```
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                         07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-628-380-8
                                                US-08-628-380-8
                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
0
                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                   Gaps
                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.3%; Score 66; DB 2; Length 18; 100.0%; Pred. No. 3.3e-05; ive 0; Mismatches 0; Indels
                                                94.3%; Score 66; DB 1; Length 18; 100.0%; Pred. No. 3.3e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION 1436
PRIOR APPLICATION 1436
PRIOR APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY, AGENT INFORMATION:
NAME: JACKSON ESQ., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECHONE: 201 487-5800
TELECHONE: 201 343-1684
TELECHONE: 133521
INPORMATION FOR SEQ ID NO: 8:
SEGURNCE CHARACTERISTICS:
                                                                                                                                                                                              RESULT 2
US-08-485-948-8
'Sequence 8, Application US/08485948
'Patent No. 5855882
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 11; Conservative
                                                Query Match
Best Local Similarity 100.0
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                   1 CFQWQRNMRKV 11
                                                                                                                                               1 CFOWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                    à
```

CFOWORNMRKV 11

```
ö
Sequence 8, Application US/08628380

Patent No. 5891341

GENERAL INFORMATION:
APPLICANT: LI, YONG MING
APPLICANT: CLASSARA, HELEN
APPLICANT: CLASSARA, HELEN
APPLICANT: CRAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION ENDFRODUCTS, AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

94.3%; Score 66; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FIGHT FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin. Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     947-1-008 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1
FELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-475-055-8; Sequence 8, Application US/08475055; Patent No. 5962245; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      411 Hackenback Avenue
                                                                                                                                                                                                                                           Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: ACENIS
TITLE OF INVENTION: ENDPROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNMRKV 11
```

us-09-743-107b-79.rai

```
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                      TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
ADPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.3%; Score 66; DB 2; Le
100.0%; Pred. No. 3.3e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/475,055 FILING DATE:
                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFÓWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                     07601
                                                     CITY: Hac
STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
```

```
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "thiol group of
Cys residue at location 2 connected by disulfide bond with
thiol group of Cys residue at location 19"
                                                         .uwbER: US/07/755,161A
19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER:
FILING DATE:
PRELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. CHECK JT.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
TELECHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITS:
UNITS:
FRATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys reconstruction of the content of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
SUFTWARE: DisplayMrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
```

94.3%; Score 66; DB 1; Length 20;

```
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: Libid group of Cys residue at location 2"
PUBLICATION INFORMATION:
                                 OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.3%; Score 66; DB 1; Length 20; 100.0%; Pred. No. 3.7e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: CHIDA, TOSHIAKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT IRPORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
RECLOMMONICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08204487
Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAMAMOTO, NAOKI
NAKASHIMA, HIDEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: THIBEAULT: 53 STATE STREET BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 11; Conservative
LOCATION: 2
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CFOWORNMRKV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BOST
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                      JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-204-487-1
                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                     ó
                     Indels
                                                                                                                                                                                              Sequence 3, Application US/07891174;
Patent No. 5317084;
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
  Pred. No. 3.7e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIPECATION 530
PR.OR APPLICATION 530
PR.OR APPLICATION UMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REPERENBE/DOCKET NUMBER:
TELECHONE: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
  Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
CHROMOSOME/SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                    D.C.
T. U.S.A.
                                                           1 CFQWQRNMRKV 11
                                                                                           2 CFQWQRNMRKV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY:
                                                                                                                                                                               US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
                                                               δ
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                         Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                               1 CFQWQRNMRKV 11
                                                                                                                                               2 CFQWQRNMRKV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CFOWORNMRKV 12
                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-381-984-24
   US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION
                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/08256771
Patent No. 565691
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                                                  94.3%; Score 66; DB 1; Length 20;
100.0%; Pred. No. 3.7e-05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                            /note= "ANTIBACTERIAL PEPTIDE DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARR: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Waren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Warren M. Cheek T.
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                         LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                        Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                               single
                                                                                                                                 MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                        COCATION: 1.20
CTHER INFORMATION:
CTHER INFORMATION:
US-08-204-487-1
                                                                                                                                                                         NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1RY: U.S.A.
20005
                                                                         TYPE: amino acid STRANDEDNESS: sir
                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                              1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                     2 CFQWQRNMRKV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washi
STATE: D.C.
COUNTRY: U.
                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                à
```

```
·.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                              RESULT 9
US-08-256-711-25
J Gequence 25, Application US/08256771
Fatent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
STREET: D.C.
STREET: D.C.
STREET: D.C.
STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                        í,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | IDENTIFICATION METHOD:
| OTHER INFORMATION: /note= "Cys residues are protected to
| OTHER INFORMATION: prevent disulfide bond"
| US-08-256-771-25
94.3%; Score 66; DB 1; Length 20; 100.0%; Pred. No. 3.7e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.3%; Score 66; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 3.7e-05; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: LIBM Compatible
COMPUTER: LIBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: UJY 22, 1994
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER:
PRILNG DATE:
RILING DATE:
RILING DATE:
```

φ

```
Sequence 4, Application US/09508734

Patent No. 6423509

GRNERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Waseful microcranism thereof
TITLE OF INVENTION: Waseful microcranism thereof
TITLE OF INVENTION: Useful microcranism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 12090-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR APPLICATION NUMBER: RR1998-29351
PRIOR FILING DATE: 1998-07-13
PRIOR FILING DATE: 1998-07-13
FRIOR FILING DATE: 1998-07-13
SCOTWARE: Kopatentin 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /note= "cysteine residues at positions 2 orner information: /note= "cysteine residues at positions 2 orner information: and 19 are chemically modified to prevent disulfide linkage" US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%; Score 66; DB 1; Length 20; 100.0%; Pred. No. 3.7e-05; tive 0; Mismatches 0; Indels
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
         805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Check, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CFOWORNMRKV 12
STREET: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
                                                                              U.S.A.
                                                                                                     20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "cysteine residues at positions 2 OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

94.3%; Score 66; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                               ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
PILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
            Sequence 24, Application US/08381984
Patent No. 5864555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITITLE OF INFUNITION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NUMB: WALKEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CFOWORNMRKV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                       STREET: 805 Fift
                                                                                                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                                                                                20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                      STATE:
```

```
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.3%; Score 66; DB 1; Length 25; 100.0%; Pred. No. 4.6e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                 33,367
                                                                                  REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: AMINO ACID
      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek Jr
REGISTRATION UMBER: 33,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                             TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CFOWORNMRKV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION: useful microorganism thereof

TITLE APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 1090-06-06-01

PRIOR PILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR PILING DATE: 1999-07-13

PRIOR PILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 6

LENGTH: 24
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.3%; Score 66; DB 4; Length 24; 100.0%; Pred. No. 4.4e-05;
                                                                                                   94.3%; Score 66; DB 4; Length 22;
100.0%; Pred. No. 4e-05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                        Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1991090:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
LENGTH: 22
TYPE: PRT
ORGANISM: Homo mapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                   1 CFQWQRNMRKV 11
                                                                                                                                                                                                                         2 CPOWORNMRKV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CFOWORNMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-07-755-161A-10
                                                                                                                                                                                                                                                                                      RESULT 13
US-09-508-734-6
                                                             US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-508-734-6
                                                                                                     Query Match
                                                                                                                                                                                     ð
                                                                                                                                                                                                                           සු
```

ó;

Gaps .; 0

```
US-07-891-174-10
                                                                                                                          JOURNAL:
                                                                                                                                           VOLUME:
                                                                                                                                                              ISSUE
                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent TITLE OF SEQUENCES: 10 CORRESPONDENCES: 11 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderorth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Displaykrite
SOFTWARE: Displaykrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION TA:
APPLICATION DATE: 300
PRIOR APPLICATION DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REPERNEK/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
RESULT 15
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLGY: linear MOLECULE TYPE: HYPOTHETICAL: ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified site LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified site LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                  ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY:
```

```
DENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of of other information of cornected by disulfide bond with of other information: thiol group of cys residue at location 4"

PUBLICATION INFORMATION: thiol group of cys residue at location 4"

PUBLICATION INFORMATION:

TITLE:

JOURNAL:

VOLUME:

PARE:

PARE:

PARE:

PARE:

PUBLICATION DATE:

PUBLICATION DATE:

PUBLICATION DATE:

MELEVANT RESIDUES IN SEQ ID NO:

US-07-891-174-10

Query Match

At CFOWGRNRKV 11

Db 4 CFOWGRNRKV 11

Db 4 CFOWGRNRKV 11

Db 4 CFOWGRNRKV 14

Search completed: February 21, 2003, 07:50:35

Job time: 8.7 8ecs
```

```
(without alignments)
35.508 Million cell updates/sec
                                                                                                                                                                                                              February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Grant G / ptodata / 2 / pubpaa / USOB NEW PUB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB NEW PUB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOG NEW PUB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOG NEW PUB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOG PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOG PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
/ cgn2 G / ptodata / 2 / pubpaa / USOB PUBCOMB.pep: *
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156504 segs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications_AA:*
                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                          US-09-743-107B-79
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Appli Sequence 58, App] 47985, Sequence 2, Appl Sequence 30, Sequence 23, Sequence 20, Sequence 58, Sequence 58, Sequence 8, Sequence 58, Sequence 6, Sequence 2, Description Sequence 2 Sequence 3 Sequence 2 Sequence 8 Sequence 2 Sequence Sequence Sequence US-09-798-869-20 US-10-023-096-2 US-09-798-869-6 US-09-798-869-5 US-09-798-869-23 US-09-798-869-4 US-09-798-869-4 US-09-798-869-22 US-09-798-869-22 US-09-798-869-29 US-09-798-869-20 US-09-798-869-30 US-09-798-869-30 US-09-888-320-2 US-10-066-273-58 US-10-066-494-58 US-09-904-536-8 SUMMARIES Query Match Length DB Result

Appl

Sequence 9, Appli Sequence 11, Appl Sequence 13, Appl Sequence 14, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appli Sequence 11, Appli Sequence 119, Appl Sequence 24, Appli Sequence 24, Appli Sequence 30, Appli	32 28 10,
10 US-09-904-536-9 10 US-09-904-536-11 10 US-09-904-536-12 10 US-09-904-536-14 10 US-09-904-536-15 10 US-09-904-536-15 10 US-09-904-536-16 10 US-09-904-536-10 10 US-09-904-536-10 10 US-09-904-536-10 10 US-09-904-536-11 10 US-09-904-649A-6	10 US-09-981-649A-32 10 US-09-981-649A-28 9 US-09-881-579-10
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	554 559 607
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	51.4 51.4 51.4
๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗	36 36
0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.3%; Score 66; DB 9; Length 15; 100.0%; Pred. No. 3.3e-05; rive 0; Mismatches 0; Indels
                                    Sequence 2, Application US/09798869
Fublication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A44049-PCT-USA-A
FULRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
SOFTWARE: FRAESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: RALDUR SVEINBJ (RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFOWORNMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-20
RESULT 1
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

ő

0;

Gaps

0;

Length 694;

94.3%; Score 66; DB 9; Length 694 100.0%; Pred. No. 0.0012; trive 0; Mismatches 0; Indels

```
11; Conservative
                                                                            1 CFOWORNMRKV 11
                                                                                                             22 CFÓWORNMRKV 32
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-798-869-3
                                                                                                                                                                                                9-698-861-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                   Matches
                                                                                                               OP
                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
ATITLE OF INVENTION: Cloning, Expression, and Uses of Human IIILE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                                      DB 9; her.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Jacobson, Price, Holman & Stern
400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                    Query Match 94.3%; Score 66; DB Best Local Similarity 100.0%; Pred. No. 5.3 Matches 11; Conservative 0; Mismatches
            FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT TILING DATE: US/01-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR RILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSSESEE FOR WINDOWS VERSION 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE, DOCKET NUMBER: 10505/P58185C
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 400 Seventh S. CIIY: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSE: Jacobson,
    APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                          ; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CFOWORNMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-023-096-2
                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens; OTHER INFORMATION: sequence)
US-09-798-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.9%; Score 58; DB 9; Length 15; illarity 90.9%; Pred. No. 0.00072; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.1%; Score 54; DB 9; Length 15; 72.7%; Pred. No. 0.0034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-38
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                           APPLICANT: JORGALION SIGGRA SPENDSEN
APPLICANT: GYSTEIN REKDAL
APPLICANT: GYSTEIN REKDAL
APPLICANT: ABALDUK SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A3449-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 201-02-27
PRIOR PLING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GE9818938.4
PRIOR FILING DATE: 1998-08-21
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
Sequence 6, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: APLIDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CFOWOWNINKY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: CAPRINE
```

```
Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGHTD SVENDEN
APPLICANT: AYTEIN REKUAL
APPLICANT: BALDUR SVEINDS (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
                                                                                                                                           Sequence 4, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 65...
For 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQRNMRKV 11
1 CFOWORNMRKV 11
                                     3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CLRWONEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: MURINE
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-798-869-22
                                                                                                                         US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEC ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
ପୁପ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
  à
                                   음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·,
ó
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: synthetic peptide (modified form of homo sapiens ; OTHER INFORMATION: sequence) US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 9; Length 25;
Pred. No. 0.0054;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.7%; Score 46; DB 9; Length 15; Best Local Similarity 63.6%; Pred. No. 0.073; Matches 7; Conservative 2; Mismatches 2; Indels
  Indels
  1,
                                                                                                                                                                                                                                          APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEIRBJ (RNSSON
APPLICANT: LARS VORLAND
ITTLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREESEQ for Windows Version 4.0
SSOFTWARE: 255
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/0979869
Fublication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: GYSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVENDEN
APPLICANT: BALDUR SVENDRINGNENSON
APPLICANTON NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
FRIOR FILING DATE: 1999-08-31
FRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FARLSEQ for Windows Version 4.0
SEQ ID NO 7
LENGRIH: 15
2; Mismatches
                                                                                                                                                                                     Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
8; Conservative
                                          1 CFQWQRNMRKV 11
                                                                                 3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYÓWORRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: CAPRINE
                                                                                                                                           RESULT 6
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
  Matches
                                          à
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.3%; Score 45; DB 9; Length 15; 63.6%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.3%; Score 45; DB 9; Length 25; 63.6%; Pred. No. 0.17; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
GENERAL INFORMATION:
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUNG SVEINBJ(RNSSON)
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CTJ/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PELICATION NUMBER: PCT/GB99/02851
PRIOR PELING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
```

```
APPLICANT: Beary III, Clifton E. APPLICANT: Debarber, Andrea E. APPLICANT: Debarber, Andrea E. APPLICANT: Debarber, Andrea E. APPLICANT: Mobili, Khishmuzi APPLICANT: The Government of the United States of America APPLICANT: as represented by The Secretary of the APPLICANT: as represented by The Secretary of the APPLICANT: as represented by The Secretary of the APPLICANT: Bepartment of Health and Human Services TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis CURRENT APPLICATION NUMBER: US/09/888,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type BtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.3%; Score 38; DB 9; Length 489; 54.5%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.34; 2; Indels cive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                           JEAUKALL INFOGRATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVELNBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CDT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FABELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 2
LENGTH: 489
TWDE: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
Sequence 30, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09888320
; Publication No. US20030013090A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 COKWPRRMRKM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine ; OTHER INFORMATION: sequence)
US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.34; 2; Indels live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 9; Length 15; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                            APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-21
PRIOR FILING DATE: 1999-08-21
PRIOR FILING DATE: 1999-08-21
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 8
LENDER DATE: 1999-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
RIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
RIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
RIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
SOFTWARE: FRSENCE FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/09798869; Publication No. US20030022821A1
                                              Sequence 8, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5%,
-%a 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CLRWOWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-798-869-29
       RESULT 10
US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 29
```

RESULT 11

ð

TYPE: PRT

; 0

ô

RESULT 12 US-09-798-869-30

ð

```
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENERMENE: P3130R107
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT FILING DATE: 2002-02-01
PRIOR PAPLICATION NUMBER: 10/002,796
PRIOR PLICATION DATE: 2001-11-15
PRIOR PAPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R FILING DATE: 1997-12-16
R APPLICATION NUMBER: 60/074086
R FILING DATE: 1998-02-09
R APPLICATION NUMBER: 60/074092
R FILING DATE: 1998-02-09
R APPLICATION NUMBER: 60/079294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059588
FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/066840
FILING DATE: 1997-11-25
APPLICATION NUMBER: 60/069694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/062285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/062816
FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/063082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/063329
FILING DATE: 1997-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/097000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/063733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/066364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/081049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/095998
                                                                                                                                                                                                                                                                                                                                                                                                          Nicholas F. Paoni
Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
Avi J. Ashkenazi
Kevin P. Baker
David A. Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colin K. Watanabe
P.Mickey Williams
William I. Wood
                                                                                            Dan L. Eaton
Napoleone Ferrara
                                                                                                                                                                                                                 Mary E. Gerritsen
Audrey Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-10-17
                                                                                                                                                                                                                                                              Paul J. Godowski
Austin L. Gurney
                                                                                                                                                                                                                                                                                                             Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
                                                                                                                                                                       Wei-Qiang Gao
Hanspeter Gerber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997-10-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-11-2
                                                                          Luc Desnoyers
                                                                                                                                           Sherman Fong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zemin Zang
                                                                                                                                                                                                                                                                                                                                                                                      James Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
                                                           APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
OTHER INFORMATION: MAP TO AL086701.14
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EST_HUMAN HIT: AM294800.1, EVALUE 1.00e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.9%; Score 37; DB 10; Length 21; 83.3%; Pred. No. 3.2; 1: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49117
SOFTHARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47985
LENGTH: 21
                                                                                                                          THILE DEPERBREE A BOOMIGA -X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR PEDLICATION NUMBER: US 60/180,312

PRIOR PELLING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-05

PRIOR PLING DATE: 2000-06-03

PRIOR PLING DATE: 2000-06-07

PRIOR PLING DATE: 2000-06-07

PRIOR PLING DATE: 2000-06-07

PRIOR PLING DATE: 2000-09-07

PRIOR PLING DATE: 2000-09-07

PRIOR PLING DATE: 2000-09-07

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PRIOR PLING DATE: 2000-09-21

PRIOR PRIOR PLING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR FILING DATE: 2001—01-30

DR APPLICATION NUMBER: PCT/US01/00661

DR FILING DATE: 2001—01-30

DR APPLICATION NUMBER: PCT/US01/00670

DR PILING DATE: 2001—01-30

OR APPLICATION NUMBER: US 60/234,687

OR PILING DATE: 2000—09-21

OR APPLICATION NUMBER: US 99/608,408

OR PILING DATE: 2000—06-30

OR APPLICATION NUMBER: US 99/608,408

OR APPLICATION NUMBER: US 99/608,408

OR APPLICATION NUMBER: US 99/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-01-29
                   Rank, David R.
Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION N
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CFOWRR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-47985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWOR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/099811

Sequence 58, Application US/10066500 Patent No. US20020177165A1 GENERAL INFORMATION:

RESULT 15 US-10-066-500-58

PLICATION NUMBER: 60/099803

FILING DATE: 1998-09-09

1998-08-18

LING DATE:

us-09-743-107b-79.rapb

```
PRIOR APPLICATION NUMBER: 60/099812

PRIOR FILING DATE: 1998-09-10

PRIOR PELING DATE: 1998-09-17

PRIOR PELING DATE: 1998-09-17

PRIOR PELING DATE: 1998-09-17

PRIOR PELING DATE: 1998-10-28

PRIOR PELING DATE: 1998-10-20

PRIOR PELING DATE: 1998-10-20

PRIOR PELING DATE: 1999-00-10

PRIOR PELING DATE: 1999-00-10

PRIOR PELING DATE: 1999-10-20

PRIOR PELING DATE: 1999-10-20

PRIOR PELING DATE: 1999-10-10-29

PRIOR PELING DATE: 1999-10-20

PRIOR PELING DATE: 1999-0-11-404

PRIOR PELING DATE: 1999-0-10-20

PRIOR PELING DATE: 1999-0-10-30

PRIOR
```

Search completed: February 21, 2003, 08:08:07 Job time : 11.55 secs

ö

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.169 Million cell updates/sec

US-09-743-107B-79 70 1 CFQWQRNMRKVA 12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri:* 73:* PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	rent la company de la contra del contra de la contra del contra de la contra del la con	JC2323	1	lactoferrin pr	T08030 dynein beta heavy	AD2346 hypothetical prot	protein kinas		ornithine de	T28820 hypothetical prote	265 proteason	hypo	hypothetical	AI2343 hypothetical prote					E70848 probable oxidore			₽	S75233 ABC transporter sl			T48933 WD repeat domain	conserved	
OI EO	١.		2					·														•		2 T			ď	`
Length D	711	708	33	707	4568	298	200	121	435	932	205	282	397	464	489	515	543	996	303	361	511	531	266	570	829	1051	119	70.
% Query Match	94.3		72.9		H.	0.09	æ	55.7	'n.	55.7	54.3	54.3		54.3		54.3	4.	54.3	ά.	52.9	ď	52.9	Ċ,	52.9	52.9	52.9	51.4	, Lu
Score	99	54	51	45	43	42	41	39	39	39	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	36	40
Result No.	τ	73	m	4	Ŋ	9	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	ac

vif protein - simi flt3 ligand - huma	hypothetical prote cell cycle arrest	hypothetical sh3-c probable cytochrom	hypothetical prote	nypotnetical prote trimethylamine-N-o	GTP-binding regula	phytochrome C - so hymothetical prote	inositol 1,4,5-tri	polymyxin B resist	carcinoembryonic a	hypothetical prote
S07989 I38440	T22597 A39654	T39801 B84514	T17324	C84325 G82168	S52418	T14803	A49873	AG0794	D33876	H70.978
0.0	77	01 01	01 0	N 17	0	7 0	1 (1	7	0	73
214 235	306	501 518	558	584 820	846	1135	2671	85	114	222
51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	50.0	50.0	50.0
36	36 36	36 36	36	36 36	36	9 4	36	35	32	32
30 31	3.2 3.3	3.4 3.5	36	38	6 E	4, 4 0 L	4.2	43	44	45

н	
H	
5	E
ES	Z

lactotransferrin precursor [validated] - human

C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000 C;Accession: G01394; S11228; Ā45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R;Cho, Y. submitted to the EMBL Data Library, March 1994

A;Reference number: G06820 A;Accession: G01394

A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA

A; Residues: 1-711 <CHO>

A,Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237 R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucled: Acids Res. 18, 5288, 1990
A,Title: Complete nucleotide sequence of human mammary gland lactoferrin. A;Reference number: S11228; MUID:90384839; PMID:2402455

A; Accession: S11228

A; Molecule type: mRNA

A;Residues: 1-148, T',150-422, C',424-711 <REY>
A;Cross-references: EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416
R;Terg, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
MAD: Endocrinol. 6, 1969-1981, 1992
A;Title: Differential molecular mechanism of the estrogen action that regulates lactofer:
A;Reference number: A45401; MUID:93125571; PMID:1480183

A; Accession: A45401

A; Molecule type: DNA A; Residues: 1-15 <TEN>

A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A;Experimental source: placenta A;Experimental source: placenta A;Note: sequence extracted from NCBI backbone (NCBIP:122202) R;Powell, M.J.; Ogden, J.E. Nucleic Acids Res. 18, 4013, 1990 A;Title: Nucleotide sequence of human lactoferrin cDNA. A;Reference number: S10324; MUID:90326549; PMID:2374734

A; Accession: S10324

A; Molecule type: mRNA

A;Residues: 3-711 <PON>
A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Bjochem. J. 276; 349-355, 1991
A;Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066

 λ_i Status: nucleic acid sequence not shown; not compared with conceptual translation λ_i Molecule type: mRNA λ_i Residues: 20-31 <ST1> A; Accession: S15853

A;Accession: S20841 A;Molecule type: protein A;Residues: 20-28,'X',30-31 <ST2>

```
Score 54; DB 2,
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: lactotransferrin
                                      77.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:J03298
R;Liu, Y.; Teng, C.T.
                                                                                                                                                                                                                                                                                                                                                                                                           lactoferrin - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.9
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lactoferrin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 CLRWONEMRKV 47
                                                                                                                                                                                                                                    38 CYOWORRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 CYÓWOKKWIRKI 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFQWQRNMRKV 11
                                                                                                                                                                      1 CFQWQRNMRKV 11
                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 3-707 < PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA A; Residues: 1-15 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A28438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A41205
                                                                                                                                                                                                                                                                                                                                                                        S52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                             ò
                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: UC2323
B;C;Peb-1995 #sequence_revision 203, 1324-1332, 1994
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A;Accession: UC2323; MUID:94380047; PMID:8093048
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: mRNA

A, Residues: 3-701, SWKPVN/ <PAN>

A, Experimental source: normal breast tissue

R, Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;

Bur. J. Blochem. 145, 659-666, 1984

A, Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth

A, Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A,Note: this is the final paper in a series
R,Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Blochem. 241, 303-308, 1996
A,Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                        F.
                                                                                                                                                                                                                                                                                                                                     A, Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of 1
A;Eference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Residues: 1-708 <LEP>
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; dycoprotein
C;Keywords: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 436-487,'A', 489-711 cRAD>
A;Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Keywords: duplication; glycoprotein; iron binding; milk F;1-19/Domain: signal sequence #stautus predicted <85G> F;20-711/Product: lactotransferrin #status experimental <MAT> F;21-356/pomain: transferrin repeat homology <TRH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A61169; MUID:91235214; PMID:1674448
A;Accession: A61169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 3q21-3q23
C;Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S74119; MUID: 97054624; PMID: 8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.3%; Score 66; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:119368; OMIM:150210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 CFOWORNMRKV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S74119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactoferrin - qoat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: LTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Unl-1955 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Oian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Bicchim. alophys. Acta 1434, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a A;Reference number: S52107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41205
C;Accession: A28438; A41205
K;Pentecoet, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactorransferrin is the major estrogen inducible protein of mouse uterine secre
A;Reference number: A92596; WUID:87280033; PMID:3611056
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A.Hitle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A.Reference number: A41205, MUID:92042099; PMID:1939212
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fil-19/Domain: signal sequence #status predicted <SIG>
F;20-707/Perduct: lactotransferrin #status predicted <MAT>
F;5188-699/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 1; Length 707; Pred. No. 4.6; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.9%; Score 51; DB 2; Length 33; 63.6%; Pred. No. 0.019; ive 3; Mismatches 1; Indels
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-33 <QIA>
C;Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M74778
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
2; Mismatches
```

C; Accession: S42867

```
C; Superfamily: ornithine decarboxylase
C; Keywords: carbon-carbon lyase; carboxy-lyase; phosphoprotein; polyamine biosynthesis; ]
R;Baur, B.; Winter, K.; Fischer, K.; Dietz, K. submitted to the EMBL Data Library, March 1994
A;Description: Molecular cloning and characterization of several protein kinases from pl
A;Reference number: $42864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Panagrellus redivivus
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Accession: S5547; S52784
R;von Besser, H.; Niemann, G.; Domdey, B.; Walter, R.D.
Biochem. J. 308, 635-640, 1995
A;Title: Molecular cloning and characterization of ornithine decarboxylase cDNA of the A;Reference number: S55347; MUID:95290001; PMID:7772052
                                                                                                                                                                                                             A; Cross-references: EMBL:230330; NID:9457708; PIDN:CAA82991.1; PID:9457709
C; Superfamily: Arabidopsis thaliana protein kinase T518.9; protein kinase homology C; Kaywords: ATP; phosphotransferase; protein kinase F; 71-379/Domain: protein kinase homology < KIN>
F; 71-379/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C5B.
A,Reference number: AB2577; PMID:11743193
A,Accession: AH3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:AE008689; PIDN:AAL45598.1; PID:g17743317; GSPDB:GN00187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: X82199; NID: 9758641; PIDN: CAA57683.1; PID: 9758642
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó.
                                                                                                                                                                                                                                                                                                                                                                                                  Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ornithine decarboxylase (EC 4.1.1.17) - Panagrellus redivivus
                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 2
Pred. No. 9.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB Pred. No. 17; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.7%;
                                                                                                                                                                                                                                                                                                                                                                                               58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.55
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWORNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 CLAWORRNRVS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-500 <BAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-435 < VON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 WORNERKLA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-121 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 WORNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: AH3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S55347
                                                                                                                                A; Accession: S42867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: Atu4804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetica:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CiSpecies: Nostoc sp.
Anote: Nostoc sp.
Anote: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
CiDate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
CiAccession: AD2346
KiRaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
                                                                                                                                                                              C,Accession: T08030
R,Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes. A;Reference number: Z16302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: IX
A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3882/3; 4240/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-298 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         profein kinase (EC 2.7.1.-) - spinach
C;Species: Spinacia oleracea (spinach)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 19-Jul-2002
                                                                                                                                                      C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: T08030
                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4568 «MIL»
A;Cross-treferences: EMIL;U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
A;Experimental source: strain 21gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 4568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.0%; Score 42; DB 2; Length 298; 77.8%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Superfamily: dynein heavy chain, ciliary
C;Keywords: nuclectide binding, P-loop
F;1919-1926/Region: nuclectide-binding motif A (P-loop)
F;2202-2209/Region: nuclectide-binding motif A (P-loop)
F;2530-2537/Region: nuclectide-binding motif A (P-loop)
                                                                                               dynein beta heavy chain - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.4%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1852 CFÓWÓSQLRYI 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 FHWORNYRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FOWORNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: alr4323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: ODA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S42867
```

ă

Matches

dd

à

```
A;Note: Nostocs Sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Date: 14-Dec-2001
R;Xaneko, T: Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, É
N, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans
A;Reference number: AB1807; WUID:21595285; PMID:11759840
                hypothetical protein MYPU_5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession. F90580
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pull
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SC66T3.04 - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Accession: T3554

R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Bubmitted to the EMBL Data Library, June 1999

A;Reference number: Z21576

A;Reference number: Z21576

A;Status: Preliminary; translated from GB/EMBL/DDBJ

A;Mocession: T35361

A;Mocession: Data Library translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Residues: 1-397 <MUR>
A, Cross-references: EMBL:AL079348; PIDN:CAB45460.1; GSPDB:GN00070; SCOEDB:SC66T3.04
                                                                                                                                                                                                                                                                                                        A;Residues: 1-282 <KUR>
A;Cross-references: GB:AL445566; PID:g14089965; PIDN:CAC13723.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule_type: DNA
A;Residudes: 1-464 <KUR)
A;Crost-references: GB:BA000019; PIDN:BAB76003.1; PID:g17133440; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein all4304 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2; Pred. No. 45; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 2
Pred. No. 32;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental gource: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC66T3.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 FAWONNIKKI 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 WRRNIRKAA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WORNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: MYPU 5500
A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: AI2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26S proteasome SU BS [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
C;Species: nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: B90094
C;Accession: S: Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: CESP:F07C3.1
A;Map position: 5
A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o;
                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-205 <DOU>
A,Cross-references: GB:AF165818; NID:g13794510; PIDN:AAK39885.1; GSPDB:GN00150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T28820
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-932 <FAV>
A;Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A;Experimental source: strain Bristol N2; clone F07C3
                                                                                                                                                                                                                                                                                                                                                                      Cispecies: Caenorhabditis elegans
Cipate: 29-0ct-1999 #text_change 29-0ct-1999
Cipacession: T28820
R;Favello, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F07C3.
A;Reference number: Z20528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
F;76/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 2; Length 932;
Pred. No. 70;
                                                  DB 2; Length 435; 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                               hypothetical protein F07C3.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.7%; Scor.
70.0%; Pred. No. ..,
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB Pred. No. 23; 2; Mismatches
                                                                                                       1; Mismatches
                                                  Score 39;
Pred. No.
                                               55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           579 FOWORSARLV 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Genome: nucleomorpu
C; Keywords: nucleomorph
                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FOWORNMRKV 11
                                                                                                                                                            3 OWORNMRKVA 12
                                                                                                                                                                                                               61 OWORTMPRVA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 CPFWERNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWORNM 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: E90094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: prsB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

Matches

δ g RESULT 11

RESULT 12

g à

ö

0;

```
0
                                                                                                    Gaps
                                                                                                       0;
                                                         Query Match 54.3%; Score 38; DB 2; Length 464; Best Local Similarity 54.5%; Pred. No. 53; Matches 6; Conservative 2; Mismatches 3; Indels
C,Genetics:
A,Gene: all4304
```

2 FOWORNMRKVA 12

|||| :: | 378 FQWQVNQKRAA 388

셤

probable monooxygenage - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Uul-1998 #sequence_revision 17-Uul-1998 #text_change 22-Oct-1999
C;Accession: C70655
R;Collo. S.T.; Brosch, R.; Parkhill, J.; Gantles, C.; Harris, D.; Gordon, S.
C;Accession: C70655
R;Collo. S.T.; Brosch, R.; Parkhill, J.; Gantles, S.; Hamiln, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Natures 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-489 <COL>
A;Cors-references: GB:Z83664; GB:AL123456; NID:93261687; PIDN:CAB06212.1; PID:e301250; A;Experimental source: strain H37RV
C;Genetics:
A;Genetics:
A;Genetics: Query Match 54.3%; Score 38; DB 2; Length 489; Best Local Similarity 54.5%; Pred. No. 56; Matches 6; Conservative 2; Mismatches 3; Indels

1 CFQWQRNMRKV 11 Š

°

0; Gaps

253 COKWPRRMRKM 263

임

Search completed: February 21, 2003, 07:47:51 Job time : 10.65 secs

Run on:

```
OgtumO camelus dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             saccharomyc
bacillus st
sorghum bic
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arabidopsis
homo sapien
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  broad bean
methylobaci
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synechocyst
vibrio chol
simian immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             mus musculu
chlamydomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chlamydia m
arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homo sapien
bubalus bub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              panagrellus
liberibacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          пошо варіеп
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brome mosai
schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equus cabal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        salmonella
bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ovis aries
                                                             February 21, 2003, 07:25:55; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q39565
Q77811
P49725
P41187
P37143
Q19910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q15398
Q21988
P03588
Q10201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P93528
Q14573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P12505
P49771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P37589
P12342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P26898
P30453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09pjj9
Q9fg65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09ulc6
077698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P26448
008328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P57070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               039017
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                  112892 segs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BUB2_YEAST
GIGGA_BACST
PHYCS CORBI
IP3T HUWAN
PMRD_SALTY
IL12A_BOVIN
IL12A_BOVIN
IL12A_BOVIN
IN34 HUWAN
SYH_CHLWU
SYH_CHLWU
SYH_CHLWU
SYH_CHLWU
YOO! ARATH
YOOS HUWAN
YOOS CABEL
                                                                                                                                                                                                                                                                                                                                                                                                                             TRFL HUMAN
TRFL CABHI
TRFL CAMDR
TRFL MOUSE
DYHB CHLRE
TRFL HORSE
DCOR PANRE
RPOB LIBAF
VIA BBMV
UIA BBMV
DHOM METGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKYL_CABEL
YJ19_SYNY3
LOLB_VIBCH
VIF_SIVS4
FL3L_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YBX7 SCHPO
NPHN HUMAN
                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                              Minimum DB seg length: 0
Maximum DB seg length: 200000000
                                                                                                          US-09-743-107B-79
                                                                                                                             1 CFQWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                         SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485
1135
2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                 Sequence:
                                                                                                                                                                                     Searched:
```

Result

No.

Q58878 methanococc	Q10353 SChizosacch p12452 himan immin	P20878 human immun	Q55185 synechocyst	P16710 vaccinia vi	071154 diatraea sa	Q9xzl8 drosophila	084281 chlamydia t	035186 rattus norv	Q9jsz7 neisseria m	Q9k0y2 neisseria m
YE83 METJA	KL24 SCHPO	VIF HV2ST	Y495 SYNY3	VA16 VACCV	VNS2_DSDNV	NLA DROME	NORC CHLTR	CATK_RAT	MURG NEIMA	MURG_NEIMB
₩.	-		H	Н	н	Н	Н	Н	н	н
152	192	215	246	275	275	292	316	329	355	355
48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6
34	4. c	34	34	34	34	34	34	34	34	34
34	9 2	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

ALIGNMENTS	FL	21-UUL-1986 (Rel. 01, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)	Lactotransferrin precursor Lactoferroxin B; Lactoferro	Homo sapiens (Human). Eukaryota; Metazoa; Chordata;	Mammalia; Eutheria; Primates; Catarrhini NCBI_TaxID=9606;			Rey M.W., Woloshuk S.L., de Boer H.A.,	Complete incleding Bequence of indical manimary Nucleic Acids Res. 18:5288-5288(1990).	2 SECTENCE FROM N 2		4 Cho Y.Y.; Thesis (1994). Genetic Engineering Research Institute / Taeion, Korea.	[3]	SEQUENCE		[4]	TISSUE=Mar	Liang Q., Jimenez-Flore	Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A.		א אפו א., אמט ס., גמסס ז.א.; ["Human neutrophil lactoferrin coding and 5' flanking region DNA	sequences."; chmittod /ppp_1000) to the pwp1/Company/Indiatabase			Cheng H., Chen X., Huan L.; "cDNA cloning and sequence analysis of human	Submitted (DEC-2000) to the	SEQUENCE FR TISSUE=Proc	Straubberg K.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. VM [8]	_
	A LIKE	1111	BER	888	888	Z Z	2 X	25	4 점	Z 0	I KG	X Z	2	2 2	掘	EN C	7 2	RA E	Z ZZ	2 th	22	Z Z	RT	3 2	RP RC	R R	E.	A B B B	Z Z Z	į

homo варіеп

us-09-743-107b-79.rsp

```
MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker B.N.;
"Structure of human lactoferrin: crystallographic structure analysis
                                                                                                                                                                                                                                                                                                                                                                 "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis B., Schutz K., Gnol L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Dragan X., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan X., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U Biaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,
                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and
expression of mRNA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mutagenesis of the histidine ligand in human lactoferrin: iron
                                                                                                                                                                      Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F., Legrand D., Spik G., Montreuil J., Jolles P.; "Human lactotransferrin: amino acid sequence and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haridas M., Anderson B.F., Baker E.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding properties and crystal structure of the histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'An 88 amino acid long C-terminal sequence of human
                                                        Powell M.J., Ogden J.E.; "Nucleotide gequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 670:243-254 (1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                             comparisons with other transferrins.";
Eur. J. Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and refinement at 2.8-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                              Nucleic Acids Res. 18:4013-4013(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97156796; PubMed=9003186;
                                                                                                                                                      MEDLINE=85076667; PubMed=6510420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 609-711.
MEDLINE=82262043; PubMed=7049727;
                    TISSUE-Mammary gland;
MEDLINE-90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lactotransferrin.";
FEBS Lett. 142:107-110(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 436-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 237-711 FROM N.A.
SEQUENCE OF 3-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253-->methionine mutant
                                                                                                                                SEQUENCE OF 20-711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resolution
                                                                                                                                                                                                                                                                                                                                                   Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jolles
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is no no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOFERROXIN A SHOWS PREPERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
                                                                                                                                                                                                                                                                                                                                             Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
El Matri L., Lwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.; Fiser-Kupfer M., Nagata M., Nakayasu K.,
"Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy: exclusion of linkage to lactoferrin gene.";
Mol. Vision 4:31-32(1998)
-!-FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                             MEDILINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
              Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
"Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change.";
Acta Crystallogr. D 54:1319-1335(1998).
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- DOMAIN: COMPOSED OF TWO HOMOLOGGUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                   Agric. Biol. Chem. 54:1803-1810(1990).
                                               Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                  CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF332168; AAG48753.1; -. BC015822; AAH15822.1; -. BC015823; AAH15823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X53961; CAA37914.1; -. EMBL; U07643; AAB60324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M83202; AAA59511.1; -.
M83205; AAA58656.1; -.
M18642; AAA86665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M73700; AAA59479.1; -. X52941; CAA37116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAA37116.1; -. AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M93150; AAA36159.1; -.
                                                                                                                                                                                                                                                                                                                     VARIANTS THR-30 AND ARG-48.
                                                                                                                                                                                                                                                                     from human lactoferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-94.
31-AUG-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1LCF; 31-AUG-94.
1LCT; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-97.
21-APR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1LFH; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1LFI; 31-OCT-93.
1LGB; 31-AUG-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1LFG; 31-JUL-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96-NON-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEHUL
                                                                                                                                                                                                                                                                                                                                    PubMed=9873069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U95626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1BKA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1DSN;
1HSE;
                                   wamori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POB;
POB;
POB;
POB;
POB;
```

m

```
RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HD DATA BEACH BEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                       dira hircus (Goat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U53857, AAA97958.1; --
EMBL, X78902, CAA5517.1; --
EMBL, X78902, CAA55517.1; --
EMBL, X7800156, Transferrin.
Pfam, PF00405, transferrin, 2.
PRINTS, PR00422, TRANSFERRIN.
SMART; SM0094, TR FER, 2.
PROSTIE; P800206; TRANSFERRIN 1; 2.
PROSTIE; P800206; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein, Metal-binding; Repeat;
                                                ·
0
          94.3%; Score 66; DB 1; Length 711; 100.0%; Pred. No. 0.00027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LACTOTRANSFERRIN
                                                                                                                                                                                                         708 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΒY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.
BY
BY
BY
                                               11; Conservative
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
708
363
708
64
55
217
                                                                                 1 CFOWORNMRKV 11
                                                                                                                39 CFOWORNMRKV 49
                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=9925;
                                                                                                                                                                                                       CAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                    RESULT 2
TRFL_CAPHI
                                               Matches
                                                                                                                                                                                                                       ò
                                                                                                                셤
```

```
TISSUE=Mammary gland;
Paramasivam M., Srintvasan A., Singh R., Sahani M.S., Singh T.P.;
Paramasivam M., Srintvasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (UN1-1999) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUBMILY BICARBONATE (BY SIMILARITY).
-!- SUBGELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 1; Length 708; Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 -> V (IN REF. 2)

L -> R (IN REF. 2)

C -> R (IN REF. 2)

F -> P (IN REF. 2)

S -> P (IN REF. 2)

D -> G (IN REF. 2)

D -> G (IN REF. 2)
                                                                                                                                                                                                                                                        BY SIMILARITY.

BY SIMILARITY.

IRON 1 (BY SIMILARITY).

IRON 1 (BY SIMILARITY).

IRON 1 (BY SIMILARITY).

IRON 2 (BY SIMILARITY).

ANION (BY SIMILARITY).

N-LINKED (GLCNAC...) (CONTROL (GLCNAC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   708 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9TUMO; Q9MZS5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                            SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                               SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                    SIMILARITY
                                                                                                                                                                                      SIMILARITY
  77358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFOWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 CYÓWORRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                         2211
2712
4714
4714
6144
6144
3300
3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495
564
56
88
124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAMDR
DISULFID
                                                 DISULFID
                                                                                                                            DISULFID
                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                        DISULFID
                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                       METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRFL_CAMDR
                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
```

0;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                             EMBL; AJ131674; CAB53387.1; -.
BNSD; AF65879; AAF82241.1; -.
HSSP; O77811; 1B1X.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR0042; TRANSFERRIN.
SMART; SM0094; TREX, 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 3; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%; Score 49; DB 1; Length 708; 72.7%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F - S (IN REF. 2).
G -> A (IN REF. 2).
LLS -> PLF (IN REF. 2).
L -> F (IN REF. 2).
A -> PLF (IN REF. 2).
A -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
ALINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
LACTOTRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.

BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
METAL
SOLUTION OF THE STATE OF THE ST
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu Y., Tenger...;
Liu Y., Tenger...;
Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880:1880:1880:1991)
-!-FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-!-FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                         MEDIJINE-87280033; PubMed-3611056;
Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBUNIT: MONOMER.
-:- SUBCELLULAR LOCATION: Secreted.
-:- DOMALIN: COMPOSED OF TWO HOMOLOGOUS DOMALINS.
-:- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
LACTOTRANSFERRIN.
1.
TREL MOUSE STANDARD; PRT; 707 AA. P08071; P70590; Q61799; Q922P2; Created) C1-3MG-1988 (Rel. 08, Created) C1-3MG-2002 (Rel. 41, Last sequence update) L5-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                   uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D88510; BAA13633.1; --
EMBL; BC06694; AAH66904.1; --
EMBL; M74778; AAA39427.1; --
PIR; A28438; A28438.
HSSP; P02788; LCE6.
MGD; MG1:66837; Ltf.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, PRO0422; TRANSFERIN.
SMART; SMO0094; TR FER; 2.
PROSITE; PS00205; TRANSFERIN_1; 1.
PROSITE; PS00206; TRANSFERIN_2; 2.
PROSITE; PS00207; TRANSFERIN_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92042099; PubMed=1939212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03298; AAA40525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF00405, transferrin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-14 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
707
357
                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 7
                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Uterus;
                                                                                                                                                                                                                              FISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
CHAIN
REPEAT
```

0;

Gaps

.,

2; Indels

1; Mismatches

8; Conservative

Matches

B 65

Ŋ

us-09-743-107b-79.rsp

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain genes.";
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILLA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=54274778; PubMed=8006077;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYNEIN HAS ATPASE ACTIVITY.
SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii.
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MR -> IQG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.3%; Score 45; DB 1; Length 707; 63.6%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F26AE0340A4C19A8 CRC64;
                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANION (POTENTIAL).
ANION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q (IN REF. 2).
T (IN REF. 2).
T (IN REF. 2).
D (IN REF. 1).
G (IN REF. 2).
V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07.007-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 4568 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                           413
544
513
613
1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ODA4 OR ODA-4 OR SUP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449
629
707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 CLRWONEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3055;
    DYHB CHLRE
Q39565;
                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                   DISULFID
    REPEAT
DISULFID
                                                          DISULFID
                                                                                                  DISULFID
                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                           DISULFID
                                                                                                                                                                DISULFID
                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                   METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYHB_CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SO A FEET TO BE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFORTINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.; "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                           COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                          EMBL; U02963; AAA19956.1; -.
InterPro, IPR004273; Dynein_heavy.
Fam, PR03028; Dynein_heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 4568;
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                              519961 MW; 9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.; "CDNA sequence of mare lactoferrin."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                   COLLED COLL (POTENTIAL)
COLLED COLL (POTENTIAL)
COLLED COLL (POTENTIAL)
                                                                                                                                                                                                                      COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCULIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99296631; PubMed=10366507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.4%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                      293
11175
11175
11650
11825
2045
2045
3162
3162
3162
2209
2209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1852 CFÓWOSOLRYI 1862
                                                                                                                                                                                                                                                                                                                                                                                                                              4568 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                               1778
                                                                                                                                                                                                                                                                                                          22831
3106
3339
3648
1919
                                                                                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissum=Milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRFL HORSE
077811;
                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP_BIND
NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRFL_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

CDNA of the nematode Panagrellus redivivus.";

Biochem. J. 308:635-640(1995).

-I. CARALYNIC ACTIVITY: L-ORITHINE = putrescine + CO(2).

-I. CORACTOR: PYRIDOXAL PHOSPHATE.

-I. PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY.

MEDINE-95290001; PubMed=7772052; von Besser H., Niemann G., Domdey B., Walter R.D.; "Molecular cloning and characterization of ornithine decarboxylase

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Panagrolaimidae; Panagrellus.

Panagrellus redivivus.

[1] SEQUENCE FROM N.A.

NCBI_TaxID=6233;

01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) Ornithine decarboxylase (EC 4.1.1.17) (ODC).

```
ö
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                          ILIC, L., L., LEED-37.

FINITERING, IPRO1156; Transferrin.

FAM., PR0405; transferrin.

PRINTS; PR04022; TRANSFERRIN.

SNART; SM00094; TR FER; 2.

PROSITE; PS00206; TRANSFERRIN_1; 2.

PROSITE; PS00206; TRANSFERRIN_2; 2.

PROSITE; PS00207; TRANSFERRIN_3; 1.

Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.

NON TER .

SIGNAL <1 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.6%; Score 41; DB 1; Length 695; 63.6%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07BB84D50E1B165D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LACTOTRANSFERRIN.
1.
2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON 1 (BY 5 IRON 1 (BY 5 IRON 1 (BY 5 IRON 2 (BY 5 IRON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANION (BY
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 N
75991 MW;
                                                                                                                                                                                           EMBL; AJ010930; CAA09407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                               PDB; 1B1X; 02-DEC-98.
PDB; 1B7U; 02-FEB-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431
463
487
497
508
579
631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
98
198
259
259
401
401
601
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         )ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -;- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE DECARBOXYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001183; Decarbxylse2.

Pfam; PF00278; Orn_DAP_Arg_deC; 1.

Pfam; PF002784; Orn_Arg_deC_N; 1.

PRINTS; PR01179; ODADCREMIASE.

PROSITE; PS00878; ODR_DC_2 1; 1.

PROSITE; PS00879; ODR_DC_2 2; 1.

PROSITE: PS00879; ODR_DC_2 2; 1.

PS00879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-NCV-1995 (Rel. 32, Last sequence update)
01-NCV-1995 (Rel. 40, Last aequence update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liberibacter africanus (Liberobacter africanum).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Rhizobiaceae, Candidatus Liberibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Nelspruit; Planet P., Jagoueix S., Bove J.M., Garnier M.; Planet P., Jagoueix S., Bove J.M., Garnier M.; "Detection and characterization of the African Citrus Greening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 1; Length 435;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BBB093C1EF7FEFA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF POLYAMINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47110 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X82199; CAA57683.1; -. EMBL; X95719; CAA65024.1; -. HSSP; P07805; 1F3T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 OWORNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QWQRTMPRVA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=34020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPOB LIBAF
P41187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPOB_LIBAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID
DT A
DD DT 
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

435 AA.

STANDARD;

PANRE

RESULT 7
DCOR PANRE
ID DCOR PANI
AC P49725;

ò 엄 01-0CT-1996 (Rel. 34, Created)

ó

```
EMBL; M65138; AAA42740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 WORNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHOM METGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHOM METGL
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       rpoBC operon.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dzianott A.M., Bujarski J.J.; "The nucleotide sequence and genome organization of the RNA-1 segment in two bromoviruses: broad bean mottle virus and compea chlorotic
Liberobacter by amplification, cloning and sequencing of the rplKAJL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                     SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                     CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VITOLOGY 185:553-562(1991).
-!- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
-CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN.
METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.3%; Score 38; DB 1; Length 146; 60.0%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001572; RNA_pol B.
Pfam; PF00562; RNA_pol B; 1.
PROSITE; PS01166; RNA_Pol BETA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
NON TER 146 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER 146 146
SEQÜENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-001-1993 (Rel. 26, Created)
01-001-1993 (Rel. 26, Last sequence update)
16-001-2001 (Rel. 40, Last annotation update)
16 protein [Includes: Helicase; Methyltransferase].
Broad bean mottle virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         966 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92074218; PubMed=1962437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U09675; AAA19557.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 CVOWSRGARK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=12301;
                                                                                                                                                                                                                                                      BETA' CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mottle virus."
                                                                                                                              SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bawden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bromovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V1A BBMV
Q00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIA_BBMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DETAIL DEPARTMENT OF THE PROPERTY OF THE PROPE
     à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                              1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00742; Homoserine_dh; 1.
Pfam; PF03447; NAD binding_3; 1.
PROSITE; PS01042; HOMOSER_DHGENASE; FALSE_NEG.
Oxidoreductase; NADP; Threonine biosynthesis; Isoleucine biosynthesis;
Methionine biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  semialdehyde + NaD(P)H.

-!- PATHWAY: THIRD STEP IN CONVERSION OF L-ASPARTATE TO HOMOSERINE.
HOMOSERINE PARTICIPATES IN THE BIOSYNTHESIS OF THREONINE AND THEN
ISOLEDCINE AND IN THE BIOSYNTHESIS OF METHIONINE.
-!- SIMILARITY: BELONGS TO THE HOMOSERINE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 21276;

MOLOYAMA H., MARI K., Anazawa H., Ishino S., Teshiba S.;

MOLOYAMA H., MAKI K., Anazawa H., Ishino S., Teshiba S.;

MOLOYAMA H., MAKI K., Anazawa H., Ishino S., Teshiba S.;

"Cloning and nucleotide sequences of the homoserine dehydrogenase genes (hom) and the threonine synthase genes (thrC) of the Grammagative obligate methylotroph Methylobacillus glycogenes.";

Appl. Environ. Microbiol. 60:111-119(1994).

-I - CATALYTIC ACTIVITY: L-homoserine + NAD(P) (+) = L-aspartate 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methylobacillus glycogenes.
Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
                                                                                                                                                                                                                                                                                                                                                                 . , 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%; Score 37; DB 1; Length 435; ilarity 66.7%; Pred. No. 25; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                             54.3%; Score 38; DB 1; Length 966; 50.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                          3; Indels
PIR; A41699; PIBVBB.
InterPro; IPR002588; Vmethyltransf.
InterPro; IPR000506; Viral_helicasel.
Ffam; PF01443; Viral_helicasel; 1.
Pfam; PF01660; Vmethyltransf; 1.
Helicase; ATP-binding; Transferase; Methyltransferase.
NP BIND
690 697
SEQUENCE 966 AA; 109621 MW; DF592681D7231C8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 AA; 48226 MW; 58468B0E7A81ACAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Homoserine dehydrogenase (EC 1.1.1.3) (HDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001342; Homoserine dh. InterPro; IPR005106; NAD binding 3.
                                                                                                                                                                                                                                                                                                                                                              ٠.
ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D14070; BAA40414.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 CFKENKDWTENMRSVA 362
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQ----WORNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methylobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=406;
```

9 06:51:38 2003

Tue Dec

a

```
Chaperone; Outer membrane; Lipoprotein; Transport; Protein transport;
-! - SIMILARITY: BELONGS TO THE ABC1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer-membrane lipoprotein lolB precursor
                                                                                                                                                                  InterPro; IPR004147; ABC1.
InterPro; IPR000719; Euk pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004289; AAF95326.1; -.
                                                                                                                                                                                                                                                                               52.9%;
61.5%;
                                                                                                                                                     EMBL; D90903; BAA17147.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004565; LolB.
Pfam; PF03550; LolB; 1.
                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          469 FOWORLENMLSIA 481
                                                                                                                                                                                                                                                                                                                                           2 FOWOR--NMRKVA 12
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR VC2181
                                                                                                                                                                                                                                                                                                                                                                                                                                 LOLB VIBCH
ID LOLB VIBCH
AC P57070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholerae
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIZIE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K.,

Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,

'Samada M., Tabada S.,

"Sequence analysis of the genome of the unicellular cyanobacterium

Synechocyptis sp. strain PCC6803. II. Sequence determination of the

entire genome and assignment of potential protein-coding regions.",

DNA Res. 3:109-136(1996).
                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%; Score 37; DB 1; Length 455; 50.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               Miller N., Bradshaw H.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormPep; F30B5.4; CE28552.
Hypothetical protein.
SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                               16-0cT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein F30B5.4 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                    Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein slr1919.
SLR1919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U42437; AAA83493.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                             STANDARD;
                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 CIQWELNRRR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQRNMRK 10
   111 WORDFRRVA 119
                                                                                                                                                                                                                                                                                STRAIN=Bristol N2;
Miller N., Bradsha
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1148;
                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                             Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNY3
                                                                             CAEEL
                                                                                                                                                                                                                                                                                                                                              REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
YJ19_SYNY3
                                               RESULT 11
YKYL CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=E1 Tor Ni6961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE LOLA PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NATURE 406:477-483 (2000).
-!- FUNCTION: PLAYS A CRITICAL ROLE IN THE INCORPORATION OF
LIPOPROTEINS IN THE OUTER MEMBRANE AFTER THEY ARE RELEASED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1; Length 566; Pred. No. 33; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF03109; ABC1; 1.
PROSTIE; PSS0011; PROTEIN KINASE DOM; UNKNOWN 1.
Hypothetical protein; Complete proteome.
SEQUENCE 566 AA: 65078 MW; 0CS0CC04509FDCB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE LOLB FAMILY.
```

```
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                            Simian immunodeficiency virus (F236/smH4 isolate) (sooty mangabey)
                                                                                                                                                                                                                                                                                                                          "An African primate lentivirus (SIVsm) closely related to HIV-2.", Nature 339:389-392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
11-0CT-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3
ligand) (Flt3L).
                OUTER MEMBRANE LIPOPROTEIN LOLB.
N-ACYL DIGLYCERIDE (BY SIMILARITY).
FIEF70858484177E CRC64;
                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.4%; Score 36; DB 1; Length 214; 75.0%; Pred. No. 18; ive 1; Mismatches 1; Indels
                                                           DB 1; Length 211;
                                                                                                                                                                                                                                                                                             MEDLINE=89262053; PubMed=2786147;
Hirsch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25140 MW; 9BCE884EC454BF3D CRC64;
                                                                                                                                                                                        01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Virion infectivity factor (SOR protein) (Q protein).
                                                                                                                                                                                                                                                      Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                        214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 235 AA.
                                                           Score 36; DB
Pred. No. 18;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR000475; Viral_infect.
Paran, PR00559; VIF; 1.
PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; Viral_infect; 1.
                             27 N
24379 MW;
                                                           51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X14307; CAA32484.1; -.
Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                              5; Conservative
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                   211
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S07989; S07989.
HIV; X14307; VIF$SMMH4.
                                       211 AA;
                                                                                                  2 FOWORNMRKVA 12
                                                                                                                     71 FÓWÓKSPOKLS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AA;
                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=11737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 OWRRINRK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 QWQRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FL3L HUMAN P49771;
                                                                                                                                                                      SIVS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                       SEQUENCE
                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLT31G.
                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FL3L_HUMAN
                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
KW
FT
FT
SO
                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted (isoform 2).
-!- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of human and murine flt3 ligand genomic loci."; Oncogene 11:1165-1172(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF02947; flt3_lig; 1. Cytokine; Alternative splicing; Signal; Cytokine; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=94235842; PubMed=8180375;
Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.;
"Cloning of the human homologue of the murine flt3 ligand: a growth
                                                                                                                                                                      MEDLINE=94195428; PubMed=8145851;
MEDLINE=94195428; PubMed=8145851;
MEDLINE=94195428; PubMed=8145851;
Marbinum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Lub J., Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
"Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by variant RNAS.";
Nature 368:643-648(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

MEDLINE-20343011, PubMed=10081197,
Savvides S.N., Boone T., Karplus P.A.;
"Flt3 ligand structure and unexpected commonalities of helical
"Flt3 ligand structure and unexpected commonalities of helical
buddles and cystine knots.";
Nat. Struct. Biol. 7:486-491(2000).
-!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=96032581; PubMed=7566977;
Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and 2/soluble; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SL CYTOKINE. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor for early hematopoietic progenitor cells.";
Blood 83:2795-2801(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR004213, Flt3_lig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U03858; AAA19825.1; -. ERNEL; U29874; AAA90949.1; -. EMBL; U29874; AAA90950.1; -. PDB; 1ETE; 09-JUN-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U04806; AAA17999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:3766; FLT3LG.
MIM; 600007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2535
2335
2035
2035
1111
153
(Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escobar S.;
```

```
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 161 178 DSSTIPPPMERREATA -> VETVFHRVSQDGLDLITS
FT VARSPLIC 179 235 MISSING (IN ISOFORM 2).
FT CONFLICT 72 G -> A (IN REF. 1).
SQ SEQUENCE 235 AA, 26416 MM, 718958BF693B4CECF CRC64;

Query Match 51.4%; Score 36, DB 1; Length 235;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

Search completed: February 21, 2003, 07:27:54 Job time : 5.6 secs

1 CFQWQRNMRK 10 | | | | | | 204 CLHWQRTRRR 213

장 원

```
Q9ucy5 homo sapien
Q9tr80 ovis aries
Q8yp77 anabaena sp
Q9yqc1 human immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09yqco human immun
09yqbb human immun
09yqbB human immun
09yji7 human immun
09yij2 human immun
09xi12 human immun
09xi12 human immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9qb73 yaba monkey
Q91mq5 lumpy skin
Q9dhk5 yaba-like d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sesamum ind
spinacia ol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O8tcd2 homo sapien
                                                            February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
(without alignments)
118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q41383
O90863
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries
                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9YQB9
Q9YQB8
Q9YJI7
Q9YJJ2
Q9XIJ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q41383
O90863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       091MQ5
09DHK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8YP77
                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29QB73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UCY5
Q9TR80
                                                                                                                                                                                                                                                                                                             sp arches:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_unclassified: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_bacteriap:*
                                                                                                        US-09-743-107B-79
                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
                                                                                                                              1 CFQWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                           sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp plant: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length DB
         Copyright
                                                                                                                                                                                                                                                                                                       SPTREMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                           Minimum DB B
                                                                                                                               Sequence:
                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                       Database
                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
```

0;

Gaps

. 0

Length 711;

ch 94.3%; Score 66; DB 4; Length 711 1. Similarity 100.0%; Pred. No. 0.0006; 11; Conservative 0; Mismatches 0; Indels

Best Local Similarity

Matches

Query Match

ò g

Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

SEQUENCE FROM N.A. LISSUE=PROSTATE;

SOR REPRESENTED BY SOR

O.J.M.Y.2000 (TrEMBLrel. 13, Created)
O.J.M.Y.2000 (TrEMBLrel. 13, Last sequence update)
O.J.M.Y.2000 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;

PRELIMINARY;

Q9UCY5

OS DE DE CO

RESULT 2

	‡ 0	57.1	469	6	Q38115	Q38115 bacteriopha
	39	ď.	105	10	Q9XFD5	O9xfd5 oryza sativ
σı	99	55.7	121	16	Q8U6K3	
0	6	'n.	279	16	O8XSE2	O8xse2 ralstonia s
Н	39	'n.	306	4	Q8TAX2	homo sanien
7	39	55.7	372	10	081653	
8	9.0	55.7	459	4	ONZN60	Ognzwo homo sapien
4	68	55.7	460	4	O9NZW3	рошо
2	9	55.7	466	4	O9NUS2	D TOU
Q	39	'n	488	10	088934	4 dins
7	9.0	55.7	632	4	094937	
28	39	55.7	932	ស	019153	019153 caenorhabdi
6	38		81	72	090884	4
0	38		205	ω	Q98RR2	O98rr2 quillardia
_	38	54.3	208	72	Q8US46	9
2	38		282	16	Q98Q19	
m	88	54.3	294	11	Ø3DCM6	
₹#	88	4	341	Ħ	Q8R2A4	O8r2a4 mus musculu
'n	88	54.3	376	12	Q9Q8X2	
9	88	54.3	376	12	090834	emoxym
7	88	54.3	397	16	Q9XAX9	
. 60	88	54.3	464	16	O8YP95	
	8	54.3	489	16	P96223	mycobacte
	8	54.3	515	10	022185	
41 3	80	54.3	543	10	022188	
	80	54.3	570	10	085487	
	80	4	2186	ហ	906N6O	+
	7	N	æ		090489	σ
45	2	C	109	7	741,740	himman
))		1 1 1	וותווומוו
					ALIGNMENTS	•
RESULT 1						
Q8TCD2						
ID Q8TCD2		PRELIMINARY	NARY;		PRT: 711 AA.	
AC OSTCD2;						
	002	(TrEMBLrel			Created)	
	005	(TrEMBLrel			n ecuence ni	
	005	(TrEMBLrel		21,	Last annotation update)	
DE Lactotransferrin.	nste	rrin.				
OS Homo Bablens (Human)	iens a·	(Human	/ . Chordata.	1		
	9	Firthoria		ממרמ המנים	; crannata; vertebrata; buteleostomi;	ureleostom1;
NCBI	TaxID=9606:	606:	1117.7.2	ב ה ה		Homo.
	l t	- - -				

ö

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 ÓWNŘTLŘKVÁ 87
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11676;
                                                                                                                                                          163 FHWORNYRK 171
                                                                                                                                      2 FQWQRNMRK 10
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11676;
                                                                                                                                                                                                                                  01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09YQC0
                                                                                                                                                                                                               Q9YQC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ODAAGO
                                                                                                                                                                                                      Q9YQC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                          ð
SOW KE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                        ó
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                              "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazōa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                        ;
0
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.9%; Score 51; DB 6; Length 33; 63.6%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                 Score 57; DB 4; Length 38;
Pred. No. 0.0013;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                        InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Hypothetical protein Alr4323.
                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactorin (Fragment).
Ovis aries (Sheep).
                                                                                                                                                                                                                                                                      33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                          100.0%; Pred. No. v.v.
                                                                                                                                                   Score 57;
                                                                           seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE=95127729; Pubmed=7827104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001156; Transferrin.
                                SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                    81.4%;
                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                       Mammalia, Butheria, Ceta.
Bovidae, Caprinae, Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 CYQWQKXCMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=103690;
                                                                                                                                                                                                           21 FOWORINMRKV 30
                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; 077698; ICE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 7; Conser
                                                                                                                                                                                              2 FOWORNMRKV 11
            NCBI TaxID=9606;
   Mammalia;
                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                     Sato I.;
                                                                                                                                                                                                                                                                                  O9TRB0;
                                                                                                                                                                                                                                                                       Q9TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
Q8YP77
                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE-99440505; PubMed=9765386;
Pasquier C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J.,
Puel J., Izopet J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular evidence for mother-to-child transmission of multiple variants by analysis of RNA and DNA sequences of human immunodeficiency virus.";

J. Virol. 72:8493-8501(1998).

BMBL; AJ008835; CAA08937.1;

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120:

1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PASDLINES-198440505, PubMed=9765386;

PASQLISE C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J.,

Puel J., Izopet J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                           .;
0
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 15; Length 109;
Pred. No. 3.8;
                                                                                                                                                                                                                                    h 50.0%; Score 42; DB 16; Length 298; Similarity 77.8%; Pred. No. 7.2; 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AA; 12015 MW; EEOCA3E4A0A0D0EB CRC64;
                                                                                                    DNA Res. 8:205-213(2001).

EMBL; AP003596; BAB76022.1;

Hypothetical protein; Complete proteome.

SEQUENCE 298 AA; 34513 MW; 64036E6852299A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retrôviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 10, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O1-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Envelope protein (Fragment)
```

0

```
|| | :||||
78 QWNRTLRKVA 87
                                                                                                                                                                                                                                                                                                                                                                                                        3 QWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 OWNRTLRKVA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9YJI7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
Q9YIJ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
Q9YJ17
        RAY RET RET OR KENT RET OR KENT RET SO DE RET 
                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                             dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PH PH PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                               2; Indels '0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98440505; PubMed=9765386;
MEDLINE=98440505; C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J.,
Puel J., Izopet J.;
"Molecular evidence for mother-to-child transmission of multiple
variants by analysis of RNA and DNA sequences of human
"Molecular evidence for mother-to-child transmission of multiple variants by analysis of RNA and DNA sequences of human immunodeficiency virus.";
J. Virol. 72:843-861(1998).
EMBL; AJ008839; CAA08301.1;
InterPro; IPR00777; GP120.
Pfam; PF00516; GP120.
Pfam; PF00516; GP120.
Pfam; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.0%; Pred. No. 3.8;
Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.6%; Score 41; DB 15; Length 109; 70.0%; Pred. No. 3.8; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AA; 12053 MW; 8217D3EA2DFD4C4B CRC64;
                                                                                                                                                                                          109 AA; 12012 MW; FB18E6E4AB546FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSYQB8 PRELIMINARY; PRT; 109 AA.
QSYQB8;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCB _TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodeficiency virus.";
J. Virol. 72:8493-8501 (1998).
Bmbi, Ando8843; CAA08305.1; -.
InterPro; IPR000777, GP120.
Pfam; PF00516; GP120; 1.
Pfam; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 70.0 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        3 QWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                78 OWNRTLRKVA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 OWNRTLRKVA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                    NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9YQB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
Q9YQB8
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9YQB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98440505; PubMed=9765386;

MEDLINE-98440505; PubMed=9765386;

MEDLINE-98440505; PubMed=9765386;

A Pasquiar C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J., Izopet J., Izo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
MEDLINE=98440505; PubMed=9765386; Pasquier C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J., Pasquier C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J., Puel J., Izopet J.; Izopet J.; Everyoet J.; Everyoet J.; Everyoet J.; Everyoet J.; Pason C. Manan Everyor S., Manan Everyor J., Gpl20. Peam; PRO0516; Gpl20, Gpl20. Peam; PRO0516; Gpl20, Manan Everyor S., Manan Everyor Ev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.6%; Score 41; DB 15; Length 109; 70.0%; Pred. No. 3.8; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.6%; Score 41; DB 15; Length 109; 70.0%; Pred. No. 3.8; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AA; 12042 MW; EE0CA3E4B04EDE1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9YIJ2 PRELIMINARY; PRT; 109 AA.
09YIJ2;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VJI7;

1-MAY-1999 (TrEMBLrel. 10, Created)

01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 70.0 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
```

4

```
L SUMMITTED MAR. 1994) to the EMBL/GenBank/DDBJ databases.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
HEAST, 20303, CAA82991.1; --
HESP; POSIJ2; LCTP.
R INTERPO: IPRO00719; ENk pkinase.
R InterPro; IPRO00290; Ser Lhr_pkinase.
R InterPro; IPRO00290; Ser Lhr_pkinase.
R Ffam; PF00069; pkinase; I.
R Pfam; PF00069; pkinase; Z.
R Pfam; PF000001; Euk pkinase; Z.
R PRODON; PRO00001; Euk pkinase; Z.
R PROSITE; SM00123; STK: 1.
R PROSITE; PS00107; PROTEIN KINASE DOW; 1.
R PROSITE; PS00107; PROTEIN KINASE DOW; 1.
R PROSITE; PS00101; PROTEIN KINASE ST);
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
W ATP-Dinding; Kinase; Serine-protein kinase; Transferase.
Q SEQUENCE 500 AA; 57996 MW; 5579A056AC357C07 CRC64;
                                                                                                                                                                                                                                               Bukaryota, Viridiplantae. Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baur B., Winter K., Fischer K., Dietz K.; "Molecular cloning and characterization of several protein kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=NJS182;
Brandful J.A.M., Ampofo W.K., Janssens W., Adu-Sarkodie Y.,
Brandful J.A.M., Anyoni F., Aidoo S., Barnor J.S., Yamamoto N.,
Ishikawa K., Sata T., Kurata T.;
"Genetic and phylogenetic analysis of HIV-1 strains from Southern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.6%; Score 41; DB 10; Length 500; Best Local Similarity 77.8%; Pred. No. 19; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein gp120 (Fragment)
                                                                                                                                                                                                                                   Spinacia oleracea (Spinach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AJ225659; CAA12541.1;
InterPro, IPR000777; GP120.
Pfam, PF00516; GP120; 1.
                                     Q41383;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
PRELIMINARY;
                                                                                                                   01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 WORNRRKLA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WORNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11676;
                                                                                                                                                                                                  Protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from plants."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ghana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              090863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         090863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090863
DDA BARRA BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID ACC DE ACC DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.; "Molecular cloning of 11S globulin and 2S albumin, the two major seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sesamum indicum (Oriental sesame) (Gingelly).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae, euasterids I; Lamiales; Pedaliaceae; Sesamum.
                                                                                                                                                                                                                                                                    MEDLINE=98440505; PubMed=9765386;
Pasquier C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J.,
Puel J., Izopet J.;
                                                                                                                                                                                                                                                                                                                                                                               "Molecular Evidence for mother-to-child transmission of multiple variants by analysis of RNA and DNA sequences of human immunodeficiency varius type 1.",
j. Wirol. 72:8493-8501(1998).

EMBL; AJ009061; CAA08523.1; -.

EMBL; AJ008042; CAA08304.1; -.

Interpro; IPR00077; GP120.

Pfam; PF00516; GP120.

AIDS; Coat protein; Envelope protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.6%; Score 41; DB 15; Length 109; 70.0%; Pred. No. 3.8; 2; Indels Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.6%; Score 41; DB 10; Length 148; 66.7%; Pred. No. 5.2; ative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               storage proteins in sesame.";

1. Agirc. Food Chem. 47:4932-4938 (1999).

EMBL; AF091441, AAA24943.1;

InterPro; IPR003612; AAI.

InterPro; IPR0010617; Nagin.

InterPro; PR0010617; Nagin.

Fram; PF00234; tryp_alpha_amyl inhbtr.

PFRINTS; PR00496; NAPIN.

SMART; SM0499; AAI: 1.

SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 AA; 12028 MW; EE0CA3F708754E1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                         Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 70.0 les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QWQRNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 CMOWMRSMR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQRNMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
```

Q9XHP1

RESULT 11 Q9XHP1

Matches

ð

· 0

Gaps

0

9138 MW; 2D43DCD554295572 CRC64;

81 81 **AA**;

RESULT 12 Q41383

8

·,

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruges; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Capripoxvirus.
NCBI_TaxID=59509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12)
SEQUENCE FROM N.A.
STRAIN-NEETHLING 2490;
STRAIN-NEETHLING 2490;
Tulman B.R., Afforso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF325528; AAK85069.1; -.
INTERPRO; IPR004281; DUP230.
Ffam; PF03003; DUP230; 1.
SEQUENCE 377 AA; 43937 MW; FA3B4316D8B28D3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=NEETHLING 2490;
MEDLINE-2129495;
MEDLINE-2129495;
FubMed=11435593;
Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"Genome of lumpy skin disease virus.";
                                 ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; Score 40; DB 12; Length 329; 50.0%; Pred. No. 19; 1ve 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 40; DB 12; Length 377;
 Score 40; DB 15; Length 81;
Pred. No. 4.2;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                       Amano a., Miyamura T.;
"DNA sequence of Yaba virus BamH1-D fragment.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB018404; BAA88879.1;
InterPro; IRR004251; DUF230.
Pfam; PF03003; 329 329, 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 AA; 37969 MW; 03511EB8F7582FC2 CRC64;
                                                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
YB-D1L protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91MQ5 PRELIMINARY; PRT; 377 AA.
Q91MQ5,
Q01DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTM-2002 (TrEMBLrel. 21, Last annotation update)
LSDV108 putative myristylated membrane protein.
                                                                                                                                                                329 AA.
                                                                                                                                                             PRT;
   57.1%;
Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .umpy skin disease virus.
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                 Yaba monkey tumor virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 CIKWLRQKRKIA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQRNMRKVA 12
                                                            3 QWQRNMRKVA 12
                                                                              69 EWKENLRKVA 78
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            Yatapoxvirus.
NCBI_TaxID=38804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                              Q9QB73
                                                                                                                                 RESULT 14
Q9QB73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                          à
```

```
Best Local Similarity 50.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps
Qy 1 CFQWQRNMRKVA 12

Db 185 CLKWLRTKRIA 196
Search completed: February 21, 2003, 07:44:33
Job time: 20.8 secs
```

us-09-743-107b-80.rag

```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                   February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Geneseq 101002:*

1: /SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDSZ/gcgdata/geneseq_geneseqp-emb1/AA1981.DAT:*

3: /SIDSZ/gcgdata/geneseqg-emb2.AA1981.DAT:*

4: /SIDSZ/gcgdata/geneseqg-emb1/AA1983.DAT:*

5: /SIDSZ/gcgdata/geneseqg-emb1/AA1983.DAT:*

6: /SIDSZ/gcgdata/geneseqg-emb1/AA1983.DAT:*

7: /SIDSZ/gcgdata/geneseqg-emb1/AA1985.DAT:*

8: /SIDSZ/gcgdata/geneseqg-emb1/AA1985.DAT:*

9: /SIDSZ/gcgdata/geneseqg-emb1/AA1980.DAT:*

10: /SIDSZ/gcgdata/geneseqg-emb1/AA1980.DAT:*

11: /SIDSZ/gcgdata/geneseqg-emb1/AA1980.DAT:*

12: /SIDSZ/gcgdata/geneseqg-emb1/AA1990.DAT:*

13: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1991.DAT:*

14: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1991.DAT:*

15: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1991.DAT:*

16: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1995.DAT:*

16: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1995.DAT:*

17: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1995.DAT:*

18: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1995.DAT:*

19: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1995.DAT:*

10: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1996.DAT:*

10: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1996.DAT:*

10: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1996.DAT:*

10: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1996.DAT:*

10: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1996.DAT:*

10: /SIDSZ/gcgdata/geneseqg/geneseqg-emb1/AA1996.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                           64
1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                      US-09-743-107B-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                      Title:
```

ALIGNMENTS

	•				99WO-SE0123		98SE-000244	98SE-000256	98SE-000461		INVEST AB.		ttsby-Baltze		88/13.
	WO200001730-A1		13-JAN-2000.		06-JUL-1999;		06-JUL-1998;	17-JUL-1998;	29-DEC-1998;		(ASCI-) A+ SCI INVEST AB.		Hanson LA, Mattsby-Baltze		WPI; 2000-147388/13.
Į	PN	X	PD	XX	PF	X	PR	PR	PR	×	PA	X	ΡΙ	XX	DR
															<u> </u>
				Description		Human lactoferrin	Human lactoferrin	Human lactoferrin	Human lactoferrin	Human lactoferrin					
	SUMMARIES			ID	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AAY78080	AAY78071	AAY78038	AAY78046	AAY78047	AAY78096	AAY78037	AAY78048	AAY78049	AAY78036
				DB	1	21	21	21	21	21	21	21	21	21	21
				Match Length DB ID		12	12	12	12	12	12	13	13	13	14
		æ	Query	Match		100.0	92.2	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6
				re	1	64	59	28	58	28	58	58	58	58	58

Dolphin GT;

Mattsby-Baltzer I, Baltzer L,

Human lactoferrin Human lactoferrin Peptide for anti-u Human lactoferrin Human lactoferrin Human lactoferrin	1 ac	Human lactoferrin Human lactoferrin Advanced glycosyla Human lactoferrin Amino acid sequenc	lcrobia srrin-r errin d errin d errin d errin d	la ara ara e ra e ra e ra e ra e ra e ra	נו וו
AAY78050 AAY78051 AAX98554 AAY78035 AAY78062	803 806 806 803 806	0 6 6 6 6 6	H 44 M M 49 49 40	0.0000040	2000
21 21 21 21 21 21	221222	21 17 21 21 21 21	10111111111111111111111111111111111111	16 116 117 117	17 17 18 18
41 41 15 15 15 15	16 16 17	118 118 118 119	00000000	0000000	0000
8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9	888890.	88888	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	888888888888888888888888888888888888888	88890.
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11 11 12 13 13 13 13 13 13 13 13 13 13 13 13 13	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	る ろ ろ ろ み な な ら ひ ち ひ ひ ひ ひ ひ ひ ひ ひ ひ ひ ひ ひ ひ	। বা বা বা বা । বা লে বা বা

Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative. Human lactoferrin derived peptide SEQ ID NO:80. AAY78080 standard; Peptide; 12 AA 98SE-0002441. 98SE-0002562. 98SE-0004614. 99WO-SE01230, 25-APR-2000 (first entry) 30-A1. Homo sapiens. Synthetic. . 66 98; 98; 00 AAY78080; AAY78080

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                           Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections,
              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 64; DB 21; Length 12; 100.0%; Pred. No. 4.8e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammations and tumors and for use in infant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78071 standard; Peptide; 12 AA.
                                                                     Claim 22; Page 36; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-SE01230,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFOLORINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78071;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as medicinal tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                         Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                     92.2%; Score 59; DB 21; Length 12; 91.7%; Pred. No. 0.00039; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lactoferrin derived peptide SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78038 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                         Local Similarity 91.7
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFÇAÇRIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                    12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78038;
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
          888888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

.; 0

Gaps 0

ö

Tue Dec

ö

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane), inflammations add/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
             Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and auti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                    Gaps
fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                Score 58; DB 21;
Pred. No. 0.00059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baltzer L,
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 35; 102pp; English
                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                    AAY78046 standard; Peptide; 12
                                                                                                                                                                                90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                        CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                         1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13.
                                                                                                                                                                                                 Local Similarity
                                                                                                                                              12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78046;
                                                                                                                                                                                Query Match
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                     AAY78046
                                                                                                                                                                                                                                                                                                                                                                                                       ПЪ
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides an also be used fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                      Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.6%; Score 58; DB 21; Length 12; 91.7%; Pred. No. 0.00059; ative 0; Mismatches 1; Indels
                                          Length 12;
                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baltzer L, Dolphin GT;
                                         Score 58; DB 21;
Pred. No. 0.00059;
                                                                                                                                                                                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:47.
                                                                       Mismatches
                                                                                                                                                                                                        AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 73; 102pp; English
                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mattsby-Baltzer I,
                                         90.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230
                                                                                                                                                                                                                                                                      25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                     12
                                                                                                                               1 CFÓWORNWRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                       Local Similarity
nes 11; Conserv
                                                                                                     1 CFQLQRNMRKVR
            12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                        AAY78047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                     Matches
                                                                                                                                                                                          AAY78047
ID AAY7
                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                         X S
                                                                                                      à
                                                                                                                               g
```

AAY78037 standard; Peptide; 13 AA.

```
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food suffis such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammacory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                               Human, lactoferrin, modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 21; Length 12;
Pred. No. 0.00059;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolphin GT;
                                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mattsby-Baltzer I, Baltzer L,
                                                                                                              AAY78096 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 38; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002441.
                                                                                                                                                                                                                                                                                                  bactericidal; preservative.
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
1 CFQLQRNMRKVR 12
                          1 CFÓWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA;
                                                                                                                                                                                                                                                                                                                                                                                    WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1998;
                                                                                                                                                                               25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson LA,
                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                              AAY78096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                               g
à
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the industrial actoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or prevention of infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides he used on the used and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.6%; Score 58; DB 21; Length 13
91.7%; Pred. No. 0.00064;
ive 0; Mismatches 1; Indels
                                                                                                     Human lactoferrin derived peptide SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78048 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                        98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOLORIMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CFQWQRNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AA;
                                                                                                                                                                                                                                                                                   WO200001730-A1.
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000
                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1998;
                                                                   25-APR-2000
                                                                                                                                                                                                                                                                                                                      13-JAN-2000
                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78048
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             田林なななな田
```

. 0

Gaps

٥;

Best Local Similarity 83.3 Matches 10; Conservative

Matches

1 CFOLORNMRKVR 12

ð

1 CFQLQKWMKKVR 12

셤

RESULT 7

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through peptide or classification and complete the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammantions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and continued them to be used for the same purposes as lactoferrin at lower and continued the costs.
               Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                    Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                      98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                     99WO-SE01230.
                                                                           bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AA;
                                                                                                                                                                       WO200001730-A1
                                                                                                                 Ното варіепв
                                                                                                                                                                                                                                                                                                      17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                   06-JUL-1999;
                                                                                                                                                                                                                                                                                      06-JUL-1998;
                                                                                                                                                                                                             13-JAN-2000
                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
```

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the dirollation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candia infection an a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an infant and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canbe them to be used for the same purposes as lactoferrin at lower

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 18; Page 74; 102pp; English

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB.

98SE-0002441. 98SE-0004614.

99WO-SE01230

06-JUL-1999; 06-JUL-1998; 29-DEC-1998;

13-JAN-2000

WO200001730-A1

Synthetic

·,

```
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                Score 58; DB 21; Length 13;
Pred. No. 0.00064;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                        AAY78036 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                90.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                   25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                     Local Similarity 91.7
                                                                                                                                                                                                                                                                                                         CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                       2 CFOWORINMRKVR 13
                                                                                                                                                                                                                                                                  Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                      AAY78036;
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                          Н
                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                   AAY78036
ð
                                                                                                                                                                                                                                                                                                                       쉽
                                                                                                                                                                                                                                                                                                                                                                ö
```

0; Gaps

Length 13;

90.6%; Score 58; DB 21; Length 13 91.7%; Pred. No. 0.00064; live 0; Mismatches 1; Indels:

11; Conservative

Matches

Best Local Similarity

Query Match

à

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

Human lactoferrin derived peptide SEQ ID NO:49.

(first entry)

25-APR-2000

AAY78049;

AAY78049 standard; Peptide; 13 AA.

AAY78049

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                   Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%; Score 58; DB 21; Length 14; 91.7%; Pred. No. 0.00069; ttive 0; Mismatches 1; Indels
                                                                                                            Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lactoferrin derived peptide SEQ ID NO:50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78050 standard; Peptide; 14 AA.
                                                                                                                                                                                                                         Claim 12; Page 69; 102pp; English.
                                                                                                            Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-SE01230.
                              98SE-0002562.
98SE-0004614.
               98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                            (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CFOWORNMRKVR 14
                                                                                                                                            WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
                              17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JAN-2000.
                                                                                                            Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
```

```
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                              AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                   infections,
                                                                                                                               New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.6%; Score 58; DB 21; Length 14; 91.7%; Pred. No. 0.00069; iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolphin GT;
Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lactoferrin derived peptide SEQ ID NO:51.
   Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                       Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mattsby-Baltzer I,
   Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CFÓWÓRNMRKVR 14
                                                                 WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X H X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B 
          à
```

. 0

Gaps

0;

ö

Claim 18; Page 75; 102pp; English.

```
AAY78035 standard; Peptide; 15 AA.
                                                                                        25-APR-2000 (first entry)
                                                                     AAY78035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                       RESULT 14
                                     AAY78035
                                                        ò
                 AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The agent is low oln.. It can be
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR98531-54 are peptides used in an anti-ulcer agent. The a in toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                                                                                                                                              Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.6%; Score 58; DB 17; Length 15; 91.7%; Pred. No. 0.00074; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-ulcer agent contg. peptide - has low toxicity, is
                                                                                                                                                                                                                            Score 58; DB 21;
Pred. No. 0.00069;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                    AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 11; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MORG ) MORINAGA MILK IND CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heat-resistant and water-soluble
                                                                                                                                                                                                                             90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                     Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                       1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                             3 CFÓWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-318857/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                       14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP08143468-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                           AAR98554;
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                          AAR98554
8X5555555555555555558888
                                                                                                                                                                                                                                                                                                                                                                δ
```

12

CFQLQRNMRKVR

2 CFOWORNMRKVR 13

g

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the peptides are taken up in the intestine through the operation lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such and and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower can be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                            Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Match 90.6%; Score 58; DB 21; Length 15; Local Similarity 91.7%; Pred. No. 0.00074; nes 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolphin GT;
Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78062 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
                                                                                                                                                                                                                                                                                                                                                                        WO200001730-A1.
                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanson LA,
                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78062
ID AAY7
XX
AC AAY7
```

```
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                      Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0002441,
98SE-0002562,
98SE-0004614,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-SE01230.
                                  25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
SON COURSE OF COURSE SERVICE STATES SERVICE SE
```

Dolphin GT;

lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower AAY78001 to AAY78100 represent peptides having sequences based on human

15 AA;

Gaps 0; / Match
Local Similarity 91.7%; Pred. No. 0.00074;
les 11; Conservative 0; Mismatches 1; Indels Query Match Matches

ô

1 CFOLORNMRKVR 12

à g

4 CEÓWÓRNMRKVR 15

Search completed: February 21, 2003, 07:37:14 Job time : 29.35 secs

```
MOLECULE TYPE: peptide
FRATURE:
NAME: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appli
Appli
Appli
Appli
Appli
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                      (without alignments)
40.818 Million cell updates/sec
                                                                      February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence (Sequence (Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                  1: /cgr2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-204-487-3

US-08-485-948-8

US-08-462-98-8

US-08-625-8

US-08-256-771-24

US-08-256-771-24

US-08-256-771-24

US-08-381-984-25

US-08-381-984-25

US-08-381-984-25

US-08-381-984-25

US-09-508-734-4

US-07-55-161A-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-18

US-07-891-174-18

US-07-891-174-18

US-08-26-771-30

US-08-26-771-30

US-08-26-771-30

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29
                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*
                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                           US-09-743-107B-80
                                                                                                                                                 1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                Searched:
                                                                                                                                                   Sequence:
                                                                        Run on:
```

	28 30 30		9.09	54 694	9999	000	464-724-	3-464-182A-2 3-406-271-2 3-724-596-2			2, Appli 2, Appli 2, Appli	444
,	35 35 35	20 00	9.06	694 694	44	00	-421	632-2 190-2		Sequence Sequence S		<u> </u>
	3. S.	58 58	90.6	705	N N	US-08-	-655-i -655-t	640-2 640-4				11
	35	28	9.06	711	-	US-08	-154-	019-4				17:
	3 6	ω τ. α	90.0	117	H ~	US-08	-461-	333-4		Sequence 4		-d -
	38	2 60	9.06	711	n	Ö	-158-	313-4				1 1
	39	28	9.06	711	4	US-08-	-476-	798-4];
	40	22	85.9	711	н	US-08-	-145-	681-2				17:
	41	25	2.29	711	н.	US-08-	-250-	308-2				-d -
	7 7	ה ע ה ע	0.00 0.00	111	٦ ،	Š	- 404-	703-2				4.5
	4 4	יי ר	, o	711	٧ ٣	Š	456.	108-2				4 · r
	45	22	85.9	711	4.	-03	265-	577-2			Appl	1:1
						AL.	ALIGNMENTS	STN				
	RESULT 1	.487-3										
	- F02:-00:-00	1	1 4 4 4 4 5	/ OTT &	0.00	10000						
	. Datent No		3, Appilcation US/U820448 5, 5565425	n us/	N R O	0448 /						
	GENERAL	INFOR	GENERAL INFORMATION:									
-	APPL	APPLICANT:	YAMAMOTO,	O, NAOKI	OKI	!						
	APPL:	APPLICANT:	MAKASHIMA, HIDEKI	MA, HIDE	IDE	¥						
	APPL	APPLICANT:	TANAKA,		EAK	—						
	APPL	APPLICANT:	DOSAKO,	SHON, ICHI	Į,	H						
	APPL	CANT:	KAWASAKI	Н	SHI	HIRO						
	; APPL.		OCHIDA,	-	IAK	I						
	TITLE		OF INVENTION:		AL	TORS	ON A	VIKAL INFECTION AND PROLIFERATION INHIBITORS	RATION			
	NUMBER	R OF S	OF SEQUENCES:	œ		}						
	CORRI	SPONDE	CORRESPONDENCE ADDRESS:	ESS:								
	; ADI	RESSEE	PATEN	T ADM	INE	STRATOF		TESTA, HURWITZ	TZ &			
	; ADI	ADDRESSEE:	: THIBEAULT	AULT								
	; STI		53 STATE STREET	STRE	댎							
	:		BOSTON									
		STATE: M	MA									
	zIP:	02109	_									
	COMPUTER	TER RE	READABLE FORM:	ORM:								
	, MEI	MEDIUM TYPE:	PE: Flo	Floppy disk	isk							
	Ö.	COMPUTER:	2	. E	atil	ble						
	; OPI	SRATING	03	P.	DOS	-DOS/WS-DOS						
	ios ;	SOFTWARE:	PatentIn Release	In Re	lea	se #1.0,		Version #1.2	D.			
	; CURRI	SNT APE	CURRENT APPLICATION DATA:	DATA								
	, API	PLICATI		R: U	8/0	UMBER: US/08/204,48	187					
		FILING DATE:		-MAK-1	40,00							
-	TOPE C	OK/ AGING	- 6	DIA T								
	NAM .	NAME: A	CAMPERT.	DATTLA	5							
	REC	TESTRAT		3		503						
	REF	FRENCE	REFERENCE/DOCKET NUMBER	NUMBE		FJN-01	6					
	TELEC	COMPILINI	TELECOMMUNICATION INFORMATION:	NFORM	ATI	NC: NC	}					
	TEI	TELEPHONE:	(617)	(617) 248-7000	700							
	TEI	TELEFAX:	9	48-71	00	,						
	; INFORM	INFORMATION FOR	OR SEQ ID NO:	D NO:								
		-										

```
US-08-475-055-8
                                       RESULT 3
US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                      .;
0
                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: YONG MING LI
APPLICANT: TONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAIN
TITLE OF INVENTION: ACENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSE: Alauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
90.6%; Score 58; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                        Score 58; DB 1; Length 18; Pred. No. 0.00037; O; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:

CLASSIFICATION 1436

RIOR APPLICATION DATA:

APPLICATION NUMBER: 08/488,217

FILING DATE: JUNE 7, 1995

APPLICATION NUMBER: 08/418,642

FILING DATE: APRIL 7, 1995

CLASSIFICATION: 436

ATTORNEY AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 947-1-008A

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 187-5800
                                                                                                                                                                                                                                                                                         ; Sequence 8, Application US/08485948
; Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 Hackensack Avenue
OTHER INFORMATION: (20-37) "
                                                        90.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                             Query Match
Best Local Similarity 91.73
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 411 ALL COLTY: Hackensack STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQLQRNMRKVR 12
                                                                                                                                             1 CFQLQRNMRKVR 12
                                                                                                                                                                                       1 CFQWQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: YONG M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-485-948-8
                                                                                                                                                                                                                                                  RESULT 2
US-08-485-948-8
        ;
US-08-204-487-3
```

```
.
0
Sequence 8, Application US/08628380
Patent No. 5891341
GENERAL INFORMATION
APPLICANT: Li, YONG MING
APPLICANT: ULASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                    COMPUTER EDADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: APPLIL 4, 1996
CLASSIFICATION S14
PR.OR APPLICATION DATA:
APPLICATION NUMBER: US/08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION S14
APPLICATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
RELERPACE DOCKET NUMBER: 947-1-008 CIP
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.6%; Score 58; DB 2; Best Local Similarity 91.7%; Pred. No. 0.00037; Matches 11; Conservative 0; Mismatches 1.
                                                                                                                                                                            STREET: Klauber & Jackson STREET: 411 Hackensack Avenue CIIY: Hackensack STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08475055;
Patent No. 5962245;
GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDROCC.
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
```

us-09-743-107b-80.rai

```
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 2; Length 18;
Pred. No. 0.00037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
TIY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFFCATION:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/486,217
FILING DATE: 0408 7, 1995
FILING DATE: 0408 7, 1995
FILING DATE: APPLICATION NUMBER: 08/418,642
FILING DATE: APPLICATION:
APPLICATION NUMBER: 08/418,642
FILING DATE: APPLICATION:
APPLICATION:
NAME: Jackson BSq., David A.
REGISTRATION NUMBER: 26/742
REGISTRATION NUMBER: 26/742
FELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 1343-1684
                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/475,055
ALUDRESS:

LIKET: Klauber & Jackson

LIKET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-07-755-161A-3
: Sequence 3, Application US/07755161A
; Patent No. 5304633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.6%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIRAMAN
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFÓWORNWRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FRAGMENT TYPE:
US-08-475-055-8
```

```
FEATURE:
NAME/KEY: modified site
LOCATION: 19
LIDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "thiol group of
Cys residue at location 2 connected by disulfide bond with
thiol group of Cys residue at location 19"
                                                              US/07/755,161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
FILING DATE:
PRILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECPHONE: 202-371-8850
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITS:
UNITS:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note
OTHER INFORMATION: Cys red
OTHER INFORMATION: thiols
OPERATING SYSTEM: MS-DOS
                 SOFTWARE: DisplayWrite CURRENT APPLICATION DATA: APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                             FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
CELL LINE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
```

90.6%; Score 58; DB 1; Length 20;

us-09-743-107b-80.rai

```
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
                                   OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19" FRATURE: NAME/KEY: modified site LOCATION: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YAMMOTO, NAOKI
APPLICANT: YAMMOTO, NAOKI
APPLICANT: YAMMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MASKASHIMA, HIDEKI
APPLICANT: TANAKA, SHICERALI
APPLICANT: TOSAKO, SHIN'ICHI
APPLICANT: TAMASAKI, YOSHIARI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: B
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58; DB 1; Length 20;
Pred. No. 0.00042;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REPERENCE/DOCKET NUMBER: PJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION DATE: RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/08204487; Patent No. 5565425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 91.7
Matches 11; Conservative
  COCATION: 2
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
                                                                                                                                                                                                                                                                                       AUTHORS:
TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                      JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                       ö
Best Local Similarity 91.7%; Pred. No. 0.00042;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                Sequence 3, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENITON: Antimicrobial Peptides and an TITLE OF INVENITON: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE
                                                                 1 CFQLQRNMRKVR 12
                                                                                                           2 CPOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washi
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL TYPE:
                                                                                                                                                                           RESULT 6
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
                                                                 δ
```

ö

;

```
Query Match
90.6%; Score 58; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00042;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                       1 CFQLQRNMRKVR 12
                                                                                                                                                                                2 CFÓWÓRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-381-984-24
           US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                 90.6%; Score 58; DB 1; Length 20; 91.7%; Pred. No. 0.00042; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                         LOCATION: 1.20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/256,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/ORGET UNBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/25
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 amino acids
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                       NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                           US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5555591
; GENERAL INFORMATION:
    APPLICANT: Mamoru TOMITA et al.
    ITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
    TITLE OF INVENTION: PRODUCTS THEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
; IDRNITEICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 90.6%; Score 58; DB 1; Length 20; 1 Similarity 91.7%; Pred. No. 0.00042; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb computible operating System: MS-DOS SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771.
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER:
                                                                                                                                                                               NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STRET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
```

us-09-743-107b-80.rai

```
OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.6%; Score 58; DB 1; Length 20; 91.7%; Pred. No. 0.00042; live 0; Mismatches 1; Indels
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IDEN COMPATION: 1.005
COMPUTER: DISKette, 3.5 inch, 1.44 mb COMPUTER: IDEN COMPATION: DOSS SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, JT.
REGISTRATION NUMBER:
REGISTRATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, JT.
REGISTRATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, JT.
REGISTRATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, JT.
REGISTRATION NUMBER:
ATTORNEY/AGENT NUMBER:
ATTORNE
   805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-66-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1990-07-14
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09508734
Patent No. 6423509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                          Washington
                                                                                                           U.S.A.
                                                                                                                                           20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COCATION:
                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.6%; Score 58; DB 1; Length 20; 91.7%; Pred. No. 0.00042; iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Inal Comparible
COMPUTER: Inal Comparible
COMPUTER: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
                                                                                                                                                                                                                                            ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
Sequence 24, Application US/08381984 Patent No. 5804555 GENERAL INFORMATION:
                                                                                                    APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CFOWORINMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

0

ò

```
FRATURE:
NAME/KRY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: (yo residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 90.6%; Score 58; DB 1; Length 25; I Similarity 91.7%; Pred. No. 0.00052; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER:
FILING DATE:
RELECTION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                     33,367
                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INPORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified site
LOCATION: 4
LIDENTIFICATION METHOD:
OTHER INFORMATION: Cys re
OTHER INFORMATION: Cys re
OTHER INFORMATION: thiol
                     ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,3
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBBARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-755-161A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:

APPLICAT'S Samyang Genex Corporation

TITLE OF INVENTION: useful microorganism thereof

CURRENT PAPLICATION NUMBER: US/09/508,734

CURRENT PAPLICATION NUMBER: PCT/KR99/00373

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 6

LENGTH: 24

TYPE: PRIOR FILING NUMBER: TOWN CORPORATION CORPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                          ö
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58; DB 4; Length 24; Pred. No. 0.0005;
                                                                                                                                             90.6%; Score 58; DB 4; Length 22; 91.7%; Pred. No. 0.00046; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GRNERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
; UNUMERS OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; STRATE: D.C.
; COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/755,161A FILING DATE: 19910905 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 90.6%;
l Similarity 91.7%;
11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
                                                                                                                                             Query Match 90.6
Best Local Similarity 91.7
Matches 11; Conservative
                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                              1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                        2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20002
                                                                                     US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-508-734-6
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
```

ö

Gaps ., ; 0

Gaps ; 0

```
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
90.6%; Score 59; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00052;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: February 21, 2003, 07:50:35 Job time : 8.7 secs
                                                                                                                                                                                                                                                                                                                           FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CFÓWORNMRKVR 15
                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
                                                                                                                                                                                   JOURNAL:
                                                                                                                                                                                                          VOLUME:
                                                                                                                                                                                                                                                          PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OYS residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
                                     VESOUR 12

VES-07-891-174-10

Sequence 10, Application US/07891174

Patent No. 5317084

Patent No. 5317084

Patent No. 5317084

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS: 10

CORRESPONDENCE ADDRESS: 10

CORRESPONDENCE ADDRESS: 10

COUNTRY: Washington SITEET; 805 Fifteenth Street, N.W., #700

CITY: Washington SITEET: 10.S.A.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER: IBM Compatible COMPUTER: Diskette, 5.25 inch, 500Kb COMPUTER: Diskette, 1920 SOFTWARE: DisplayWrite COMPUTER: DisplayWrite COMPUTER: DisplayWrite CORRENT APPLICATION NUMBER: US/07/891,174

FILING DATE: DisplayWrite US/07/891,174

FILING DATE: 05-SEP-1991

ATPORTED TON NUMBER: US 07/755,161

FILING DATE: 05-SEP-1991

ATPORTED TON NUMBER: 33,367

RESPERENCE/DOCKET NUMBER: 33,367

TELEDROMUNICATION NUMBER: 202-371-8856

TELEBRANK: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LIBNGTH: 25 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified site LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: modified site
LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN:
```

```
5597, Ap
7, Appli
5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Appli
Sequence 20, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          (without alignments)
35.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                        February 21, 2003, 07:51:54; Search time 10.5 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              / Cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/DCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-738-626-5597
US-09-829-378-7
US-10-013-310-5
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-174-590-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-173-706-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-176-758-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-175-752-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-180-552-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-176-913-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-798-869-2
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-798-869-3
US-09-798-869-23
                                                                                                                                                                                                                                                                156504 Begs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                       US-09-743-107B-80
                                                                                                                                                                                   1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                Searched:
                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

APPP APPP APPP APPP APPP APPP APPP APP	Арр Арр Арр
00000000000000000000000000000000000000	574, 574, 574,
sednence sed	Sequence Sequence Sequence
10 110 110 110 110 110 110 110 110 110	US-10-174-585-574 US-10-174-586-574 US-10-175-747-574
, , , , , , , , , , , , , , , , , , ,	თთთ
	2 2 2 2 8 8 8 8 8 8 8 8 8
\\ \alpha \\ \al	54.7 54.7 7.40
01126459678889188899899999999999999999999999999	444 4445

ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.6%; Score 58; DB 9; Length 15; 91.7%; Pred. No. 6.7e-05; ive 0; Mismatches 1; Indels
      GENERAL INFORMATION US/0979869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKUAL
; APPLICANT: LARS VORIAND
TILLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: RALDUR SVEINBJ (RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-798-869-20
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
```

ö

Tue Dec

```
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                  90.6%; Score 58; DB 9; Length 25; 91.7%; Pred. No. 0.00011; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Jacobson, Price, Holman & Stern 400 Seventh St. N.W.
           FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: US/01-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPOME: (202) 638-666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-EEFT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: BB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Player, William E. REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 694 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington D.C.
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-10-023-096-2
LARS VORLAND
                                                                                                                                                                                                                                                                               TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
ö
                                     .
0
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens ) OTHER INFORMATION: sequence) US-09-798-869-6
                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
90.6%; Score 58; DB 9; Length 694; 91.7%; Pred. No. 0.0035; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 9; Length 15; Pred. No. 0.0021; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.1%; Score 41; DB 9; Length 15; 63.6%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOS-09-798-88-9-9

JOS-09-798-88-9-9

Publication No. US20030022821A1

GENERAL INFORMATION:

APPLICANT: (YSTEIN REXDAL

APPLICANT: (YSTEIN REXDAL

APPLICANT: ALDUR SVEINBU (RNSSON

APPLICANT: LALS VORLAND

TILLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 1999-06-31

FRIOR APPLICATION NUMBER: PCT/GB99/02851

FRIOR APPLICATION NUMBER: GB9818938.4

FRIOR APPLICATION NUMBER: GB9818938.4

FRIOR FILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 15
                                                                                                                                                                                                                 Sequence 6, Application US/09798869
Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 83.3%; es 10; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                     11; Conservative
                                                                        1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CFOWOWNMRKVR 14
                                                                                                     22 CFÓWÓRNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
   Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: CAPRINE
                                                                                                                                                                         0-698-867-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-698-861-80-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

ö

Gaps

..

us-09-743-107b-80.rapb

```
| Sequence 7, Application US/09829378 |
| Fatent No. US20020170082A1 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: FOX, Timothy |
| APPLICANT: FOX, Timothy |
| APPLICANT: FOX, Timothy |
| TITLE OF INVENITION: GENE AFFECTING MALE FERTILITY IN PLANTS |
| TITLE OF INVENITION: GENE AFFECTING MALE FERTILITY IN PLANTS |
| TITLE REFERENCE: 031229/0631 |
| CURRENT APPLICATION NUMBER: US/09/829,378 |
| CURRENT FILING DATE: 2001-05-09 |
| PRIOR FILING DATE: 2001-06-01 |
| NUMBER OF SEQ ID NOS: 10 |
| SOFTWARE: PATENTIN VET: 2.0 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 9; Length 360;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.7%; Score 35; DB 9; Length 700; 54.5%; Pred. No. 70; tive 3; Mismatches 2; Indels
              59.4%; Score 38; DB 9; Length 97; 70.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lamb, Jonathon Robert
APPLICANT: Hoyne, Gerard Francis
APPLICANT: Hoyne, Gerard Francis
APPLICANT: Ballman, Margaret Jane
TITLE OF INVENTION: Therapeutic Use
FILE REPERRNCE: 674525-2003
CURRENT APPLICATION NUMBER: US/10/013,310
CURRENT APPLICATION NUMBER: PCT/GB00/02191
PRIOR PILING DATE: 2000-06-05
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
LENGTHARE: PatentIn Version 3.1
SEQ ID NO 5
                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application US/10013310; Publication No. US20020192216A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.5%;
                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa US-09-829-378-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: House Mouse
US-10-013-310-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 CFELQREKLKI 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  666 ČEQVDŘIVŘRV 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQLQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQLQRNMRKV 11
                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                              1 CFQLQRNMRK 10
                                                                                                                       || :||| ||
73 CFLVQRNNRK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7
LENGTH: 360
                                                                                                                                                                                                 RESULT 8
US-09-829-378-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-013-310-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                  Query Match
                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                    g
                                                                                                  à
ö
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 9; Length 25; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
Indels
                                                                                                                                                                                                                                                                                         APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049 PCT-USA-A
FURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 23
LENGTH: 25
  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NOS: 5597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5597, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5597
                                                                                                                                                                            Sequence 23, Application US/09798869
PUDLICATION NO. USCO30022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REXOAL
APPLICANT: BALDUR SVENBJ (RNSSON)
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6
Matches 7; Conservative
7; Conservative
                                     1 CFQLQRNMRKV 11
                                                              3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQLQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CYÓWÓRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: CAPRINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-738-626-5597
                                                                                                                                      RESULT 6
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                       à
```

ö

Gaps

·;

ô

Gaps

0;

1 CFQLQRNMRKV 11

ਨੇ

```
848 CEQVDRNIRRY 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT APPLICATION NUMBER: US/10/176,758
                                                                                                                                                                                                                                                     APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACTIOS ENCODING THE SAME FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.7%; Score 35; DB 9; Length 882; 54.5%; Pred. No. 89; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.7%; Score 35; DB 9; Length 882; 54.5%; Pred. No. 89; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 574
LENGTH: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 574, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INPORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
                                                    Sequence 574, Application US/10174590 Publication No. US20030008352A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                           Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                    Desnoyers, Luc
                                                                                                                         APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo Sapien
US-10-174-590-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    848 CEQVDRNIRRY 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOLORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-176-758-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-10-176-758-574
                    RESULT 10
US-10-174-590-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 574
                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
```

```
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C7
CURRENY APPLICATION NUMBER: US/10/173,706
CURRENY FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 574
LENGTH: 882
                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P34.301150 NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.7%; Score 35; DB 9; Length 882; 54.5%; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 574, Application US/10173706
; Publication No. US20030022293A1
                              ; Sequence 574, Application US/10175737; Publication No. US20030013153A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desnoyers, Luc
Goddard, Audrey
Goddwski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                             Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                              Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.2
Pest Local Similarity 64.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                              APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                          Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), ORGANISM: Homo Sapien
US-10-173-706-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     848 CEQVDRNIRRV 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOLORNMRKV 11
                                                                                                                                                                                                                             Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Publication No. US20; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-173-706-574
RESULT 12
US-10-175-737-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                    APPLICANT:
APPLICANT:
```

54.7%; Score 35; DB 9; Length 882;

.. 0 us-09-743-107b-80.rapb

```
US-10-175-752-574
                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·;
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 574
LENGTH: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GERRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBRNCE 19430R1C45
CURRENT APPLICATION NUMBER: US/10/175,738
CURRENT APPLICATION NUMBER: US/10/175,738
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 5-4
LENGTH: 882
JENGTH: 882
JENGTH: 882
JENGTH: 882
JORGANISM: Homo Sapien
US-10-175-738-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                       Gaps
                       ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.7%; Score 35; DB 9; Length 882; 54.5%; Pred. No. 89; cive 3; Mismatches 2; Indels
                       2; Indels
     54.5%; Pred. No. 89;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 574, Application US/10175752
Publication No. US20030022295A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                   Sequence 574, Application US/10175738
Publication No. US20030022294A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                       Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                              Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: ||:||:|
848 CEQVDRNIRRV 858
                                                                               | |: ||:|
848 CEQVDRNIRRV 858
   Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQLQRNMRKV 11
                                                           1 CFQLQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-175-752-574
                                                                                                                                                    RESULT 14
US-10-175-738-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                             ð
```

```
0
                                        Gaps
                                        ..
Query Match
Best Local Similarity 54.5%; Pred. No. 89;
Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                  Search completed: February 21, 2003, 08:08:07 Job time : 10.55 secs
                                                                                                 848 CEQVDRNIRRV 858
                                                                            1 CFOLORNMRKV 11
```

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec Run on:

US-09-743-107B-80 64 1 CFQLQRNMRKVR 12 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 segs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* 73:* PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		probable peroxisom		lactoferrin - goat	4	lactoferrin - shee	hypothetical prote		hypothetical prote	_	hypothetical prote	hypothetical prote	hypothetical prote	probable transcrip	hypothetical prote	hypothetical prote		chalcone synthase	secY protein - red	hypothetical prote	oxi		teichoic acid bios	probable membrane	ATP-dependent deox	hypothetical prote	hypothetical prote	_	hypothetical prote
CI CI	TFHUL	T37974	T40568	JC2323	H96515	852107	T33211	AH1866	F65084	T19980	A96516	A97524	AB2743	G64908	B85720	E90897	AI3401	T03612	847440	AG2342	T31292	T28852	AE1210	849965	A39432	T29970	æ		E98038
DB	Н	N	ď	~	7	7	7	7	~	N	7	7	7	N	ď	~	N	7	7	~	(7	~	N	~	N	~	~1	~1	Ŋ
Length		223	238	708	887	33	335	187	252	346	887	153	178	228	228	228	249	389	409	508	519	664	969	921	1166	47	57		. 81
Match		64.1	64.1	64.1	62.5	59.4	59.4	57.8	57.8	57.8	7	9	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	54.7	54.7	54.7	54.7
Score	58	41	41	41	40	38	38	37	37	37	37	36	36	36	36	36	36	36	36	36	36	36	36	36	36	35	35	35	35
No.	-1	7	٣	4	Ŋ	9	7	80	Φ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	60S ribosomal prot	ribosomal protein	hypothetical prote	hypothetical prote	hypothetical prote	probable malate de	malate oxidoreduct	hypothetical prote	embryogenic callus	probable ribonucle	hypothetical prote	2-amino-4-hydroxy-	protein ZK1073.2 [hypothetical prote
D95003	E71547	T00407	A42840	T15387	S77802	D86255	A81933	C81173	S50977	T49924	F81411	T34468	F72425	F89732	D71436
0	N	C)	Н	N	N	N	N	~	7	7	~	7	0	~	0
104	151	159	179	234	267	295	426	426	431	445	644	795	129	189	273
54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	53.1	53.1	53.1
35	35	35	35	35	35	35	35	35	35	35	35	35	34	34	34
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

```
lactotransferrin precursor [validated] - human
N.Alternate names: lactoferrin
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C;Accession: G01394; S11228; Ā45401; S10324; S15853; S20841; S07160; A61169; A31000; S74 R;Cho, Y.
                                                                                                                                                                                                                                                                                                                                   A) Submitted to the EMBL Data Library, March 1994

A) Reference number: G06820

A) Accession: G01394

A) Status: preliminary; translated from GB/EMBL/DDBJ

A) Molecule type: mRNA

A) Rosidues: 1-711 -CHHD.

A) Rosidues: 1-711 -CHHD.

A) Cross-references: EMBL: U07643; NID: G467236; PIDN: AAB60324.1; PID: G467237

R) R, Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A) Fittle: Complete nucleotide sequence of human mammary gland lactoferrin.

A) Reference number: S11228; MUID: 90384839; PMID: 2402455
```

A; Accession: S11228

A; Molecule type: mRNA A; Residues: 1-148, Tr.,150-422, Cr.,424-711 <REY>
A; Cross-references: EMBL.X53961; NID:934415; PIDN:CAA37914.1; PID:934416
B; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
R; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
A; Title: Officerential molecular mechanism of the estrogen action that regulates lactofer: A; Reference number: A45401; MUID:93125571; PMID:1480183

A;Accession: A45401 A;Molecule type: DNA A;Residues: 1-15 <TEN>

A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A;Experimental source: placentá A;Note: sequence extracted from NCBI backbone (NCBIP:122202) R;Powell, M.J.; Ogden, J.E. Nucleic Acids Res. 18, 4013, 1990 A;Title: Nucleotide sequence of human lactoferrin cDNA. A;Reference number: S10324; MUID:90326549; PMID:2374734

A,Accession: \$10324 A;Molecule type: mRNA A;Residues: 3-711 <POW>

A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem, J. 276; 349-355, 1991
A;Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066

A; Status: nucleic acid sequence not shown; not compared with conceptual translation A;Accession: S15853

A; Molecule type: mRNA A; Residues: 20-31 <ST1>

A; Molecule type: protein A; Residues: 20-28, 'X', 30-31 <ST2>

```
64.1%;
63.6%;
                                                                                                                                                                                                                              64.1%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |::||:| :|:
155 CYELQQNSKKIK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 CYELOONSKKIK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQLQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 CYQWORRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SPDB:SPBC582.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: JC2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lactoferrin - goat
         A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
H96515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: protein
A,Rolecule type: protein
A,Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4,
A,Residues: 20-140,140-169, 171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4,
B,Note: Linis is the final paper in a series
R;Houen, G; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A,Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A,Reference number: 874119; MUID:97054624; PMID:8898921
A,Residues: 'G',22-24', R',26-27,'XX',30-32 <HOU>
A,Residues: 'G',22-24', R',26-27,'XX',30-32 <HOU>
A,Residues: 'G',22-24', R',26-27,'XX',30-32 <HOU>
A,Residues: 'G',22-24', R',26-27', XX',30-32 <HOU>
A,Residues: 'G',23-24', R',26-27', XX',30-32 <HOU>
A,Residues: 'G',24-24', R',26-27', XX',36-27', R',26-27', XX',30-32 <HOU>
A,Residues: 'G',24-24', R',26-27', 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;360-699/Domain: transferrin repeat homology 
F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 436-487, 24, 489-711 <RAD>
A; Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
A; Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
A; Panella, T.J.; S37-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 3-701, SWRPVN 'ARNA
A;Residues: 3-701, SWRPVN 'ARNA
A;Residues: 3-701, SWRPVN 'ARNA
A;Experimental source: normal breast tissue
R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Br. J. Blochem: 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A;Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                   띹
R,Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
Ajritle: Isolation of lactoferrin cDNA from a human myeloid library and expression of A,Reference number: S07160; MUID:88001031; PMID:3477300
A,Accession: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: BMBL:Z69909; PIDN:CAA93785.1; GSPDB:GN00066; SPDB:SPAC19G10.03c A;Experimental source: strain 972h-; cosmid c19G10 C;Genetics: A;Genetics: A;Gene: SPDB:SPAC19G10.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable peroxisomal membrane protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000 C;Datession: T37974 R;Murphy, i.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, March 1996 A;Reference number: 221759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; DB 1; Length 711; Pred. No. 0.0053; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:119368; OMIN:150210
A;Map position: 3421-3423
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; tron binding; milk
C;Keywords: duplication; glycoprotein; iron binding; milk
F;1-150/Domain: signal sequence #status predicted <21G>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T37974
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 CFÓWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-223 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: LTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

```
Rice Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
Arithe. Characterization of the goat lactoferrin cDNA; assignment of the relevant locus A; Reference number: JC2323; MUID:94380047; PMID:8093048
A; Accession: JC2323
A; Molecule type: mRNA
A; Residues: 1-708 < LEP>
C; Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: duplication; glycoprotein
F;359-696/Pomain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: Jacession: T40568
Riwood, V.; Rajandram, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
A;Reference number: Z21937
A;Reference number: Z21937
A;Accession: T40568
A;Accession: T40568
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-238 - WMO>
A;Residues: 1-238 - WMO>
A;Residues: SMBL:AL096788; PIDN:CAB46672.1; GSPDB:GN00067; SPDB:SPBC582.09
A;Experimental source: strain 972h-; cosmid c582
C;Genetics: Grap.cop.cop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SPBC582.09 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
A;Introns: 10/3; 170/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
C;Keywords: peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 2
A;Introns: 15/3; 25/3; 185/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 708; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.1%; Score 41; DB 2; Length 238; 41.7%; Pred. No. 3.1;
                                                                                                                                                      Length 223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                      1; Indels
                                                                                                                                                  Score 41; DB 2;
Pred. No. 2.9;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
```

m

o;

```
hypothetical protein b2984 - Bscherichia coli (strain K-12)
C;Species: Bscherichia coli
C;Scession: F65084
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science D.J.; Mat, B.; Shao, Y.
Science number: Ascherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Residues: 1-252 <BLAT>
A, Cross-references: GB. AB000381, GB. U00096, NID. g2367181; PIDN. AAC76020.1; PID. g1789357, A, Experimental source: strain K-12, substrain MG1655
C, Superfamily: conserved hypothetical protein b2986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C,Accession: AH1866
A,Cross-references: EMBL:AF067944; PIDN:AAC17673.1; GSPDB:GN00023; CESP:Kl0C9.6
A;Experimental source: strain Bristol N2; clone Kl0C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:BA000019; PIDN:BAB72439.1; PID:g17129826; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein all0481 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                               ..
0
                                                                           A,Gene: CESP:K10C9.6
A,Map position: 5
A,Introns: 163/2; 313/1
C,Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2; Length 252; Pred. No. 19;
                                                                                                                                                                                              59.4%; Score 38; DB 2; Length 335; 60.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 2; Length 187;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 57.1%;
B; Conservative
                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 CFSLRRMANLRKVQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOLOR -- NMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:| |||:|
168 FELPTNMRKMR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                       217 ČVÓMHŘNÍMKK 226
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             1 CFOLORNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 FQLQRNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: F65084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: all0481
                                                          C;Genetics:
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                         q
lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S2107
R;Olan, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Accession: S52107; MUID:95127729; PMID:7827104
A;Accession: S52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                   A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-887 <STO>
A, Cross-references: GB: AE005173; NID: 95668806; PIDN: AAD46032.1; GSPDB: GN00141
C, Genetics:
A, Gene: F16N3.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Dec-2000
C;Accession: T33211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 887;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 2; Length 33;
Pred. No. 1.7;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Du. Z.; Maggi, L. submitted to the EMBL Data Library, May 1998 A.Description: The sequence of C. elegans cosmid K10C9. A.Reference number: Z21302 A.Recession: T33211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein K10C9.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB;
Pred. No. 18;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    659 CHQIERNERNVR 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: protein
A,Residues: 1-33 <QIA>
C,Superfamily: transferri
C,Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQLQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 CYOWOKKWRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOLORNWRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 1
```

g

ö

1;

C, Genetics:

N

à

```
probable transcription regulator ydfH - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G64908
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Map position: circular chromosome
C,Superfamily: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase; 2-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:AE000251; GB:U00096; NID:g1787814; PIDN:AAC74613.1; PID:g1787821
                                                                                                                                                                                                                                                                                                                                A;Gene: AGR C 2500
A;Map positIon: circular chromosome
C;Superfamily: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase; 2-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cjāccession: AB2743
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monker, D.; Kutyavin, T.; Levy, R.; Li, M.; McCleller, Rarp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                  ţ
                      m
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein folk [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ster, E.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-153 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87146.1; PID:g15156416; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE008688; PIDN: AAL42360.1; PID: g17739767; GSPDB: GN00186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: G64908
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-228 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 178;
Pred. No. 21;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               h
Similarity 41.7%; Pred. No. 18;
5; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 56.2%;
Local Similarity 41.7%;
Les 5; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 CLDIERGMKRVR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 CLDIERGMKRVR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-178 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
                                                                                                                                              A;Accession: A97524
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: AB2743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: folk
                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein AGR_C_2500 [imported] - Agrobacterium tumefaciens (strain C58, Cere C;Species: Agrobacterium tumefaciens C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: A97524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Alature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: Z81484; PIDN: CAB03971.1; GSPDB: GN00023; CESP: C47A10.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE005173; NID: 95668804; PIDN: AAD46030.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F16N3.17 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A96516
                                                                                                                                                 hypothetical protein C47Al0.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .`
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.8%; Score 37; DB 2; Length 346; 54.5%; Pred. No. 26; 2; Indels ative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 2;
Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary; translated from GB/EMBL/DDBJA,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 5
A,Introns: 77/2; 154/3; 179/3; 215/3; 281/1; 302/3
                                                                                                                                                                                                                                                                                   R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19207
A;Accession: T19980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: clone C47A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        659 CHOIEKNERNVR 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
'Local 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 YOLEANMENIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-887 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-346 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: C47Al0.6
                                                                                                                                                                                                                                                       C; Accession: T19980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
```

A; Gene: F16N3.17

RESULT 12

ò 셤

```
ó:
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                               0;
                                                                                                                                                        Query Match 56.2%; Score 36; DB 2; Length 228; Best Local Similarity 41.7%; Pred. No. 27; Matches 5; Conservative 5; Mismatches 2; Indels
A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
A;Gene: ydfH
C;Superfamily: hypothetical protein b1540
C;Superfamily: bydothetical protein b1540
```

1 CFOLORNMRKVR 12

à

|:||::|: | 110 CYQLEQNLHQQR 121

q

BB572c.

BB572c.

BB572c.

BB572c.

BB572c.

C;Species: Escherichia coli

C;Species: B572c

B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

11er, L.; GGrobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Accession: B8572c

B772c

B772c

B

A,Gene: ydfH C,Superfamily: hypothetical protein b1540

Gaps ; Query Match 56.2%; Score 36; DB 2; Length 228; Best Local Similarity 41.7%; Pred. No. 27; Matches 5; Conservative 5; Mismatches 2; Indels

ö

1 CFQLQRNMRKVR 12

ò

|:||::|::| 110 CYQLEQNLHQQR 121 QC Op

Search completed: February 21, 2003, 07:47:53 Job time : 11.65 secs

```
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-80 64 1 CFQLQRNMRKVR 12 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ption	P02788 homo sapien		Q10333 schizosacch		-		047950 neurospora	Q46842 escherichia	Q01115 leptosphaer	P77577 escherichia	-					Q11109 caenorhabdi	P53661 mycoplasma		002799 sus scrofa	P11531 mus musculu	097592 canis famil	P11532 homo sapien	Q10353 schizosacch		P52689 klebsiella		P75028 symechocyst				-	٠.	O30807 rhizobium m
SUMMARIES	О	TRFL HUMAN	TRFL HORSE	YBM9_SCHPO	TRFL CAMDR	TRFL_CAPHI	URE1_LACFE	NUKM NEUCR	YGHR_ECOLI	FRO LEPAU	YDFH ECOLI	SECY_CYACA	YIB7_YEAST	ADDB_BACSU	SPCR_HUMAN	RK27 TOBAC	YX02_CAEEL	Y125_MYCCA	DEGY_CAEEL	STA2_PIG	DMD_MOUSE	DMD_CANFA	DMD HUMAN	RL24_SCHPO	UL31_HSVSA	LTRA KLEPN	I1BC_FELCA	PCXA SYNY3	YAGF_SCHPO		LPXB CHLPN			MAO1_RHIME
	DB	i	Н					Н	Н	Н	Н	-	Н	Н													Н					Н	н	Н
	gth	711	695	238	708	708	573	226	252	992	228	410	921	1166	3674	179	234	267	795	864	3678	3680	3685	192	261	309	410	440	510	554	604	604		770
de	Query Match	9	70.3	64.1	64.1	64.1	59.4	57.8	57.8	57.8	56.2	56.2	56.2	56.2	56.2	54.7	54.7	54.7	54.7	53.1	53.1	53.1	53.1	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6
	Score	58	45	41	41	41	38	37	37	37	36	36	36	36	36	32	35	35	35	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33
	Result No.]]]	7	ю	4	Ŋ	9	7	8	δ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q9bzf2 homo sapien P10220 herpes simp	Q05961 rattus norv P11928 mus musculu	Q8y052 raistonia s P10152 bos taurus	Q09688 schizosacch	295990 nepartus u Q9fln4 arabidopsis	Q58771 methanococc	droso	Q9nr22 homo sapien
RP7_HUMAN	OAS1_RAT	392 RALSO	A16_SCHPO	C27_ARATH	76 METUA	33A_DROME	1M4_HUMAN
O E	00	\$ \$	χ;	2 2	Ħ	R	Æ
44	нн,		н.		Н	-	Т
842 3164	358	115	177	198	245	267	334
51.6	50.8	50.0	50.0	20.0	20.0	50.0	50.0
33	32.5	3 B	32	3.2	32	32	32
3.34 5.4	36	3 3 3 3	40	4 4 1 2	43	44	45

ALIGNMENTS

RESULT 1 TREL HUANN AC 026KZ AC 026KZ AC 026KZ DDT 21-JU DT 115-JU DDT 115-J
--

N

```
McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parrell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., La Bastida M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Ritzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Glacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X.-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                  "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of
                                                                                                                                                                                                                                                                                        PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE=82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=82262043; PubMed=7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W., Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Mutagenesis of the histidine ligand in human lactoferrin: iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88001031; PubMed=3477300;
Rado T.A., Wel. X., Benz B.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library an
expression of mana during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
                                                                                                                    SEQUENCE OF 20-711.
SEQUENCE OF 20-711.
MEDLINE=85076667; PubMed=6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F., Legrand D., Spik G., Montreuli J., Jolles P.;
Legrand D., Spik G., Montreuli J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural comparisons with other transferrins.";
".- J Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding properties and crystal structure of the histidine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haridas M., Anderson B.F., Baker E.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "An 88 amino acid long C-terminal sequence of human
                                                        Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 670:243-254(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-99190892; Pubmed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97156796; PubMed=9003186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=7049727;
                      IISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lactotransferrin.";
FEBS Lett. 142:107-110(1982)
                                                                                                                                                                                                                                                                                                                                                                                                               N- and C-terminal domains.";
      SEQUENCE OF 3-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 -- >methionine mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 609-711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jolles P.;
                                                                                                                                                                                                                                                                                                                                                        Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [15]
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUNCTION: LACTOFERROXINS A, BAND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N., Qumaiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y., Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F., Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F., Hejtmancik J.F., Teng C.T.; Kaiser-Kupfer M., Nagata M., Nakayasu K., Hejtmancik J.F., Teng C.T.; corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene."; Mol. Vision 4.31-22 (1998).

Mol. Vision 4.31-22 (1998).
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                               MEDLINE-91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                    MEDLINE=99192677; PubMed=10089508; Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker B.N.; "Structure of human apolactoferrin at 2.0-A resolution. Refinement
                                                                                                                                                                                                                                             and analysis of ligand-induced conformational change.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i-SUBCELLULAR LOCATION: Secreted.
-i-DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i-SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agric. Biol. Chem. 54:1803-1810(1990).
                                                                                                                                                                                                                                                                            Acta Crystallogr. D 54:1319-1335(1998)
                                                                                   Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M83205; AAAS8656.1; -. M18642; AAA86665.1; -. AF332168; AAG48753.1; -. BC015822; AAH15822.1; -. BC015823; AAH15823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M73700, AAA59479.1; -.
X52941; CAA37116.1; -.
U95626; AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X53961; CAA37914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U07643; AAB60324.1; -. M93150; AAA36159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M83202; AAA59511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS THR-30 AND ARG-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                           from human lactoferrin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1LCF; 31-AUG-94.
1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -OCT-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9873069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S11228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1HSE;
1VFD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1LGB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1IGC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1BKA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1LFH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1LFI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1DSN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resolution.";
J. Mol. Biol. 289:303-317(1999).

-!- FUNCTION TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

-!- FUNCTION TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUALLY BICARBONATE.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ010930; CAA09407.1; -.

R PDB; 1B1X; 02-DEC-98.

R PDB; 1B7U; 02-FEB-99.

R InterPor; 1D2-FEB-99.

R InterPor; 1D2-FEB-99.

R PRINTS; PR00405; transferrin. 2.

PRINTS; PR00405; TRANSFERRIN.

R SMART; SM00094; TR FER; 2.

R PROSITE; PS00205; TRANSFERRIN. 1; 2.

R PROSITE; PS00205; TRANSFERRIN. 3; 1.

R PROSITE; PS002007; TRANSFERRIN. 3; 1.

Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.

T NON TER. 4. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99296631; PubMed=10366507;
Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                    ;
0
Query Match 90.6%; Score 58; DB 1; Length 711; Best Local Similarity 91.7%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Paramasivam M., Singh T.P.;
"CDM, sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLUTAR LOCATION: Secreted.
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                           Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6995
6950
6950
511
204
204
                                                                    1 CFOLORNMRKVR 12
                                                                                                  39 CPÓWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Milk;
                                                                                                                                                                                      TRFL HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                      077811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                      à
```

```
MEDLINE=21848401; PubMed=11859360;

MEDLINE=21848401; PubMed=11859360;

Mod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Sgouros J., Peat N., Hayles J., Basker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Haanlin N., Haartis D., Hidalpo J., Hodgson G.,

Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Moorey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Moorey P., Moule S., Saunders D., Qeall M.A., Rabbinowitsch E.,

Rutherford K., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Taylor R.G., Tivey A., Malsh S.V., Marren T., Whitchead S.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mulbert H.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Beger P., Zimmermann W., Wedler H., Mambutt R., Purnelle B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                70.3%; Score 45; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                     07BB84D50E1B165D CRC64;
                                                                                                                                                                                             IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypotherical protein C582.09 in chromosome II.
SPBC582.09.
                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 CAKFORNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                    695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHPO
                                                                                                                                       DISULFID
                                                                                                                                                                    DISULFID
                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                   DISULFID
                                                                                DISULFID
                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       010333;
                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                    METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YBM9 SCHPO
                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YBM9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

HSSP; 077811; 1B1X.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Mammary gland;
Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (JUN-1999) to the EMBL/Genbank/DDBA databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORP PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!- SUBBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOWAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
NCBI TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1; Length 238; Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            11 protein.
238 AA; 26479 MW; 58095AA8CD708180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camelus dromedarius (Dromedary) (Arabian camel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9TUMO: Q9MZS5;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             708 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL096788; CAB46672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ131674; CAB53387.1; -. EMBL; AF165879; AAF82241.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.1%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 CYELQQNSKKIK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CFOLORINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 4
CAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
      ð
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capra hircus (Goat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                           ransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.1%; Score 41; DB 1; Length 708; 66.7%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  F -> S (IN REF. 2).
G -> A (IN REF. 2).
G -> P (IN REF. 2).
LLS -> PLF (IN REF. 2).
L -> F (IN REF. 2).
A -> P (IN REF. 2).
A -> P (IN REF. 2).
A -> Q (IN REF. 2).
                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
AMION (BY SIMILARITY).
AMION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                   ANION (BY SIMILARI
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC.
                                                                                                         LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRFL_CAPHI STANDARD; PRT; 708 AA. Q29477; Q29479; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                               SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                               SIMILARITY
                                                                                                                                                                                                                                               SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
      Interpro; IPR001156; Transferrin.
Pfam; PR00402; TRANSFERIN;
SWART; SW00094; TR FER; 2.
PROSITE; PR00205; TRANSFERRIN 1; 2.
PROSITE; PS00205; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                 | | || |:|||
38 CAQWQRRMKKVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Best Local B; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                         594
261
3304
492
506
609
642
708 AA;
                                                                                                                                                                                                                                                                                                                                                                                   482
252
385
537
                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                     DISULFID
                                                                                                                                                                          DISULFID
                                                                                                                                                                                     DISULFID
                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                METAL
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                 DISULFID
                                                                                     Signal.
                                                                                              SIGNAL
                                                                                                      CHAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRFL_CAPHI
ID_TRFL_CI
AC 029477
DT 15-DEC.
DT 15-DEC.
DT 15-UN
DE Lactot:
GN CAPF.
OS CAPF.
                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                               METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                         TETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
엄
```

```
LACFE
               CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                         CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                   SEQUENCE
                                                                                      CARBOHYD
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P269<u>2</u>9;
                                                                                                                                                                                                                                                                                                                                                                                                                                            URE1_LACFE
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URE1
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHILD THE LEAD OF THE PROPERTY OF THE PROPERTY
ð
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@ibs-sib.ch).
                                                                                                                                                               P SEQUENCE FROM N.A.

TISSUB_Ammary gland;

MEDLINE=94380047; PubMed=8093048;

A MEDLINE=94380047; PubMed=8093048;

A MEDLINE=94380047; PubMed=8093048;

T "Characterization of the goat lactoferrin cDNA. Assignment of the "Characterization of the goat lactoferrin cDNA. Assignment of the "Characterization of the goat lactoferrin cDNA. Assignment of the "characterization of the goat lactoferrin cDNA. Assignment of the "characterization of the granteny group.";

E Biochem. Biophys. Res. Commun. 203:1324-1332(1994).

C AN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALL'S BICKNATEY).

--- SUBURIT: MONOMER (BY SIMILARITY).

--- SUBCELLULAR LOCATION: Secreted.

--- SUBCELLULAR LOCATION: Secreted.

--- SUBCELLULAR ENDORSED OF TWO HOMOLOGOUS DOMAINS.

--- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U53857, AA97958.1; -.
EMBL, X78902, CAA55317.1; -.
EMBL, X78902, CAA55317.1; -.
EMBL, X78902, CAA55317.1; -.
InterPro, IRROULISE, Transferrin.
Pfam, PF00405, transferrin, 2.
PRINIES, PR00429, TRANSFERRIN.
SMART, SM0094, TR FER, 2.
PROSITE; PS00206, TRANSFERRIN 1; 2.
PROSITE; PS00206, TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                          TISSUE=Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
LACTOTRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.
BY SIMILARITY.
                 Bovidae; Caprinae; Capra.
NCBI TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
METAL
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WETAL
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=JCM 5869;
SUZUKI K., Takahashi M., Imamura S., Ishikawa T.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.

-!- CATAINTIC ACTIVITY: Urea + H(2)0 = CO(2) + 2 MH(3).

-!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).

-!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).

-!- PTW: Lys-222 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).

-!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | HSSP; F41.6.7, | HSSP
                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Acid urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 708;
Pred. No. 2.7;
2; Mismatches 2; Indels
                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTT

I -> V (IN REF. 2) .

L -> R (IN REF. 2) .

C -> K (IN REF. 2) .

F -> P (IN REF. 2) .

F -> P (IN REF. 2) .

D -> G (IN REF. 2) .

D -> G (IN REF. 2) .

W, F2EDBA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
ANION (BY SIMILARITY).

N-LINKED (GLCNAC. .) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D10605; BAA01460.1; -. HSSP; P41020; 1UBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactobacillus fermentum
        |:| || || || CYQWQRRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQLQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1613;
```

φ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITRE=97188515; PubMed=9037100;
Lewis M.T., Morgan L.W., Feldman J.F.;
Lewis M.T., Morgan L.W., Feldman J.F.;
"Analysis of frequency (frq) clock gene homologs: evidence for a
helix-turn-helix transcription factor.";
Mol. Gen. Genet. 253:401-414(1997).
-!- FUNCTION: CIRCADIAN CLOCK COMPONENT INVOLVED IN THE GENERATION OF
BIOLOGICAL RHYTHMS, IN PARTICULAR IN RHYTHM STABILITY, PERIOD
LENGTH, AND TEMPERATURE COMPENSATION. BEHAVES AS A NEGATIVE
ELEMENT IN CIRCADIAN TRANSCRIPTIONAL LOOP (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FRQ FAMILY.
                                                                                                                                                                                                                                                          MEDLINE-97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                         Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Bscherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leptosphaeria australiensis.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Leptosphaeriaceae; Leptosphaeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.8%; Score 37; DB 1; Length 252; 57.1%; Pred. No. 5.4; 1; Indels iive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; ATP-binding; Complete proteome. NP BIND 28 35 ATP (POTENTIAL). SEQUENCE 252 AA; 28151 MW; E9C49E970425C758 CRC64;
    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ATP-binding protein yghR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     992 AA
                                                                                                                                                                                                                                                                                                                                                                                                        !- SIMILARITY: TO E.COLI YGHS AND YGHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000381; AAC76020.1; -.
EcoGene; EG13002; yghR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U28377; AAA69151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                       277:1453-1474 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frequency clock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 CFSLRRMANLRKVQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOLOR--NMRKVR 12
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
Les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 66919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                    Escherichia coli.
                                                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRO LEPAU
Q01115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                       Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRQ_LEPAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1411:142-146(1999).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
-!- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                Gaps
                                                                                                                                                                                                                                                                                      047950;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 41, Last sequence update)
15-UTM-2002 (Rel. 41, Last annotation update)
NADH-ubiquinone oxidoreductase 19.3 kDa subunit, mitochondrial
precursor (BC 1.6.5.3) (BC 1.6.99.3) (Complex I-19.3KD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRION (POTENTIAL).
NADH-UBIQUINONE OXIDOREDUCTASE 19.3 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ001520; CAA04802.1; -.
InterPro; IPR002096; Cmplx1_20kDa.
Pfam; PF01058; oxidored_q6; 1.
PROSITE; PS01150; COMPLEX1_20K; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide; Iron-sulfur; 4Fe-45.
TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sousa R., Barquera B., Duarte M., Finel M., Videira A., "Characterisation of the last Fe-S cluster-binding subunit of Neurospora crassa complex I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1; Length 226; Pred. No. 4.8;
                                          Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24972 MW; E48CB09C64AAAFC6 CRC64;
573 AA; 61805 MW; 2D2619781C39E54B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRON-SULFUR (4FE-4S)
                                        Score 38; DB 1;
Pred. No. 8.4;
                                                                                                                                                                                                                                                                   226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                2; Mismatches
                                          59.4%; Score 38; 58.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99233617; PubMed=10216160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                  Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
102
166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ?
                                                                                                                                                               379 CWOLASKWKKVR 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOLORKMRNTK 218
                                                                                                                         1 CFQLQRNMRKVR 12
                     101
102
166
196
196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGHR_ECOLI
ID YGHR_ECOLI
                                                                                                                                                                                                                                                                   NUKM NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                            RESULT 7
NUKM NEUCR
```

252 AA.

PRT;

STANDARD;

RESULT 8

셤

ð

Matches

.. H

Gaps

; 7

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                               Biological rhythms; Transcription regulation; Nuclear protein.

DOMAIN 550 554 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

DOMAIN 868 890 ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97426617; PubMed=9278503;
Blatther F. R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blatther F. R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Kriley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Man B., Shao Y.;
Man E., Shao Y.;
When complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21074935, PubMed=11206513,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Belch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 280-440.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                         Score 37; DB 1; Length 992;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                              992 AA; 107559 MW; 98E029B585F83AFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.75.77;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

01-NOV-1997 (Rel. 36, Last sequence update)

Hypothetical transcriptional regulator ydfH.

YDFH OR B1540 OR Z2157 OR ECS2149.

Escherichia coli, and

Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                           57.8%;
                                                                                                                                                                           EMBL; U25851; AAB96844.1; -
                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                       504 FOLSRDGRKVR 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                               2 FOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDFH ECOLI
ID YDFH ECOLI
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5555555558 F F S
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                       STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258706;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Sohiba T., Racomplete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Rhodophyta, Bangiophyceae, Porphyridiales, Porphyridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vogel H., Fischer S., Valentin K.-U.; Model for the evolution of the plastid sec apparatus inferred from "A model for the evolution of the plastid sec apparatus inferred from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                    0157.H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
-!- SIMILARITY: BELONGS TO THE GNIR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM0345; HTH GNTR; 1.
PROSITE; PS00043; HTH GNTR FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.2%; Score 36; DB 1; Length 228; 41.7%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 57 H-T-H MOTIF (POTENTIAL).
228 AA; 26565 MW; 8CFF8EB3BCF9AF84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H-T-H MOTIF (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P46249; O9MD55;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preprotein translocase secY subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20496959; PubMed=11040290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97134960; PubMed=8980520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secY gene phylogeny.";
Plant Mol. Biol. 32:685-692(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D90798; BAA15246.1; -.
EMBL; D90797; BAA15242.1; -.
EMBL; AE005351; AAG56222.1; -.
EMBL; AP002557; BAB35572.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000251; AAC74613.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EcoGene; EG13820; ydfH.
InterPro; IPR000524; HTH GntR.
Pfam; PF0032; GntR; 1.
PRINTS; PR00035; HTHGNTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 CYOLEONLHOOR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyanidium caldarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
DNA BIND 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=RK-1;
                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2771;
                                                                                                                                                                                                                                                                                                                                                                                            REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=RK-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyanidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
SECY_CYACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOUR READER OF R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

.. H

Gaps

4,

1; Indels

```
56.2%; Score 36; DB 1; Length 921; 53.3%; Pred. No. 34;
921 AA; 105491 MW; DDFA550E22E846A0 CRC64;
                                                                                                                        2; Mismatches
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                          647 CFQLLRNLTCNSRKI 661
                                                                                                                                                                                 1 CFQLQRNM----RKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kooistra J., Venema G.;
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168;
                                                                                                                     8.
                                                                                                                                                                                                                                                                                                                                                                                        ADDB_BACSU
P23477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=OG1;
      SEQUENCE
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                  BACSU
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDB.
                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                  ADDB
      S
                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                           7. Mol. Evol. 51:382-390(2000)
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. PROBABLY INTERACTS WITH OTHER PROTEINS TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE CHLOROPLAST ENDOPLASMIC RETICULUM (CER) MEMBRANES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288C / AB972;
Barrell BG. Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connoc K., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis B., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitchead S.,
                                     "The structure and gene repertoire of an ancient red algal plastid
                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast. -!- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomyoota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FFB-1995 (Rel. 31, Created)
01-FFB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last amnotation update)
Hypothetical 105.5 kDa protein in RPL2B-SNL1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein transport; Transmembrane; Chloroplast; Translocation.
CONFLICT 149 H199 MISSING (IN REF. 1).
SEQUENCE 410 AA; 46242 MW; 7CB0130175B1DF03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 AA.
            Gloeckner G., Rosenthal A., Valentin K.-U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.2%; Score 36; DB 50.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TICRPAMS; TICR00967; 3a05018007; 1.
PROSITE; PS00755; SECY 1; 1.
PROSITE; PS00756; SECY 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF022186; AAF12924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00303; SECYTRNLCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z46881; CAA86975.1; -. SGD; S0001279; YIL017C. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002208; SecY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002208; Si
Pfam; PF00344; secY; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 CFELSNNLKK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQLQRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P40547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YIB7_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

8

```
RAM Kunst R., Ogasawara N., Maczer I., Albertini A.M., Alloni G.,

Runst R., Ogasawara N., Messieres P., Bolotin A., Borchert S.,

Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Raverdo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Raverdo V., Bertero M.G., Caldwell B., Capuano V., Carter N.M.,

Radio S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Radio S.K., Codani J.J., Fabret C., Ferraria E., Foulger D.,

Ratiz C., Fujita M., Fujita Y., Fuma S., Galistis E., Foulger D.,

Radiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Radiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Radiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Radiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Radiseppi G., Guy B.J., Magna S., Mallo M.F., Itaya M., Jones L.,

Radiseppi G., Guy B.J., Magna S., Mauel C., Medigue C.,

Radishi Y., Kochter P., Koningstein G., Krogh S., Kumano M.,

Ratita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Radia N., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Radia N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

Radion D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

Ratic S., Polleich S., Schroeter R., Scoffone F.,

Schiguchi J., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

Rateuchi M., Tamakoshi A., Tanamacho H., Yamane K., Yasumoto K., Yata K.,

Hardeuchi M., Tamakoshi A., Tanamane K., Yasumoto K., Yata K.,

Hardeuchi M., Tamakoshi A., Tarkagi T., Tarkagara P., Togaroni A.,

Togato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

Ramiters P., Wanbutt R., Wedler E., Wedler H., Yamane K., Yasumoto K., Yata K.,

Hardeuchi M., Tamamoto H., Yamane K., Yasumoto K., Yata K.,

Hardeuchi M., Tamakoshi A., Tanamane C., Vannier E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Weller Gram.-Positive B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATURE 390:249-256(1997).
-!- FUNCTION: THE ENZYME COMPLEX MAY HAVE A WIDE VARIETY OF CATALYTIC ACTIVITIES INCLUDING ATP-DEPENDENT EXONUCLEASE, ATP-STIMULATED
                                                                                                                                                                                                                                                                                                                                                     "Cloning, sequencing, and expression of Bacillus subtilis genes
involved in ATP-dependent nuclease synthesis.";
J. Bacteriol. 173:3644-3655(1991).
                                                                                                                                               Bacillus subtilis.
Racteria, Firmicutes; Bacillales; Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noback M.A., Terpstra P., Holsappel S., Venema G., Bron Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                              (Rel. 20, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                            MEDLINE=91267926; PubMed=1646786;
                                              01-NOV-1991 (Rel. 20, Last sequen
15-JUN-2002 (Rel. 41, Last annota
ATP-dependent nuclease subunit B.
                        01-NOV-1991 (Rel. 20, Created)
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-RETENON N.A.

TISSUB-RELIA, Gerebellum, and Spinal cord;
TISSUB-RELIA, Gerebellum, and Spinal cord;
TISSUB-RELIA, Gerebellum, and Spinal cord;
MEDLINE-20347255; PubMed=10764729;
A Stabach P.R., Morrow J.S.;
Tidentification and characterization of beta V spectrin, a mammalian ortholog of Drosophila beta H spectrin.";
Tortholog of Drosophila Beta H spectra Beta H spectrin.";
Tortholog of Drosophila Beta H spectrin.";
Tortholog of Drosophila Beta H spectra Beta H spectrin.";
Tortholog of Drosophila Beta H spectrin.";
Tortholog of Drosophila Beta H spectra Beta H spectra Beta H spectrum.";
Tortholog of Drosophila Bet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A39432; A33432.
Subtilist; BG10465; addB.
InterPro; IFR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Brdonuclease; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                         SUBUNIT: THE B.SUBTILIS ATP-DEPENDENT NUCLEASE COMPLEX IS FORMED BY ONE B SUBUNIT IN CONJUNCTION WITH ONE A SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spectrin beta chain, brain 4 (Spectrin, non-erythroid beta chain 4)
(Beta-V spectrin) (BSPECV).
ENDONUCLEASE, ATP-DEPENDENT HELICASE AND DNA-DEPENDENT ATPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1; Length 1166; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
-!- SIMILARITY: CONTAINS 2 CALPONINY-HOMOLOGY (CH) DOMAINS.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 31 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1166 AA; 134631 MW; 1A57BBE81A08AB4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3674 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA repair; Complete proteome.
NP BIND 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M63489; AAA22200.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y14081; CAA74481.1; -. EMBL; Z99109; CAB12902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||: |:| :
486 FQLQKRMKKAK 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTBN5 OR SPTBN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPCR HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPNRC6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPCR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
   g
```

```
0
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                        Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein.
1 279 ACTIN-BINDING (BY SIMILARITY).
DOMAIN 54 159 CH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3533 3641 PH.
3674 AA; 416832 MW; 8COFDFAODD0C7C18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.2%; Score 36; DB 1; I
50.0%; Pred. No. 1.5e+02;
ive 3; Mismatches 3;
                                                                                                                                                                                                                                                               SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
                                                                                                                                                                                                                                                                                                  SPECTRIN 5.
SPECTRIN 6.
SPECTRIN 7.
SPECTRIN 9.
SPECTRIN 9.
        entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECTRIN 31
                                                                                                                                                          SMART; SM00033) CH; 2.
SMART; SM00233 PH; 1.
SMART; SM00150; SPEC; 29.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; FALSE_NEG.
PROSITE; PS50021; CH; 2.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                   InterPro; IPR001589; Actbind actnin. InterPro; IPR001715; Calponin-like. InterPro; IPR001715; Calponin-like. InterPro; IPR001849; PH. InterPro; IPR002017; Spectrin. InterPro; IPR001605; Spectrin. Pfam; Pr00169; PH; 1. Pfam; Pr00435; spectrin, 30. Pfam; Pr00435; spectrin, 30. PRINTS; PR00683; SPECTRINPH.
                                                                                                                                                                                                                                                                                                                                                                    SPECTRIN
SPECTRIN
SPECTRIN
SPECTRIN
SPECTRIN
SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECTRIN
                                                                                                                                                                                                                                                                                             SPECTRIN
                                                                                                                                                                                                                                                                                                                                                            SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECTRIN
                                                                                                                                                                                                                                                       CH 2
                                   EMBL; AF233523; AAF65317.1; -.
                                            HSSP; Q01082; 1BKR.
Genew; HGNC:15680; SPTBNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2574
2680
2785
2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2290 CLQLRRRLREFR 2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2470
2576
2682
2787
2787
                                                                                                                                                                                                                                                                                                                                                                                                                                    2255
2312
2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666
                                                              MIM; 605916; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                      DOMAIN
REPEAT
                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                            RPEAT
                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
à
```

RESULT 15 RK27_TOBAC

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                         Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Espermatophyta; Magnoliophyta; edicotyledons; core eudicots; Asteridae; enasteridae; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                            Elhag G.A., Bourque D.P.; "Nuclear-encoded chloroplast ribosomal protein L27 of Nicotiana rabacum: cDNA sequence and malysis of mRNA and genes."; Biochemistry 31:6856-6864[1992].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.7%; Score 35; DB 1; Length 179; 63.6%; Pred. No. 9.2;
                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FB2-1996 (Rel. 33, Last annotation update)
50S ribosoomal protein L27, chloroplast precursor (CL27).
RPL27 OR RPL27A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50S RIBOSOMAL PROTEIN L27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D6A30E2E90CB3FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF01016; Ribosomal L27; I.
PRINTS, PR00063; RIBOSOMALL27.
TIGREAMS; TIGR00062; L27; I.
PROSTITE; PS00831; RIBOSOMAL L27; I.
RIBOSOMAL RAMOST.
PRT; 179 AA.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 52-68.
STRAIN=cv. Petit Havana; TISSUE=Leaf;
MEDLINE=92345244; PubMed=1339289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M75731; AAA34115.1; -.
EMBL; M96473; AAA34104.1; -.
PIR; A42840; A42840.
InterPro; IPR001684; Ribosomal L27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN 52 179 5
SEQUENCE 179 AA; 19664 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.6 Matches 7; Conservative
STANDARD;
RK27 TOBAC
```

152 FRLORERRKAR 162

2 FOLORNMRKVR 12

à

; 0

0; Gaps

3; Indels

1; Mismatches

Search completed: February 21, 2003, 07:27:55 Job time : 5.6 secs

```
RESULT 2
Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qatcdz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9tr80 ovis aries
Q9h860 homo sapien
G51888 caenorhabdi
Q986f6 lactobacill
Q8Yzh9 anabaena sp
Q9uut7 yarrowia li
O45308 ceenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8xju2 clostridium
Q9sx86 arabidopsis
Q9ltn4 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q98x85 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91g17 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ucy5 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8tcd2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogvzą6 drosophila
Q95sh7 drosophila
                                                                                                                              February 21, 2003, 07:25:55; Search time 20.8 Seconds (without alignments) 118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                       671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9SX85
Q9LG17
Q9TR80
Q9H960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   061888
0956F6
08YZH9
09UUT7
045308
08XJU2
095X86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9VZQ6
Q95SH7
                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8TCD2
Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_bhage:*
sp_plant:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                    US-09-743-107B-80
                                                                                                                                                                                                                                                                              1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPIREMBL 21:*
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6622.66
6622.66
6622.76
6626.76
6626.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.76
6636.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11443
                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 4 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
```

Q8ufp3 agrobacteri Q8ygg0 brucella me Q43595 oryza sativ Q9vff6 drosophila Q8ypa5 anabaena sp	OBEOUG BPALINGOMODIA Q99/MB caenorhabdi Q99/MB caenorhabdi Q8y833 listeria mo Q9yr08 drosophila	404	4 L 2 D L 9	OSS87 avran rotav OSKOd8 neisseria m QSJve6 neisseria m Q2124 saccharowyc OSLA7 arabidopsis Q9flf7 arabidopsis Q8flf7 arabidopsis Q861W9 oryza sativ Q9phn6 campylobact
QBUFP3 QBYGG0 Q43595 Q9YFF6 QBYPA5	Q86000 Q9N9K2 Q9GYM8 Q8Y833 Q9VR08	Q2JV34 Q97PW0 Q97TB1 Q59956	Q9H7E7 O84177 O22165 Q9VPD0 Q9AWM7	055587 09K0D8 09JVE6 012124 09ELE7 08S1W9
9 H H H P P P P P P P P P P P P P P P P	12 L 22 12 14	999	4 10 110 10 10 10	100000000000000000000000000000000000000
244 244 384 288 208	675 675 3680	57 81 104 129	130 151 192 293 295	2 4 4 4 4 4 72 6 D 43 42 44 6 4 O 6 6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	54.7 54.7 54.7 54.7	7. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
, , , , , , , , , , , , , , , , , , ,	, w w w w w	, w w w w		
11 118 20 21 21	22 2 2 2 2 2 4 3 4 4 4 4 4 4 4 4 4 4 4 4	30 30 31 31	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	20 0 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

```
Gaps
                                                                                                Lactotransferrin.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY_2000 (TYEMBLrel. 13, Created)
01-MAY_2000 (TYEMBLrel. 13, Last sequence update)
01-JUN-2001 (TYEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                  82.8%; Score 53; DB 4; Length 711; 90.9%; Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; -.
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                 Last annotation update)
                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 AA.
711 AA
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                  01-07N-2002 (TrEMBLrel. 21, Created)
01-07UN-2002 (TrEMBLrel. 21, Last seq
01-07UN-2002 (TrEMBLrel. 21, Last ann
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 CFQWQRNMRKV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQLQRNMRKV 11
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               TISSUE=PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UCY5
OSTCD2
```

·.

```
01-DEC-2001 (
01-DEC-2001 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F16N3.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG14969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09SX85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09SX85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095SH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095SH7
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9SX85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095SH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                             Q
SORETERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDLINE=20196006; Pubmed=10731132;

RADAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADAMS M.D., Celniker S.E., Holt R.A., Schburner M., Henderson S.N.,

George R.A., Lewis S.E., Richards S., Champe M., Henderson S.N.,

RADAMS M. Lewis S.E., Richards S., Champe M., Feelffer B.D.,

RADAMS M. M. Lewis S.E., Marker E.G., Helt G., Champe M., Pefelfer B.D.,

RADAMS M. M., Basu A., Baxenelale G., Bayraktaroglu L., Beasley E.M.,

RADEILOY R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RADEILOY R.M., Cawley S., Dahlke C., Brownsort L.B., Bothakov S.,

RADERON K.Y., Dubam D.A., Buller H., Cadieu E., Center A., Chamira I.,

RADAMS M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chamira I.,

RADAMS M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chamira I.,

RADAMS M., Cawley S., Dahlke C., Perriara S., Pleischmann W.,

RADAMS M., Gariellan A.E., Garg N.S., Galbart W.M., Glasser K.,

A Glodek A., Gony F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RADAMS M., Marvey D., Heiman T.U., Hermandez J.R., Housen C.,

RADAMS M., Mony M., Murphy B., Murphy L., Marnel B.E., Kadira C.D., Kraft C., Kravitez S., Kullb D., Lai Z.,

RADAMS M. Mony M., Murphy B., Murphy L., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Shul H.,

RADAMS M. Nelson K.A., Nixon K., Nolsein F., Shen H.,

RADAMS M., Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Sunk F.,

RASHIBER R., Statelling A.C., Stapleton M., Stupski M.P., Sunk F.,

RASHIBER R., Statelling A.C., Stapleton M., Stupski M.B., Sunk S.,

RASHIBER R., Tector C., Turner R., Vencer B., Wang A.H., Wang X.,

RADAMS M., Mang R., Meinstock G.M., Weissenbach J.,

RADAMS M., Wang R., Meinstock G.M., Weinsten B., Wang X., Robert R., Mang Z.-Y., Wassarman D.A., Weinsten B.C., Stapletor R., Mang Z.-Y., Wassarman D.A., Weinster B., Weinster B., Murphy B., Wan
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                        "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 4; Length 38;
Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                       nestro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 AA.
                                                                                                                                                                                                      J. Legal Med. 49:281-293(1995).
P02788; 1BKA.
                                                                                                       MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                  76.6%;
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 FOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 FOWORINMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                         seminal plasma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BERKELEY;
                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                  Sato I.;
                                                                                                                                                                                                                    Jpn. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90ZA60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAPARA RA
     OX
OX
OX
RR
RR
RR
RR
DR
DR
DR
DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
;
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyladons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicacea, Arabidopsis.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                            0
                                                                                                                                                                                                    DB 5; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.5%; Score 40; DB 5; Length 315; 58.3%; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 AA; 34892 MW; DF66E013854AEA50 CRC64;
                                                                                                                          EMBL; AE003477; AAF47763.1; -.
FlyBase; FBgn0035440; CG14969.
SEQUENCE 253 AA; 27767 MW; D50BD3A60E0F0428 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                        62.5%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 1 (TrEMBLrel. 1 (TrEMBLrel. 2
                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 CFDLQDNMNRTR 178
                                                                                                                                                                                                                                                                                                                          105 CFDLQDNMNRTR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOLORNMRKVR 12
                                                                                                                                                                                                                                                                                     1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F16N3.18 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
```

ö

Gaps

1;

Indels

2; Mismatches Pred. No. 25;

66.78;

61.7%; Score 39.5; DB 10; Length 735;

```
EMBL; AC002304; AAF79335.1; -.
InterPro; IRRO01128; Cytochrome_P450.
Pfam; PF00067; P450; P450.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
Heme; Moncoxygenase; Oxidoreductase.
SEQUENCE 735 AA; 84661 MW; 4718F6202974F811 CRC64;
                                                                                                                                   Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                             165 CYDLQRNDMRKI 176
                                                                                                                                                                                 1 CFOLORN-MRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              원
                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi B., Conn L., Conway A., Gorzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liuu A., Liuu J., Liu S., Makharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi B., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome
                                                                                                                                                                                                                Gaps
 Lee J., Liu A., Li J., Kremenetskaia I., Gonzalez A., Altafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hänsen N., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                              0
                                                                                                                                                                             62.5%; Score 40; DB 10; Length 887; 58.3%; Pred. No. 24; ive 2; Mismatches 3; Indels
                                                                        "Arabidopsis, thaliana chromosome 1 BAC F16N3 sequence."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AC007519; AAD46032.1; -.
InterPro; IPR002048; EF-hanb; UNKNOWN 1.
SEQUENCE 887 AA; 100064 MW; 533510830A4A5099 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ecker J.R.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   735 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                               Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                             659 CHQIERNERNVR 670
                                                                                                                                                                                                                                              1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ecker J.R.;
Submitted (APR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecker J.R.;
Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scker J.R.;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                  Q9LG17;
                                                                                                                                                                                                                                                                                                                                                   09LG17
                                                                                                                                                                                                                                                                                                                    RESULT 6
Q9LG17
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
ISOGUENCE FROM N.A.
ISOGUENCE T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project.";
Submitted (ANG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK023050; BAB14376.1;
SEQUENCE 125 AA; 13445 MW; 66AICDDS774E7BD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin (Fragment)
Lactoferrin (Fragment)
Lactoferrin (Fragment)
Eukaryota aries (Sheep)
Bukaryota Aries (Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.4%; Score 38; DB 4; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.4%; Score 38; DB 6; Length 33; 54.5%; Pred. No. 2.3; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.,
Biochim. Biophys. Acta 1243:25-32 (1995).
HSSP: 077698; 10R2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FL112988 fis, clone NT2RP3000880.
Homo sapiens (Human).
   33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95127729; PubMed=7827104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                   Mammalia, Butheria, Ceta
Bovidae, Caprinae, Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQLQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                  SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  096H6Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09H60
   Q9TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
```

```
Local Similarity 63.6 ses 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           379 CWOLASKMKKVR 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 FELPTINMRKMR 178
                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 FOLORNMRKVR 12
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anabaena sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBYZH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09UUT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8YZH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC DE COLOR OF COLOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8YZH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactobacillus fermentum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·,
                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Du Z., Maggi L.;
"The sequence of C. elegans cosmid K10C9.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Urease (EC 3.5.1.5) (Urea amidohydrolase).
                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 38.7 kDa protein.
                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.4%; Score 38; DB 5; 60.0%; Pred. No. 23;
                                                                                                                                                                                      335 AA.
   Pred. No. 8.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99069613; PubMed=9851916;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                      6; Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 CVOMHRŇMKK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQLQRNMRK 10
   Best Local Similarity
                                                       1 CFQLQRNMRK 10
                                                                                          70 CFSLOONFKK 79
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=BRISTOL N2
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09S6F6;
                                                                                                                                                                                                       061888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9S6F6
                                                                                                                                                                                    061888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                        Matches
                                                                                                                                             RESULT 9
061888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09S6F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Subunit NUKM of procein NADH:ubiquinone oxidoreductase (Complex I)
Precursor (EC 1.6.99.3).
NUKM.
STRAIN=TK1214;
Coton E., Visser J.J., Van Vuuren H.J.J.;
"Urease operon of Lactobacillus fermentum.";
"Urease operon of Lactobacillus fermentum.";
submitted (24N-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: UREA + H(2)O = CO(2) + 2 NH(3).
-!- COPACTOR: EACH CHAIN BINDS TWO NICKEL IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
EMBL, AF120718; AAD22480.1; -.
HSSP; P41020; 1UBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21595285; PubMed=11759840; Kaneko T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanbe A., Iriguchi M., Ishikwa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%; Score 37; DB 16; Length 187; 63.6%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Čyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                    InterPro; IPR01924; UreaseA.
Pfam; PF00449; urease, 1.
Pfam; PF00449; urease, C; 1.
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS01145; UREASE 2; 1.
Hydrolase; Metal-binding; Nickel.
SEQUENCE 573 AA; 61823 MW; 4D325C6C4A21559C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 8:205-213(2001). _

EMBL, AP003582; BABV2543-1, -.

Hypothetial protein; Complete proteome.

SEQUENCE 187 AA; 21356 MW; 85C13C2EC8831DA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.4%; Score 38; DB 2; 58.3%; Pred. No. 39; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.6%; Pred. No. Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein All0481.
```

us-09-743-107b-80.rspt

SEQUENCE FROM N.A.

NCBI_TaxID=4952;

```
SEQUENCE FROM N.A.

C STRAIN=CV. COLUMBIA;

A VSOCESKAIA V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J., Liu A., Li J., Kremenetskaia I., Gonzalez A., Altafi H.,
A Araujo R., Brooks S., Buehler E., Chao O., Conn L., Conway A.B.,
Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C., Rowley D.,
Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A.,
A Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC F16N3 sequence.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
R EMBL, AC007519; AAD46030.1; --
R InterFro. IPROGOG48; EF-hand.
R PROSITE; PSO0018; EF-hand.
PROSITE; PSO0018; EF-HAND; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                    Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                              Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.8%; Score 37; DB 16; Length 565; 70.0%; Pred. No. 60; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0456; args; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
Ligase; Complete proteome.
SEQUENCE 565 AA; 64626 WW; 2626BD869B6ED66E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         flesh_eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP03131; BAB81367.1;
InterPro; IPR001278; Arg tRNA-synt_1c.
InterPro; IPR001220; Lectin_legB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               887 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005148; N.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03485; N-Arg; 1.
Pfam; PF00750; tRNA-synt ld; 1.
PRINTS; PR01038; TRNASXNTHARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Match
Best Local Similarity 70.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
   PRELIMINARY;
                                                                                            Arginine-tRNA ligase.
                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=13 / TYPE A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQLORNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 CFOLAKVMRK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F16N3.17 protein.
                                                                                                                                                                                       NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                    PubMed=11792842;
                                                                                                                ARGS OR CPE1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98XS60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98XS60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                            STRAIN=E 150;
MEDLINE=204939569; PubMed=10924914;
Diafarzadeh Andabili R., Kerscher S., Zwicker K., Radermacher M.,
Lindahl M., Schaegger H., Brandt U.;
"Biophysical and structural characterization of proton-translocating
"MaDH-Dehydrogenase (complex I) from the strictly aerobic yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT NUKM OF PROTEIN NADH:UBIQUINONE OXIDOREDUCTASE (COMPLEX 1).
C976335ECFD686ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.8%; Score 37; DB 5; Length 346; 54.5%; Pred. No. 37; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%; Score 37; DB 3; Length 210; 63.6%; Pred. No. 23; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; 28144; CAB03971.1; -.
Interio: IRR000344; Sra_chemo_Ce.
Pfam; PF02117; Sra; 1.
SEQUENCE 346 AA; 40696 MW; 5EA98035D4E93B5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                     346 AA
```

Created) PRT;

01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20,

Caenorhabditis elegans.

C47Al0.6 protein.

C47A10.6

SEQUENCE FROM N.A.

A STREET OF STRE

Basham V.M.;

PRELIMINARY;

045308; 045308

RESULT 13

210 AA; 23430 MW;

SEQUENCE

Conservative

Matches

Query Match Best Local Similarity

192 FOLORKMRNTK 202

g

à

2 FOLORNMRKVR 12

MEDLINE=99069613; PubMed=9851916;

SEQUENCE FROM N.A.

Local Similarity 54.5

Matches

Query Match

:||: ||| :| 230 YQLEANMRNIR 240

RESULT 14

Q8XJU2

2 FOLORNMRKVR 12

ð

ö

Gaps

;

0; Gaps Query Match
Best Local Similarity 50.0%; Pred. No. 94;
Matches 6; Conservative 3; Mismatches 3; Indels

0;

OY 1 CFOLORNMRKVR 12 | | ::: | | | | Db 659 CHQIEKNERNVR 670

Search completed: February 21, 2003, 07:44:35 Job time : 22.8 secs

us-09-743-107b-81.rag

```
Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | SIDS2/gcgdata/genesed/genesedp.embl/AA1990.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1991.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1991.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1993.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1994.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1994.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1994.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1996.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1996.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1999.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1999.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1999.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1999.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1999.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA1999.DAT:
| SIDS2/gcgdata/genesed/genesedp.embl/AA2000.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSZ/gcgdata/geneseq-geneseqp-embl/AA1982.DAT:*
4: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
7: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
9: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
11: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
12: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
13: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
14: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                    908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78048
AAY78049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78036
AAY78050
AAY78051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78047
AAY78037
                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78038
                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Geneseq 101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                      1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                            US-09-743-107B-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
68
68
68
68
68
68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
7
10
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
```

Peptide for anti-u Human lactoferrin	Human lactoferrin Human lactoferrin Human lactoferrin Khuman lactoferrin Amino acid sequenc Human lactoferrin Amin acid sequenc	oferrin-rela oferrin deri oferrin deri oferrin deri ne lactoferr ne lactoferr ne lactoferr parasitic l parasitic l	crin-deri crin-deri crin-deri crin-deri crin deri crin deri crin deri
AAR98 AAY78 AAY78 AAY78 AAY78 AAY78 AAY78	AAY 7806 AAK6935 AAW1339 AAW1339 AAY7803 AAY6886 AAY7803	AAR44 AAR48 AAR57 AAR57 AAR84 AAR864 AAR866	AAK5789 AAR818 AAR806 AAR876 AAR876 AAW261 AAW140 AAW703
-444444444	400000	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
110000000000000000000000000000000000000	200000	000000000000000000000000000000000000000	000000000000000000000000000000000000000
10 10 10 10 10 10 10 10 10	0.0.0.0.0.0.0.0.0	, w w w w w w w w w w w w w w w w w w w	
	888888888 0000000000000000000000000000		88888888 00000000000000000000000000000
11 11 11 11 11 11 12 13	1 2 2 2 2 2 2 2 2 3 2 4 3 2 5 4 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6	2 C C C C C C C C C C C C C C C C C C C	0 C C C C C C C C C C C C C C C C C C C

ALIGNMENTS

```
anti-tumour;
                                                                                                         Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumou
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                           Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                      Human lactoferrin derived peptide SEQ ID NO:81.
                    AAY78081 standard; Peptide; 12 AA
                                                                                                                                                                                                                                                                         98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                98SE-0004614.
                                                                                                                                                                                                                                                    99WO-SE01230
                                                                25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147388/13.
                                                                                                                                                                                                      WO200001730-A1.
                                                                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                           06-JUL-1998;
                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                     17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                             13-JAN-2000.
                                           AAY78081;
RESULT 1
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colltis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 71; DB 21; Length 12; 100.0%; Pred. No. 2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78038 standard; Peptide; 12 AA.
                                                                Claim 22; Page 36; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bactericidal, preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWOKNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFÓWOKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L7-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78038;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

AAY78001 to AAY78100 represent peptides having sequences based on human

Claim 12; Page 70; 102pp; English.

÷

Gaps .. 0

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used
        hadrontian. The peptides are cased up to the interaction consists through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                Gaps
lactoferrin. The peptides are taken up in the intestine through
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                         95.8%; Score 68; DB 21; Length 12; 91.7%; Pred. No. 7.4e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78046 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laim 15; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWOKNIMIRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                       12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78046;
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78046
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
$$$$$$$$$$$$$$$$$$$$$$$
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through louding to specific lactoferrin receptors and are then transported through the direculation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                       0;
fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, lactoferrin, modification, infection, inflammation, tumour;
food, infant formula, anti-inflammatory; anti-microbial, anti-tumour;
urlnary tract infection, collitis, Candida infection, fungicidal;
bactericidal, preservative
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                   Length 12;
                                                                                                                                                                  Score 68; DB 21; Length 14, Pred. No. 7.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                 AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 73; 102pp; English
                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                   95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-SE01230
                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                       1 CFOWOKNMRKVR 12
                                                                                                                                                                                                                                                                                          1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ношо
                                                                                                                                                                                                                                                                                                                                                                  AAY78047
   8$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                       ò
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                     Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                           Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 21; Length 13;
Pred. No. 8e-05;
1; Mismatches 0; Indels
                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dolphin GT;
                                          Score 68; DB 21;
Pred. No. 7.4e-05;
                                                                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                AAY78037 standard; Peptide; 13
                                          95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0004614
                                                                                                                                                                                                                                                                            25-APR-2000 (first entry)
                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB.
                                                                                                                          1 CFOWORNMRKVR 12
                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
                                                          Local Similarity
                                                                                                        1 CFQWQKNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AA;
             12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                               AAY78037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
              Sequence
                                          Query Match
                                                                       Matches
                                                                                                                                                                                                   AAY7803
                                                                                                                                                                                    RESULT
XX
SO
                                                                                                         à
                                                                                                                                   g
```

Tue Dec

AAY78049 standard; Peptide; 13 AA

(first entry)

25-APR-2000

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the direction. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower.
                                                                                                                                                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 21; Length 13;
Pred. No. 8e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                 Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                         AAY78048 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0004614.
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guery Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB.
1 CFOWOKNMRKVR 12
                  2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-1998;
                                                                                                                                                                                               25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                           AAY78048;
                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                         δ
                              q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Datacoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections or fragment urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on human
                                                                                                                        Human, lactoferrin, modification, infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78001 to AAY78100 represent peptides having sequences based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.8%; Score 68; DB 21; Length 13; 91.7%; Pred. No. 8e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                            Human lactoferrin derived peptide SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78036 standard; Peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                     98SE-0002441.
                                                                                                                                                                                                                                                                                                                     99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                   98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWOKUMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AA;
                                                                                                                                                                                                                                                      WO200001730-A1
                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                     06-JUL-1998;
                                                                                                                                                                                                                                                                                     13-JAN-2000
                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY7803
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BXXXXXX
```

; 0

Gape .; 0

RESULT 7

CFQWQKNMRKVR 12

à

```
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78001 to AAY78100 represent peptides having sequences based on human
             Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                               98SE-0004614.
                                                                                                                                                                                                                                                                  98SE-0002562.
                                                                                                                                                                                                                 99WO-SE01230.
                                                                                                                                                                                                                                                98SE-0002441.
                                                                 bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                WO200001730-A1.
                                                                                                  Homo sapiens.
                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                                06-JUL-1998;
                                                                                                                                                                                                                                                                  17-JUL-1998;
                                                                                                                                                                                                                                                                               29-DEC-1998;
                                                                                                                                                                                 13-JAN-2000
                                                                                                                   Synthetic.
```

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower 95.8%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 8.6e-05; ive 1; Mismatches 0; Indels Best Local Similarity 14 AA; Sequence Query Match

ò

11; Conservative Matches

3 CFOWORNMRKVR 14

1 CFQWQKNMRKVR 12

ð

AAY78050 standard; Peptide; 14 AA. 25-APR-2000 AAY78050; RESULT 9 4AY78050

Human lactoferrin derived peptide SEQ ID NO:50.

(first entry)

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; pactericidal; preservative 99WO-SE01230.

06-JUL-1999;

13-JAN-2000.

WO200001730-A1.

bactericidal; preservative.

ношо варіепв

Synthetic.

Homo sapiens

```
lactoferin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a wucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                          AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                     infections
                                                                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                                   Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 75; 102pp; English.
                                                                                                                                        98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                     99WO-SE01230
                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                  WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 AA;
                                 WO200001730-A1
                                                                                                     06-JUL-1999;
                                                                                                                                                                           29-DEC-1998;
                                                                                                                                                          7-JUL-1998;
                                                                    13-JAN-2000
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
```

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colliis; Candida infection; fungicidal; Gaps .; 0 95.8%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 8.6e-05; ive 1; Mismatches 0; Indels Human lactoferrin derived peptide SEQ ID NO:51. AAY78051 standard; Peptide; 14 AA. 25-APR-2000 (first entry) Local Similarity 91.7 1 CFOWOKNIMRKVR 12 3 CFOWORNMRKVR 14 AAY78051; Query Match Matches RESULT 10 AAY78051 Best

·.

Gaps . 0

. 0

```
ö
                                                                                                                                                                                                                                AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                    Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                              New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-ulcer agent contg. peptide - has low toxicity, is heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68; DB 21;
Pred. No. 8.6e-05;
1; Mismatches 0
                                                                                                      Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                                                                       Claim 18; Page 75; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MORG ) MORINAGA MILK IND CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 11; 11pp; Japanese.
                                                                                                    Hanson LA, Mattsby-Baltzer I,
            98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7'
                                                                       (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-318857/32.
                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQKNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP08143468-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L7-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-1994;
             06-JUL-1998;
17-JUL-1998;
                                           29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR98554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR98554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
6
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                  .;
0
              The agent is low
                             It can be
                                                                                                                                                                                                                                                                                                                                                                                                                               Human, lactoferrin, modification, infection, inflammation; tumour, food; infant formula, anti-inflammatory; anti-microbial, anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                Gaps
                                                                                                                                                  ٥:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
          AAR99531-54 are peptides used in an anti-ulcer agent. The agin toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                              Score 68; DB 17; Length 15; Pred. No. 9.2e-05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                    AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattsby-Baltzer I,
                                                                                                                95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                     25-APR-2000 (first entry)
                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                 1 CFQWQKNMRKVR 12
                                                                                                                                                                                                     2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                Query Match
Best Local Similarity
                                                                                 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                    AAY78035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                  Sequence
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                    3888838
                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                 엄
```

AAY78063 standard; Peptide; 15 AA.

RESULT 14

AAY78063 ID AAY7

(first entry)

25-APR-2000

AAY78063;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactoferrin. The periodes are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                            Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colltis; Candida infection; fungicidal; bactericidal; preservative.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.8%; Score 68; DB 21; Length 15; 91.7%; Pred. No. 9.2e-05; ive 1; Mismatches 0; Indels
Score 68; DB 21; Length 15
Pred. No. 9.2e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dolphin GT;
                                                                                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer
                                                                                                                                                                   AAY78062 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mattsby-Baltzer I,
 95.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-SE01230.
                                                                                                                                                                                                                                (first entry)
                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                           1 CFOWOKNMRKVR 12
                                                                             4 CFQWQRNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFOWOKNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-147388/13.
            Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1998;
                                                                                                                                                                                                                                25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                  AAY78062;
Query Match
                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                          Ношо
                                                                                                                                                      AAY78062
                                                                                                                                                                                                ò
```

```
·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 95.8%; Score 68; DB 21; Length 15; 1 Similarity 91.7%; Pred. No. 9.2e-05; 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dolphin GT;
                                                                   Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78031 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                   98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                    98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                98SE-0002562
                                                                                                                                                      bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                    (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 AA;
                                                                                                                                                                                                                                           WO200001730-A1.
                                                                                                                                                                                                                                                                                                                06-JUL-1999;
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                 06-JUL-1998;
                                                                                                                                                                                                                                                                            13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson LA,
                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78031
ID AAY
XX
AC AAY
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula such eused as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower cannot be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                            Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                               Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 68; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-SE01230.
                                  25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
NAMES OF THE PROPERTY OF THE P
```

0; Gaps 95.8%; Score 68; DB 21; Length 16; 91.7%; Pred. No. 9.8e-05; ive 1; Mismatches 0; Indels Local Similarity 91.7 tes 11; Conservative Query Match Best Loca Matches à

ö

1 CFQWQKNMRKVR 12

|||||:|||||| 5 CFQWQRNMRKVR 16

g

Search completed: February 21, 2003, 07:37:14 Job time : 28.35 secs

```
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                   February 21, 2003, 07:25:59; Search time 8.65 Seconds (without alignments) 40.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence (Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence (Sequence (Sequence )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-204-487-3

US-08-455-948-8

US-08-475-055-8

US-08-475-055-8

US-08-204-487-1

US-08-204-487-1

US-08-204-487-1

US-08-204-487-1

US-08-256-771-24

US-08-256-771-24

US-08-381-984-25

US-09-508-734-4

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-8

US-09-508-734-8

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-7

US-08-464-182A-5

US-08-464-182A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                             US-09-743-107B-81
71
                                                                                                                                                                                                                                                                                                                                                1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                 Copyright
                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $\times \text{B} \tex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
```

54 2 US-08-464-182A-2 694 3 US-08-406-271-2 694 4 US-09-421-632-2 694 4 US-09-421-632-2 705 2 US-08-655-640-2 708 2 US-08-655-640-2 711 1 US-08-154-019-4 711 3 US-08-464-167-4 711 3 US-08-464-167-4 711 1 US-08-464-167-4 711 1 US-08-464-167-4 711 3 US-08-464-167-4 711 1 US-08-451-703-2 711 1 US-08-451-703-2 711 1 US-08-451-703-2 711 1 US-08-451-703-2 711 2 US-08-456-106-2 711 3 US-08-456-106-2	ALIGNMENTS	S-08-204-487-3 S-08-204-487-3 S-08-204-487-3 Sequence 3, Application US/08204487 Patent No. 5565425 GENERAL INFORMATION: APPLICANT: YAMAMOTO, NAOKI APPLICANT: WAXASHIMA, HIDEKI APPLICANT: MAXASAKI, KSHUERAKI APPLICANT: MAXASAKI, KSHUERAKI APPLICANT: MAXASAKI, KSHUERAKI APPLICANT: MAXASAKI, YOSHIHAK TITLE OF INVENTION: UNHIBITORS NUMBER OF SEQUENCES: 8 COURRESCEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & COURTY: BOSTON STATE: MAS COUNTY: BOSTON STATE: THE STREET CITY: BOSTON STATE: THE STREET COUNTY: BOSTON STATE: THE STREET COMPUTER: READABLE FORM: MEDIUM TYPE: PLOPEY disk COMPUTER: READABLE FORM: MEDIUM TYPE: PATENTION MAYARION: SOFTWARE: PATENTION MAYARION: APPLICATION NUMBER: 32,503 REFERENCE/DOCKET NUMBER: FAN-019 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION	. / / ACT - HITMAN T.ACTOREBETN DESCRIPTION
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		T. 1	Č
228 3333333433334432 44449333466688 5443266688668866886688668866886688668866886		RESULT 1 US-08-204-487-3 US-08-204-487-3 PAPELICANT: NAVABA APPLICANT: NAVABA APPLICANT: NAVABA APPLICANT: NAVABA APPLICANT: NAVABA APPLICANT: TANAW APPLICANT: TANAW APPLICANT: TANAW APPLICANT: TANAW APPLICANT: DOSAW CONMUTER: DASA COUNTRY: USA CONFOURS: ISM COMPUTER: PREE COMPUTER: LEBRA TELEPONE: (617) INFORMATION FOR SEQ SEQUENCE TELEFAX: (617) INFORMATION FOR SEQ SEQUENCE TYPE: AMINO ACC STRANDENBESS: TOPOLOGY: 1 INGE MOLECULE TYPE: PREE NAME/KEY: PREE NAME/KEY: PREE	LOCATION:

us-09-743-107b-81.rai

```
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWOKNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , FRAGMENT TYPE:
US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                               07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-475-055-8
                                                                      US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08485948
Patent No. 585882
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YOUG MING LI
APPLICANT: ANTHONY CERANT
TITLE OF INVENTION: ADERNYS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                              .;
ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                  / Match 95.8%; Score 68; DB 1; Length 18; Local Similarity 91.7%; Pred. No. 4.5e-05; Albert 1; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
95.8%; Score 68; DB 2; I
Best Local Similarity 91.7%; Pred. No. 4.5e-05;
Matches 11; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                947-1-008A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIPCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
FILING DATE: ARRIL 7, 1995
FILING DATE: ARRIL 7, 1995
CLASSIFICATION NUMBER: 08/418,642
FILING DATE: ARRIL 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,747-1-00
TELEFRONCE/DOCKET NUMBER: 947-1-07
TELEFRONE: 201 487-5800
TELEFRAX: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNMRKVR 12
                                                                                                                                                     1 CFOWOKNMRKVR 12
                                                                                                                                                                                           1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                            US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                        Query Match
                                                                                             Best Loca
Matches
                                                                                                                                                       ð
```

q

```
.
0
                                                                    APPLICANT: LI, YONG MING
APPLICANT: VLASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08475055
Patent No. 5562245
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YOUR MING LI
APPLICANT: ANTHONY CERAMI
ITILE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
ITILE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.8%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 4.5e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FQ Compatible
OPERATING SYSTEM: FQ-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: April 4, 1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26,742
RR: 947-1-008 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 512
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
ATTORNET/AGENT INFORMATION:
NAME: JGACKBON EGG., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERNCE/DOCKET NUMBER: 26,742
REFERNCE/DOCKET NUMBER: 947-1-008
TELEPHONE: 201 487-5600
TELEPHONE: 201 343.1684
TELEPHONE: 201 343.1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
Sequence 8, Application US/08628380
Patent No. 5891341
GENERAL INFORMATION:
                                                                                                                                                                                                                                             STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
```

```
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 2; Length 18; Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REPERNICH/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRLL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
; Patent No. 5304633
                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
CORRESPONDENCE ADDRESS:
                                                                               STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE: US-08-475-055-8
                                                                                                COUNTRY: U
```

```
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" FUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8650
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: modified site
TOCATION: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                        TELEPHONE: 202-371-885
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 19
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
INDIVIDUAL ISOLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY:
```

95.8%; Score 68; DB 1; Length 20;

g à

```
NAME/KEY: modified site
LOCATION: 19
LOCATION: 10
LOCATION: Cyg residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cyg residue at location 2"
AUTHORS:
              IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMANOTO, NAOXI
APPLICANT: NAKASHIWA, HIDEKI
APPLICANT: MOSUCHI, WATAKU
APPLICANT: TANKA, SHIGRAU
APPLICANT: TANKA, SHIGRAU
APPLICANT: TANKA, SHIGRALI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UNUNTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: UNIBITORS
UNMBER OF INVENTION: INHIBITORS
UNMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 1;
Pred. No. 5e-05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REGISTRATION FOURER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
                                                                                                                                                                                                                                                                                                      TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: M
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                          0;
Pred. No. 5e-05;
                                                                                                                                                                      ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATE: 05.82P-1991
FILING DATE: 05.82P-1991
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek Jr.
REGISTRATION NUMBER: 33.367
REGISTRATION NUMBER: 33.367
REJECHNOMINICATION INFORMATION:
TELECHNOMINICATION INFORMATION:
TELECHNOMINICATION INFORMATION:
TELECHNOMINICATION INFORMATION:
TELECHNOMINICATION INFORMATION:
TELECHNOMINICATION INFORMATION:
TELECHNOMINICATION INFORMATION:
              Best Local Similarity 91.7%;
Matches 11; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                              2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
CHROMOSOME/SEGMENT;
MAP POSITION:
                                                                           1 CFOWOKNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
```

```
US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-381-984-24
                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: AMTIMICROBIAL AGENTS AND METHOD FOR TREATING TITLE OF INVENTION: PRODUCTS THEREMITH
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                   Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 5e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cyg residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/256,771 FILING DATE: July 22, 1,994 PION APPLICATION DATA:
APPLICATION NUMBER: PRICATION DATA:
APPLICATION NUMBER: PRICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Ji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWOKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CFÓWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                               Sequence 25, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION: CAPPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING TITLE OF INVENTION: PRODUCTS THEREWITH NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS: ADDRESSE: Menderoth, Lind & Ponack
                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . LOCATION:
.: LOCATION:
.: IDENTIFICATION METHOD:
.: OTHER INFORMATION: /note= "Cys residues are protected to
.: OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25
95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 5e-05; 1ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 5e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                        1 CFQWQKNIMRKVR 12
                                                                                                                   2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFOWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20005
                                                                                                                                                                                                       RESULT 9
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
```

Tue Dec

```
OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and

TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION: useful microorganism thereof

TITLE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 5e-05; 0; Indels tive 1; Mismatches 0; Indels
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
       805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGIESTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 12
SOFTWARE: KOPATENTIN 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CFQWQRNMRKVR 13
                                                                             20005
                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-508-734-4
                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: /note= "the specified peptide as well as ; OTHER INFORMATION: peptides including the specified peptide as a fragment thered US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "cysteine residues at positions
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

95.8%; Score 68; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 5e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                        GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIOXIDANT

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IDEN COMPATIBLE
OMNUTER: IDEN COMPATIBLE
OFFRATING SYGTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: APPLICATION: 252
PRIOR APPLICATION 1252
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
UNMERE OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
Sequence 24, Application US/08381984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQKNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                         D.C.
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                       20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION
                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
```

ö

ò

```
NAME/KEY: modified site
LOCATION: 21
LOCATION: 21
LOCATION: 21
LOCATION: 24
LOCATION: 24
LOCATION: 24
LOCATION: 4
LOCATION: 6
CHER INFORMATION: 6
COTHER INFORMATION: 6
COTHER INFORMATION: 6
COTHER INFORMATION: 4
LOCATION INFORMATION: 4
AUTHORS:
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
95.8%; Score 68; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 6.3e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10
                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: AMINO ACID STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL: ANTI-SENSE: FRAGMENT TYPE: CRIGINAL SOURCE:
                                                             33,367
                                                                                                    TELECOMMUNICATION INFORMATION: TELEFHONE: 202-371-8850 TELEFAX: 202-371-8856 TELEK:
                                         NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,3
REFERENCE/DOCKET NUMBER:
  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 4
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNITS:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09508734
Patent No. 64235509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
                                                                                                                                                ·,
                                                                                                                                                  Gaps
                                                                                                                                                  ö
                                                                                                  95.8%; Score 68; DB 4; Length 22; 91.7%; Pred. No. 5.5e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%; Score 68; DB 4; Length 24; 91.7%; Pred. No. 6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-755-161A-10

Squence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITT. Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILE REPERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR PILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR PILING DATE: 1998-07-13
PRIOR PILING DATE: 1998-07-13
SOFTWARE: Kopatentin 1.71
SOFTWARE: Kopatentin 1.71
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRICR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                        Best Local Similarity 91.73
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                       1 CFQWQKNMRKVR 12
                                                                                                                                                                                                               2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWOKNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20002
                                                                                                                                                                                                                                                                                                           US-09-508-734-6
                                                           US-09-508-734-4
LENGTH: 22
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
```

à

us-09-743-107b-81.rai

```
/note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
                                Sequence 10, Application US/07891174

| Patent No. 5317084
| GENERAL INFORMATION:
| APPLICAMT Mamoru TOMITA et al. TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: OF Fifteenth Street, N.W., #700 CITY: Washington STARE: D.C.
| COUNTRY: U.S.A. ZIP: D.O.S.
| COUNTRY: U.S.A. ZIP: D.O.S. COMPUTER READBLE FORM: MS-DOS COMPUTER: IBM COMPUTED: OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REFERENCE/DOCKET NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: MODIfied site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified site
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: ()not OTHER INFORMATION: (ye OTHER INFORMATION: thio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
STRAIN:
RESULT 15
US-07-891-174-10
```

```
IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

95.8%; Score 68; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 6.3e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 21, 2003, 07:50:36 Job time : 9.7 secs
                                                                                                                                                                                                                                                                                                                                       FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CFÓWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER:
                                                                                                                                                                                    JOURNAL:
                                                                                                                                                                                                         VOLUME:
                                                                                                                                                                                                                                                             PAGES:
```

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec

US-09-743-107B-81

1 CFOWOKNMRKVR 12 Perfect score: Sequence: 156504 seqs, 31069816 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

156504 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PUT NEW PUB.pep:*
3: \cgn2_6/ptodata/2/pubpaa/PUT NEW PUB.pep:*
4: \cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
5: \cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
6: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
8: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
9: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
10: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
14: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2. Appli	200	2	ı c		3.5	4	4	, ;		, ,	100	4.6	Segmence 58. Appl	Segmence 58. Anni	Segrence 58 Aprol	0 0	acducince 30, App.	Sequence 41002, A	Sequence 37353, A
ID	US-09-798-869-2	US-09-798-869-20	US-10-023-096-2	US-09-798-869-6	US-09-798-869-3	US-09-798-869-23	US-09-798-869-7	US-09-798-869-4	US-09-798-869-22	US-09-798-869-8	US-09-798-869-29	US-09-798-869-30	US-09-864-761-46393	US-10-066-500-58	US-10-002-796-58	US-10-066-273-58	TIS-10-066-494-58	110 00 00 111	US-09-864-761-41002	US-09-864-761-37353
h DВ	5	5	4	5	5	5	5	2	5	5	5	5	0 10	7	7	7	7		7	9 10
Lengt	٦	2	694	H	Η	Q	-	H	CI	-	H	-	40	74	74	747	74		•	239
Query Match Length DB	95.8	95.8	95.8	88.7	71.8	71.8	64.8	63.4	63.4	59.5	59.2	59.2	52.1	52.1	52.1	52.1	52.1	1		50.7
Score	68	68	68	63	51	51	46	45	45	42	42	42	37	37	37	37	37	70	ָ רח	36
Result No.	Н	7	3.	4	S	9	7	œ	თ	10	11	12	13	14	15	16	17	ď	9 4	13

Sequence 5, Appli Sequence 10267, A Sequence 10441, A Sequence 2, Appli		Sequence 13026, A Sequence 16, Appl Sequence 2, Appli Sequence 18, Appl	Sequence 19, Appli Sequence 2, Appli Sequence 60, Appl		Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 12, Appl Sequence 10, Appl Sequence 2, Appli
9 US-09-798-869-5 10 US-09-815-242-10267 10 US-09-815-242-10441 9 US-09-888-320-2	10 US-09-864-761-47985 10 US-09-864-761-44710 10 US-09-815-242-12129 10 US-09-815-242-12129	US-05-853 US-10-081- US-10-133-	9 US-10-133-912-19 10 US-09-265-606-2 9 US-10-001-189-60 9 US-10-028-072-38		0-176-921-3 0-137-8651-3 0-140-474-3 09-995-542-995-542-
31.9 44.34 489	525 525 525 525 525 525 525 525 525 525	351 447 723	723 760 933 1013	1013 1013 1013 1013	1013 1013 1013 2273 2310
4444 6.004 6.006 6.006	47.9 6.74 9.74 9.74	44.74 2.74 2.00 2.74	4 4 4 4 2 . 7 4 2	0.7444 0.7744 0.000	44444
3 3 2 2 2 2 2 2	ይ ይ ይ ይ 4 4 4 4 4	1 41 41 41 1 41 41 41	ი ო ო ო 4 4 4 4	0 0 0 0 0 0 4 4 4 4 4	' ಈ ಈ ಈ ಈ ಈ) ო ო ო ო ო ო
20 21 22 23	25 2 2 2 2 2 2 4 4 2 4 4 4 4 4 4 4 4 4 4	30.88	8 8 8 2 8 4 4	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3) द द द द द द 1 〇 L C E A R

ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.8%; Score 68; DB 9; Length 15; 91.7%; Pred. No. 2.8e-05; Live 1; Mismatches 0; Indels
                                                                                       APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LAKE VORLAND
TAPLICANT: LAKE VORLAND
TAPLICANT: LAKE VORLAND
TILLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSELED FOR Windows Version 4.0
                           ; Sequence 2, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
```

Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
APPLICANT: JOHN SIGHEN SVENDSEN
APPLICANT: (YSTEIN REKAAL); APPLICANT: BALDUR SVEINBJ (RNSSON) 3 CFOWORNMRKVR 14 1 CFQWQKNMRKVR 12 US-09-798-869-20 RESULT 2 à Пp

ö

```
RESULT 5
US-09-798-869-3
                                                                                                                                                                                               RESULT 4
US-09-798-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9-698-862-60-SD
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.8%; Score 68; DB 9; I
Best Local Similarity 91.7%; Pred. No. 4.6e-05;
Matches 11; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C.
         FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
FILE REFERENCE: 1001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NOS: 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10505/P58185C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASETPICATION:
FRICAR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Player, William E.
REGIETRATION UNDRER: 31,409
REFERENCE/DOCKET NUMBER: 1050:
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 639-6666
TELEPAX: (202) 339-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-10-023-096-2
LARS VORLAND
                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CHOWOKNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-023-096-2
```

```
0
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens OTHER INFORMATION: sequence)
                                                                        ·,
ch 95.8%; Score 68; DB 9; Length 694; 1 Similarity 91.7%; Pred. No. 0.0011; 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 88.7%; Score 63; DB 9; Length 15; 1 Similarity 91.7%; Pred. No. 0.00018; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 9; Length 15; 
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LAKS VORLAND
APPLICANT: LAKS VORLAND
APPLICANT: LAKS VORLAND
APPLICANT: LAKS VORLAND
APPLICANT: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: CB99818938.4
PRIOR APPLICATION NUMBER: CB9881838.4
PRIOR APPLICATION NUMBER: CB9881838.4
PRIOR APPLICATION NUMBER: CB98818938.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: (YSTEIN REXDAL
APPLICANT: ALALDY SVEINBAC(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE RERERENCE: A3404-PCT-USA-A
FILE REPERENCE: A3404-PCT-USA-A
FILE REPERENCE: A3404-PCT-USA-A
FILE OF INVENTION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR PELICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.8%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQKNMRKVR 12
                                    Best Local Similarity
Matches 11; Conserva
                                                                                                                                                 1 CFOWOKNMRKVR 12
                                                                                                                                                                                                               22 CFÓWORNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFOWOWNERVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15
TYPE: PRT
ORGANISM: CAPRINE
```

0

Gaps

0;

Indels

3; Mismatches

7; Conservative

Matches

```
63.4%; Score 45; DB 9; Length 15; 63.6%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.4%; Score 45; DB 9; Length 25; 63.6%; Pred. No. 0.25; 1; Mismatches 3; Indels
                                                                                                                                                                                                              APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: AJ4049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CTJGB99/02651
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: (YSTEIN REXDAL
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN REXDAL
APPLICANT: APLONG SVEINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCY AND SUBJECT OF 1097/199, 869
CURRENT APPLICATION NUMBER: US/09/799, 869
CURRENT FILING DATE: 2001-02-27
REIOR APPLICATION NUMBER: CT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
SROID NO 225
NUMBER OF SEQ ID NOS: 30
SOFTWARR: FRANCE OF CIT WINDOWS VETSION 4.0
                                                                                                                                                      ; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
1 CFQWQKNMRKV 11
                            3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQKNIMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWOKNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CLRWONEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-798-869-22
                                                                                                                                 US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                     Db
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: synthetic peptide (modified form of homo sapiens ) OTHER INFORMATION: sequence) US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.8%; Score 51; DB 9; Length 25; 63.6%; Pred. No. 0.027; 1; Indels cive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.8%; Score 46; DB 9; Length 15; Best Local Similarity 63.6%; Pred. No. 0.11; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN REKRAL

APPLICANT: LARS VORLAND
ITILE OF INVENTION: BLOACTIVE PEPTIDES
ITILE APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOPTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                     APPLICANT: (YSTEIN REKOAL
APPLICANT: (YSTEIN REKOAL
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT(GB99/02851
PRIOR APPLICATION NUMBER: RET(GB99/02851)
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSSISEQ for Windows Version 4.0
SCO ID NO 23
LENGTH: 25
                                                                                                                                                                                  ; Sequence 23, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION; APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 7, Application US/09798869; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.63
Matches 7; Conservative
                                1 CFQWQXXNMRKV 11
                                                                           3 CYOWORRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQKNIMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: CAPRINE
                                                                                                                                        RESULT 6
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-698-861-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

ö

;

Gaps ; 0

```
TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-46393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine protest INFORMATION: sequence)
US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.2%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.48; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.2%; Score 42; DB 9; Length 15; 63.6%; Pred. No. 0.48; artive 1; Mismatches 3; Indels
                                                                                  APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDOR SVEINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELSEQ for Windows Version 4.0
SSOTTWARE: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/09798869
| Publication No. US20030022821A1
| GENERAL INFORMATION:
| APPLICANT: (YSTEIN REKDAL
| APPLICANT: (YSTEIN REKDAL
| APPLICANT: BALDUR SVEINBJ (RNSON
| APPLICANT: BALDUR SVEINBJ (RNSON
| APPLICANT: LARS VORLAND
| TITLE OF INVENTION: BIOACTIVE PEPTIDES
| TITLE OF INVENTION: BIOACTIVE PEPTIDES
| CURRENT PELLING DATE: 2001-02-27
| PRIOR FILING DATE: 1999-08-31
| PRIOR FILING DATE: 1990-08-31
| PRIOR FILING DATE: 1990-08-31
| PRIOR FILING DATE: 1990-08-28
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: FRAESEQ FOR WINDOWS VERSION 4.0
                    ; Sequence 8, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 54...
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQKNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQKNIMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CLRWOWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-798-869-29
US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

RESULT 12 US-09-798-869-30

```
GENERAL INFORMATION
APPLICANT: Penn, Sharron G.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: URMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPERSES.OR ANALYSIS BY MICROARRAY
FILLE REFERENCE: Acond Ca. A.
CURRENT PLILING DATE: 2000-00-204
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.2%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.48; 2; Indels ive 3; Mismatches 2; Indels
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OWNSTRIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: CT/GB99/02851
PRIOR APPLICATION NUMBER: G99918938.4
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQUENCE: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 46393, Application US/09864761; Patent No. US20020048763A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQKNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CFRWOWRMKKL 13
```

```
·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130RL7
CURRENT APPLICATION NUMBER: US/10/066,500
PRIOR PILING DATE: 2002-02-01
PRIOR PELICATION NUMBER: 10/002,796
PRIOR PILING DATE: 2001-11-15
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR PLING DATE: 0/059314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                            FEATURE:

COTHER INFORMATION: MAP TO ACO18719.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PLACENTR, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 2.3

US-09-864-761-46393.1, EVALUE 9.00e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.1%; Score 37; DB 10; Length 40; 75.0%; Pred. No. 8; 1:ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
               PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PILICATION NUMBER: US 09/608,408
PRIOR PILICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 46593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58, Application US/10066500
Patent No. US20020177165A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: Luc Desnoyers
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wei-Qiang Gao
Hanspeter Gerber
Mary E. Gerritsen
Audrey Goddard
Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colin K. Watanabe
P.Mickey Williams
William I. Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 James Pan
Nicholas F. Paoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match.
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 POWDKNWR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 FQWQKNMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10-066-500-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-27
PRIOR PELING DATE: 1997-10-29
PRIOR PELING DATE: 1997-10-26
PRIOR PELING DATE: 1998-00-09
PRIOR PELING DATE: 1998-00-10
PRIOR PELING DATE: 1999-00-10
PRIOR PELING DATE: 1999-00-10
PRIOR PELING DATE: 1999-00-17
PRIOR PELING DATE: 1999-00-17
PRIOR PELICATION NUMBER: 60/14609
PRIOR PELING DATE: 1999-00-17
PRIOR PELICATION NUMBER: 60/14609
PRIOR PELING DATE: 1999-00-17
PRIOR PELICATION NUMBER: 60/14609
```

PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/886342
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: PCT/US98/14552
PRIOR FILING DATE: 1998-07-14 PRIOR APPLICATION NUMBER: PCT/US98/18824
PRIOR FILING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-14
PRIOR PLING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14 FILING DATE: 1998-09-16 APPLICATION NUMBER: PCT/US98/19437 APPLICATION NUMBER: PCT/US98/24855 PRIOR APPLICATION NUMBER: 09/158342
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR PELING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-10
PRIOR PLING DATE: 1999-10-08
PRIOR PLING DATE: 1999-10-03
PRIOR PLING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-09
PRIOR PLING DATE: 1999-03-09
PRIOR PLING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 09/254465
PRIOR APPLICATION NUMBER: 09/28465
PRIOR APPLICATION NUMBER: 09/33298
PRIOR PLING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/33298
PRIOR PLING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/33279
PRIOR PRING DATE: 1999-06-14
PRIOR PRING DATE: 1999-06-14
PRIOR PRING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14 PRIOR APPLICATION NUMBER: 09/808689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/866028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/870574
PRIOR FILING DATE: 2001-05-30 FILING DATE: 1999-11-12 APPLICATION NUMBER: 09/522342 FILING DATE: 2000-03-09 AFFALTING DATE: 2000-09-10 APPLICATION NUMBER: 09/665350 APPLICATION NUMBER: 09/709238 FILING DATE: 2000-11-08 APPLICATION NUMBER: 09/767609 FILING DATE: 2001-01-22 APPLICATION NUMBER: 09/802706 FILING DATE: 2001-03-09 PRIOR FILING DATE: 2001-05-30 PRIOR APPLICATION NUMBER: 09/872035 PRIOR FILING DATE: 2001-06-01 APPLICATION NUMBER: 09/548815 FILING DATE: 2000-04-13 FILING DATE: 2000-04-13
APPLICATION NUMBER: 09/664610 APPLICATION NUMBER: 09/403297 FILING DATE: 1999-10-18 APPLICATION NUMBER: 09/423741 APPLICATION NUMBER: 09/380138 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/380139 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/403296 FILING DATE: 1999-10-18 PRIOR FILING DATE: 1999-11-10 PRIOR APPLICATION NUMBER: 09/423844 1998-09-17 FILING DATE: 1999-08-25 FILING DATE: 1998-08-19

ö APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3.130R.IC.
CURRENT APPLICATION NUMBER: US/10/002,796
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115 Gaps ., Length 747; Query Match
52.1%; Score 37; DB 9; Length 747
Best Local Similarity 45.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR PLILING DATE: 1998-12-01
PRIOR PILING DATE: 1998-12-01
PRIOR PLILING DATE: 1998-12-25
PRIOR PLILING DATE: 1999-03-08
PRIOR PLILING DATE: 1999-03-08
PRIOR PLILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR PLILING DATE: 1999-06-02
PRIOR PLILING DATE: 1999-06-01
PRIOR PLILING DATE: 1999-09-01
PRIOR PLILING DATE: 1999-09-05
PRIOR PLILING DATE: 1999-09-05
PRIOR PLILING DATE: 1999-09-05
PRIOR PLILING DATE: 1999-09-05
PRIOR PLILING DATE: 1999-09-15 PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059589
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17 Sequence 58, Application US/10002796 Publication No. US20030032057A1 GENERAL INFORMATION: Timothy A. Stewart Daniel Tumas Colin K. Watanabe P.Mickey Williams William I. Wood APPLICANT: Avi J. Ashkenazi APPLICANT: Kevin P. Baker APPLICANT: David A. Botstein Luc Desnoyers Dan L. Eaton Napoleone Ferrara Wei-Qiang Gao Hanspeter Gerber Mary E. Gerritsen Paul J. Godowski Austin L. Gurney Ivar J. Kljavin Nicholas F. Paoni Margaret Ann Roy Jennie P. Mather Mary A. Napier Goddard Sherman Fond 311 CVRWQINSRRI 321 James Pan 1 CFOWOKNIMRKV 11 Audrey US-10-002-796-58 APPLICANT: APPLICANT ð

```
R FILING DATE: 1998-03-25
R APPLICATION NUMBER: 60/081049
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/09599
R FILING DATE: 1998-0-10
R FILING DATE: 1998-08-10
R FILING DATE: 1998-08-18
R FILING DATE: 1998-08-18
R RILING DATE: 1998-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R APPLICATION NUMBER: 60/106032
R FILING DATE: 1998-10-28
R APPLICATION NUMBER: 60/109304
R PILING DATE: 1998-11-20
R APPLICATION NUMBER: 60/125778
R FILING DATE: 1999-03-23
R APPLICATION NUMBER: 60/139695
R R FILING DATE: 1999-06-15
R APPLICATION NUMBER: 60/145070
R APPLICATION NUMBER: 60/145070
R FILING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R FILING DATE: 1997-10-29

R PELING DATE: 1998-00-114

R PELING DATE: 1998-00-14

R APPLICATION NUMBER: 09/136801

R APPLICATION NUMBER: 09/136804

R APPLICATION NUMBER: 09/136804

R FILING DATE: 1998-08-19
                                                                                             FILING DATE: 1997-10-27
APPLICATION NUMBER: 60/063733
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/066364
FILING DATE: 1997-11-21
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/066840
FILING DATE: 1997-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099803
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099811
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/063082
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/069694
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-12-16
APPLICATION NUMBER: 60/074086
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-02-09
APPLICATION NUMBER: 60/074092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-08-19
APPLICATION NUMBER: 09/136828
FILING DATE: 1998-08-19
APPLICATION NUMBER: 09/158342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-02-09
APPLICATION NUMBER: 60/079294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/100858
FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/101922
FILING DATE: 1998-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/149396
FILING DATE: 1999-08-17
APPLICATION NUMBER: 60/169495
FILING DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/145698
FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-12-07
APPLICATION NUMBER: 08/918874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/099812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-08-26
APPLICATION NUMBER: 08/933821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-09-21
APPLICATION NUMBER: 09/180997
FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997 -09-19
APPLICATION NUMBER: 08/960507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/202088
FILING DATE: 1998-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/254311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
PRIOR
```

FILING DATE: 2001-06-19
APPLICATION NUMBER: PCT/US98/14552
FILING DATE: 1998-07-14
APPLICATION NUMBER: PCT/US98/18824
FILING DATE: 1998-09-10 APPLICATION NUMBER: PCT/US98/25190 FILING DATE: 1998-11-25 APPLICATION NUMBER: PCT/US99/05028 FILING DATE: 1999-03-08 APPLICATION NUMBER: PCT/US99/12252 FILING DATE: 1999-06-02 APPLICATION NUMBER: PCT/US98/19093 FILING DATE: 1998-09-14 APPLICATION NUMBER: PCT/US98/19330 FILING DATE: 1998-09-16 APPLICATION NUMBER: PCT/US98/19437 FILING DATE: 1998-09-17 FILING DATE: 1998-11-20 APPLICATION NUMBER: PCT/US98/25108 APPLICATION NUMBER: PCT/US98/24855 PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-10-08
PRIOR PRILING DATE: 2000-11-08
PRIOR PILING DATE: 2001-01-22
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-05-26
PRIOR PELING DATE: 2001-05-26
PRIOR PELING DATE: 2001-05-30
PRIOR PELING DATE: 2001-05-26
PRIOR PELING DATE: 2001-05-30
PRIOR PELING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR PILING DATE: 1001-06-19
PRIOR PILING DATE: 1001-06-19
PRIOR PILING DATE: 1098-09-14
PRIOR PILING DATE: 1098-09-14
PRIOR PILING DATE: 1998-09-14
PRIOR PILING DATE: 1998-09-14 'ILING DATE: 1999-03-03 PPLICATION NUMBER: 09/254460 'ILING DATE: 1999-03-09 APPLICATION NUMBER: 09/254465 FILING DATE: 1999-03-05 APPLICATION NUMBER: 09/284663 FILING DATE: 1999-04-15 APPLICATION NUMBER: 09/332928 FILING DATE: 1999-06-14
APPLICATION UNBER: 09/332929
FILING DATE: 1999-06-14
APPLICATION NUMBER: 09/333075 FILING DATE: 1999-06-14
APPLICATION NUMBER: 09/333077
FILING DATE: 1999-06-14
APPLICATION NUMBER: 09/380137
FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/380138 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/380139 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/403296 APPLICATION NUMBER: 09/522342 FILING DATE: 2000-03-09 APPLICATION NUMBER: 09/548815 FILING DATE: 2000-04-13 APPLICATION NUMBER: 09/664610 FILING DATE: 1999-10-18 APPLICATION NUMBER: 09/403297 FILING DATE: 1999-10-18 APPLICATION NUMBER: 09/423741 FILING DATE: 1999-11-10 APPLICATION NUMBER: 09/423844 FILING DATE: 1999-11-12 FILING DATE: 2000-09-18
APPLICATION NUMBER: 09/665350 FILING DATE: 1998-12-01 PRIOR PRIOR

```
prior Application NUMBER: PCT/US99/20111

prior Application NUMBER: PCT/US99/20594

prior Application NUMBER: PCT/US99/20594

prior Filing Date: 1999-09-08

prior Filing Date: 1999-09-08

prior Application NUMBER: PCT/US99/21547

prior Application NUMBER: PCT/US99/21547

prior Piling Date: 1999-09-15

prior Application NUMBER: PCT/US99/28301

Query Match

$2.1\%; $core 37; DB 9; Length 747;

Best Local Similarity 45.5\%; Pred. No. 1.3e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps

Qy 1 CFQWOKNMRKV 11

Db 311 CVRWQINSRR 321

Search completed: February 21, 2003, 08:08:07

Search completed: February 21, 2003, 08:08:07
```

0;

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-81 71 1 CFQWQKNMRKVR 12 Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	lactotransferrin p	a:	1	Q		\vdash				įυ	hypothetical prote	$^{\circ}$	l pro		1 41		outer membrane lin	hypothetical prote	33.3K hypothetical	cysteine synthase	3-deoxy-manno-octu	histidyl-tRNA synt				trichohvalin like			I (E
SUMMARIES	ID	TFHUL	852107	JC2323	A28438	T08030	T19429	AB0858	C84325	T22597	D72378	AD2346	T14803	T04018	H97451	AB2670	AG3441	D82109	F90580	G86403	T47233	D71876	F81660	G86506	G72115	T28820	B85431	C97838	D71535	KHRTL
	DB C							7				2						7									2			4
	Length	711	č	708	10.	456	68.	511	287	27	283	298	113	1274	206	206	208	211	282	28	31	39.	426	75	75	933	1433	9	Н	
oko	Query Match	•	76.1	ä	63.4	B	0	59.5	σ	7	4.	4.	4.	4.	ω.	ω.	٠ ش	53.5	ъ,	ë.	e.	'n	ά.	ω.	m.	m.	ω,	52.1	ď	52.1
	Score	68	54	51	45	45	43	42	42	41	39	39	39	39	38	38	38	38	38	38	38	38	38	38	38	38	38	37	37	37
	Result No.	-	7	m	4	Ŋ	9	7	œ	6		11	12	13	14		16	17	18	19	20	21	22	23	24	25	26	27	28	

cathepsin L (EC 3.	hypothetical prote	glutamine syntheta	3-deoxy-manno-octu	probable era/thdf	hypothetical prote	diphosphate-fructo	outer capsid prote	hypothetical prote	cell cycle arrest	cytochrome P450 ho	probable tyrosine	hypothetical prote	probable protein k	cytochrome P450-li	probable cytochrom
KHMSL	T29571	G97649	E64639	T50146	T46261	T01470	A45687	T33605	A39654	T04734	C71467	S50977	B96547	T49978	B84514
Н	73	N	7	7	7	~	~	~	Н	7	7	~	N	~	7
334	361	367	393	496	570	583	749	120	306	338	415	431	476	500	518
52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7
37 52.1				37 52.1									36 50.7		

ALIGNMENTS

RESULT 1

TFHUL lactoransferrin precursor [validated] - human lactoransferrin precursor [validated] - human NiAlternate names: lactoferrin CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000 CiAccession: G01394; S11228; Ā45401; S10324; S15853; S20841; S07160; A61169; Submitted to the EMBL Data Library, March 1994 A; Accession: G01394 A; Accession: G01394 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-711 - CFHO> A; Anolecule type: mRNA A; Residues: 1-711 - CFHO> A; Anolecule type: mRNA A; Residues: 1-711 - CFHO> A; Anolecule type: mRNA A; Residues: Anolecule

A31000; S74

R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
Nucleic Acids Res. 18, 5288, 1990
A;Title: Complete nucleotide sequence of human mammary gland lactoferrin. A;Reference number: S11228; MUID:90384839; PMID:2402455
A;Accession: S11228

A, Molecule type: mRNA A, Residues: 1-148, 'T'.150-422,'C',424-711 (REY> A, Cross-references: EMBL:X53961; NID:g34416; PIDN:CAA37914.1; PID:g34416 A, Cross-references: EMBL:X53961; Nulser, D.; Panella, T. Mol. Endocrinol. 6, 1969-1981, 1992 A, Title: Differential molecular mechanism of the estrogen action that regulates lactofer: A, Reference number: A45401; MUID:93125571; PMID:1480183

A;Molecule type: DNA A;Residues: 1-15 <TEN>

A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A;Experimental source: placenta A;Experimental source: placenta A;Note: sequence extracted from NCBI backbone (NCBIP:122202) R;Powell, M.J.; Ogden, J.E. Nucleic Acids Res: 18, 4013, 1990 A;Title: Nucleicide sequence of human lactoferrin cDNA. A;Reference number: S10324; MUID:90326549; PMID:2374734

A; Molecule type: mRNA

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 20-31 <ST1>A;Residues: 20-31 <ST1>A;Accession: S20841 A; Accession: S15853

A; Melecule type: protein A; Residues: 20-28,'X',30-31 <ST2>

```
76.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.68;
      Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 63.6
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lactoferrin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M74778
                                                                                                                                       1 CFOWOKNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 CYQWQRRMRKL 48
                                                                                                                                                                                                 19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQKNIMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQKNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-15 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JC3323
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A28438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: A41205
                                                                                                                                                                                                                                                                                                                                                                   lactoferrin - goat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 436-487, 'A', 489-711 <RAD>
A; Residues: 436-487, 'A', 489-711 <RAD>
A; Cross-references: EMBL:ML8642; NID:g186815; PIDN:AAA86665.1; PID:g186855
B; Penrla, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 20-140,142-169,171-203, 'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A; Note: this is the final paper in a series
R; Houen, G.; Heegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Blochem. 241, 303-308, 1996
A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A; Reference number: S74119; MUID: 97054624; PMID: 8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: duplication; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SiG>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;39-65,39-56,135-218,177-193, 190-201, 251-265,593-699,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                          띹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Experimental source: normal breast tissue
R.Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
R.Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Bru. J. Blochen. 145, 659-666, 1984
A.Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A.Reference number: A31000, MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isoladrion and characterization of sheep lactoferrin, an inhibitor of platelet A;Accession: S52107; MUID:95127729; PMID:7827104
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-933, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: protein
A;Redues: 1-33 <QIA-
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 3q21-3q23
C,Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68; DB 1; I
Pred. No. 0.00054;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: not compared with conceptual translation A,Molecule type: mRNA
A,Residues: 3-701,'SWKPVN' <PAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Cross-references: GDB:119368; OMIM:150210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.75
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 CPÓWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A61169
                                                                                                                                A; Accession: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A31000
```

```
NAIternate names lactorransferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41205
R;Pentecost, B.T.; Teng, C.T.
J:Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactorransferrin is the major estrogen inducible protein of mouse uterine secretic anumber: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assignment of the relevant locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-708 <LEP>
C;Superfamily: transferrin repeat homology
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
C;Keywords: duplication; glycoprotein
E;355-696/Domain: transferrin repeat homology <TRH2>
F;355-696/Domain: transferrin repeat homology <TRH2>
                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Resdidues: 3-707 APBN>
A;Cross references: BMBL:J03298
R;Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb_1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;I-19/Domain: signal sequence #status predicted <SIG>
F:20-707/Product: lactotransferrin repeat homology <TRH2>
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.4%; Score 45; DB 1; Length 707; 63.6%; Pred. No. 5.9; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.8%; Score 51; DB 2; Length 708; 63.6%; Pred. No. 0.52;
Score 54; DB 2; Length 33;
Pred. No. 0.0069;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: UC2323
R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin CDNA:
A;Reference number: UC2323; MUID:94380047; PMID:8093048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 CLRWONEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
Cispecies: Halobacterium sp. NRC-1
Cibate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001
Cipate: 03-Feb-2001 #sequence_revision 02-Feb-2001
Cipate: 03-Feb-2001 #sequence 03-Feb-2001
Cipate: 03-Feb-2001 #sequence 03-Feb-2001
Cipate: 03-Feb-2001 #sequence 04-Feb-2001
Cipate: 03-Feb-2001 #text_change 03-Feb-2001
Cipate: 03-Feb-2001 #text_change 03-Feb-2001
Cipate: 03-Feb-2001
Cipat
                           R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-584 <STO>
A;Crosa-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1732C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Residues: 1-275 <WIL>
A.Residues: 1-275 <WIL>
A.Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F53H4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: i5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 2; Length 511;
Pred. No. 14;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.2%; Score 42; DB 2; Length 584; 50.0%; Pred. No. 16; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RjDobson, R. submitted to the EMBL Data Library, October 1996 A;Reference number: 219587 A;Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 CFAWDMINKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 CFTWRKDMERKR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWOKNIMIRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWOKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-511 <PAR>
                                                                                                                                                                                                                                                                                                                                     A; Accession: AB0858
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
C; Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP: F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
Пр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
```

```
dynein beta heavy chain - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: T08030
B;Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: Z16302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Nap position: IX
A;Nap position: IX
A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
A;Introns: 486/3; 3882/3; 4240/3
S;334/4; 3686/3; 3882/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
C;Reywords: nucleotide binding; P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein STX3070 [imported] - Salmonella enterica subsp. enterica serovar Ty
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z81475; PIDN:CAB03914.1; GSPDB:GN00021; CESP:C24H11.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Species: Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R'Lloyd, C.
submitted to the EMBL Data Library, November 1996
A'Reference number: Z19123
A'Reference number: Z19123
A'Reference number: Yreinslated from GB/EMBL/DDBJ
A'Molecule type: DNA
A'Molecule type: DNA
                                                                                                                                                                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4568 <MIT>
A;Cross-references: EMB::U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 2; Length 4568;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
60.6%; Score 43; DB 2; Length 681;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C24H11.8 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain 21gr C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone C24H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1852 CFÓWÓSQLŔYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 6; Conserv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 OWOKNIMIRKUR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP: C24H11.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
```

```
phytochrome C - sorghum
C;Species: Sorghum bicolor (sorghum)
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T14803
R;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet submitted to the EMBL Data Library, April 1996
A;Reference number: Z18186
A;Accession: T14803
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F17A8.60 - Arabidopsis thaliana (S.Speciese Arabidopsis thaliana (mouse-ear cress) (S.Speciese Arabidopsis thaliana (mouse-ear cress) (S.Speciese 130-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 (S.Accession: T04018 (S.Esvan, M.) Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.: submitted to the Protein Sequence Database, March 1999 A;Reference number: 215184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regula:
F;65-581/Domain: phytochrome homology <PHY>
F;321/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (st. C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens (st. C;Species: Agrobacterium tumefaciens 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: H97451
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 233-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%; Score 39; DB 2; Length 1135; 45.5%; Pred. No. 1.1e+02; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%; Score 39; DB 2; Length 1274; 60.0%; Pred. No. 1.2e+02; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   A, Residues: 1-1135 <CHI>A, Cross-references: EMBL:U56731; NID:g1800218; PID:g1800219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1274 <BEV>
A;Cross-references: EMBL:AL049482
A;Experimental source: cultivar Columbia; BAC clone F17A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.5;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       775 CLEWNKAMQKI 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWOKNIMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           968 FINWOKINKI 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FOWOKNIMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 55/3; 801/1
A;Note: F17A8.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                        ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
```

```
sugar ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: Il-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72378
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Accession: D72378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-283 <ARN>
A;Cross-references: GB:AE001721; GB:AE000512; NID:g4980922; PIDN:AAD35505.1; PID:g498092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RiKaneko, T.; Nakamura, Y.; Wolk, C.D.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A. Rice. 8, 205-213, 2001
A. Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A. Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AD2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-298 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
   57.7%; Score 41; DB 2; Length 275; 63.6%; Pred. No. 11; 2; Indels ative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.9%; Score 39; DB 2; Length 298;
66.7%; Pred. No. 28;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 2
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: TM0420
C;Superfamily: maltose transport protein malG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.98;
66.78;
                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                    262 FOWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 399, 323-329, 1999
                                                                                                                        2 FOWOKNIMRKVR 12
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 FHWORNYRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 WOKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOKNSEKIR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FQWQKNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: AD2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: alr4323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
```

```
,
0
A, Cross-references: GB: AE007869; PIDN: AAK86569.1; PID:g15155733; GSPDB:GN00169
                                                                                                                                                                                                       0; Gaps
                                                                                                                                        Query Match
Best Local Similarity 50.0%; Pred. No. 28; Matches 6; Conservative 2; Mismatches 4; Indels
                        C;Genetics:
A;Gene: AGR C 1381
A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
```

1 CFOWOKNWRKVR 12

à

88 CHWKSLRROVR 99 OP

C;Genetics: A;Gene: pdxH

A,Map position: circular chromosome C,Superfamily: pyridoxamine-phosphate oxidase

Query Match
53.5%; Score 38; DB 2; Length 206;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 4; Indels

·,

0; Gaps

1 CFOWOKNMRKVR 12

88 CFHWKSLRRQVR 99

Search completed: February 21, 2003, 07:47:53 Job time: 9.65 secs

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-81 71 Title: Perfect score:

1 CFQWQKNMRKVR 12 Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

																													٠						
	Description		damelis dro		_			-				chlamydia	-					_											owninin on	CIWILLA CAL	escherichia	SALMONELLA	haemophilus	bacillus st	saccharomyc
	scri	207700	091110	9477	P08071	7 7 9 5 6 5	077811	D93528	08r9u1	7070	91.19	084281	6797	7154	9910	Ogute7	4916	09x218	P26448	035186	1000	019020	1187	P12174	P16530	3333	P53661	P37146	157110	20233	51003	000	P44693	N.	7214
	De	100	4 0	36	Ω	Š	35) <u>6</u>	08	P5	6	8	P0	PO	010	9	ò	Č	P2	03	5	56	7.4	á	2	0	P.5.	D3	5	1 0	4 6	4 6	1 6	000	P1.7
SUMMARIES	ID	TRFL HIMAN		TRFL CAPHI	TRFL MOUSE	DYHB CHLRE	TRFL HORSE	PHYC SORBI	RL28_THETN	LOLB VIBCH	SYH CHLMU	NORG CHLTR	CATL_MOUSE	CAIL RAT	YKYL CAEEL	MSS1_SCHPO	VP4 ROTGA	NLA_DROME	BUB2 YEAST	CATK_RAT	YBX7 SCHPO	DYHC CAREL	RPOB_LIBAF	FDOI_ECOLI	PELX ERWCA	YBM9_SCHPO	Y125 MYCCA	RIR4 ECOLI	PEL2 ERWCA				TOUR BACE	GEORGE DACOL	
	DB	įH						Н											٦																
	Query Match Length	711	708	708	707	4568	695	1135	62	211	428	316	334	334	455	496	749	292	306	329	962	4568	146	211	238	238	267	319	374	434	434	475	48.5	0 0)
ж	Query Match	95.8	71.8	71.8	63.4	63.4	9.09	54.9	53.5	53.5	53.5	52.1	52.1	52.1	52.1	52.1	52.1	50.7	50.7	0	0	O	σ	49.3	49.3	σ	σ	g	49.3	49.3	49.3	49.3	49.3	O	١
	Score	9	51	51	4.5			39	38	86	80 i	37	7.5	37	37	37	37	36	36	36	36	36	32	32	35	35	35	32	35	35	35	35	35) }
	Result No.		7	m	4	2	9	7	ω (, ע	10	7 7	77	L13	T T	15	91	17	18	19	50	21	22	23	24	25	526	2.1	28	29	30	31	32	33	

[7]
SEQUENCE FROM N.A.
TISSUE=Prostate;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[8]

P14632 sus scrofa O77698 bubalus bub Q00020 broad bean P13217 drosophila Q92wi9 oryza sativ Q99wi9 oryza sativ Q99wi9 staphylococ P45390 escherichia P21159 myxococcus P12342 bos taurus
TRFL BUBBU VIA BBMV PIPA DROME PHYC ORYSA BP28 DROME RL28 BACST RL28 LISMO RL28 SISMO RL28 SISMO YRBC ECOLI PDXH MYXXA IL2A BOVIN
ਜਜਜਜਜਜਜਜਜਜ
704 708 966 1095 11137 2096 60 62 62 211 270
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
w w w w w w w w w w w w w w w w w w w
E W W W W W 4 4 4 4 4 4 4 N D C B D O L C W 4 R

ALIGNMENTS

```
PubMed=9873069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S11228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           llcT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1LFG;
1LFH;
1LFI;
1LGB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1LGC;
1BKA;
1DSN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
PDB;
              McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen E., Gibbs R., Schutz K., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzzy D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Diaga-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       and
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90064528; PubMed=2585506; Anderson B.F., Baker E.N.; Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.; Structure of human lactofernin: crystallographic structure analysis and refinement at 2.8-A resolution."; Mol. Biol. 209:711-734 (1989).
                                                                                                                                                                                                                                                                                                                                   Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                        "The present state of the human lactotransferrin sequence. Study alignment of the cyanogen bromide fragments and characterization N- and C-terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rado T.A., Wei X., Benz E.J. Jr., "Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-
253-->methionine mutant.";
                                                                                                                                SEQUENCE OF 20-711.

MEDLINE=85076667; PubMed=6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
                                                                                                                                                                                                                                                                                              PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jolles P.; "An 88 amino acid long C-terminal sequence of human
                                   MEDLINE=90326549; Pubmed=2374734;
Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 670:243-254 (1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; PubMed=10089347;
                                                                                                 Nucleic Acids Res. 18:4013-4013(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                            J. Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                    MEDLINE=82046817; PubMed=6794640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 436-711 FROM N.A. MEDLINE=88001031; PubMed=3477300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=82262043; PubMed=7049727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 142:107-110(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 237-711 FROM N.A.
  SEQUENCE OF 3-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blood 70:989-993(1987)
                        gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 609-711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lactotransferrin.";
                  TISSUE=Mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resolution."
                                                                                                                                                                                                                                                                                                                                                            Jolles P.;
RY REPRETARY FOR THE SERVICE S
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensesisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alintworth G.K., Sommer J.R., Obrian G., Han D., Ahmed M.N., Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y., Sugar J., Kunaramanickavel G., Munier F., Schorderet D.F., El Matri L., Lwaramanickavel G., Munier F., Schorderet D.F., Hejtmancik J.F., Teng C.T.; Farst M., Nagata M., Nakayasu K., Hejtmancik J.F., Teng C.T.; Farst G.T.; Far
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opicid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99192677; PubMed=10089508; Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.; Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.; "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from human lactoferrin,";
Agric. Biol. Chem. 54:1803-1810(1990).
                                                                                                                                                                                                       Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF332168; AAG48753.1; -. BC015822; AAH15822.1; -. BC015823; AAH15823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U07643; AAB60324.1; -... BMBL; M93100; AAA36159.1; -... BMBL; M83202; AAA5855.11; -... EMBL; M18642; AAA8665.1; -... EMBL; M18642; AAA86665.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M73700; AAAS9479.1; -. X52941; CAA37116.1; -. U95626; AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS THR-30 AND ARG-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X53961; CAA37914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-94.
31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-93.
```

ო

```
DISULFID
DISULFID
DISULFID
                                                                          DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                       METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                      Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                                                                                                                           STRAIN=Somal; TISSUE=Lactating mammary gland; Kappeler S.R., Ackermann M., Farah Z., Puhan Z.; "Sequence analysis of camel (Camelus dromedarius) lactoferrin."; Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR01156; Transferrin.
Pfam; PF00405; transferrin, 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PR05ITE; PS00205; TRANSFERRIN. 1; 2.
PR05ITE; PS00206; TRANSFERRIN. 2; 2.
PR05ITE; PS00207; TRANSFERRIN. 3; 2.
PR05ITE; PS00207; TRANSFERRIN. 3; 2.
                                          0;
   Query Match 95.8%; Score 68; DB 1; Length 711; Best Local Similarity 91.7%; Pred. No. 0.00024; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OTW-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.
BY
BY
BY
BY
BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ131674; CAB53387.1; -.
EMBL; AF165879; AAF82241.1; -.
HSSP; O77811; 1B1X.
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
708
3363
708
64
64
192
200
264
399
                                                                 1 CFQWQKNMRKVR 12
                                                                                                  39 CFOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384
384
384
388
388
1134
1176
1189
367
                                                                                                                                                                                CAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
                                                                                                                                                RESULT 2
TRFL_CAMDR
                                                                                                                                                                            PPAGE STATE STATE
```

```
TISSUE-Mammary gland;

MEDLINE-94380047; PubMed=8093048;

le Provost F., Nocart M., Guerin G., Martin P.;

"Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 synteny group.";

Blochem. Blophys. Res. Commun. 203:13241332(1994).

-! FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARRENAIT.

-! SUBUNIT: MONOWER (BY SINTLARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Ammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F - S (IN REF. 2)

G - A (IN REF. 2)

G - S (IN REF. 2)

ILLS - > PLF (IN REF. 2)

L - > F (IN REF. 2)

A - > P (IN REF. 2)

A - > P (IN REF. 2)

A - > Q (IN REF. 2)

A - > Q (IN REF. 2)

W, 0BOCLT5A0B69D430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                  IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC...) (N-LINKED (GLCNAC....) (N-LINKED (GLCNAC....) (N-LINKED (GLCNAC....) (N-LINKED (GLCNAC....) (N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TREL CAPHI

ID TREL CAPHI

AC Q29477; Q29479;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DUN-2002 (Rel. 41, Last annotation update)

DE Lactotransferrin precursor (Lactoferrin).
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                SIMILARITY
                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |||: |:|||
38 CAQWQRRMKKVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CFOWOKINIRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642 6
708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

0

```
Moriishi
                          RESULT 4
TRFL MOUSE
                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                             EMBL, X78902; CAASSSI7.1; -.
EMBL, X78902; CAASSSI7.1; -.
Interpror, IPRO91156; Transferrin.
Ffam, PRO0405; transferrin; 2.
PRINTS; PRO0422; TRANSFERRIN.
SNART; SN00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00206; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 1; Length 708; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I -> V (IN REF. 2).
L -> R (IN REF. 2).
Q -> K (IN REF. 2).
S -> R (IN REF. 2).
S -> R (IN REF. 2).
D -> G (IN REF. 2).
I, FZEDA3CB3539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
  TWO HOMOLOGOUS DOMAINS.
TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                         BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC)
                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                    SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
I -> V (IN
L -> R (IN
Q -> K (IN
F -> P (IN
                                                                                                                                                                                                                                                              77358 MW;
                                                                                                       EMBL; U53857; AAA97958.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.8%;
63.6%;
   DOMAIN: COMPOSED OF SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414
708 AA;
                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                               Signal.
SIGNAL
                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-14 FROM N.A.

MEDIAINE=92042099; PubMed=1939212;

Liu Y., Teng C.T.;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266:21880-21885(1991).

-I- FUNCTION: TRANSPERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ALOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pentecost B.T., Teng C.T., "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
TRFL MOUSE STANDARD; PRT; 707 AA. P08071; P70690; Q61799; Q922P2; 01-AUG-1988 (Rel. 08, Created) 15-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last amnotation update) Lactotransferrin precursor (Lactoferrin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
LACTOTRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, PO2788; 1CB6.
MD) MG1:96837; Ltf.
Interpro, IPRO1156; Transferrin.
FEam; PRO0405; transferrin; 2.
PRINTS; PRO0422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, J03298; AAA40525.1; -.
EMBL, D88510; BAA13633.1; -.
EMBL, BC006904; AAH06904.1; --
EMBL, M7478; AAA39427.1; --
PIR; A28438; A28438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
707
357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uterine secretions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIĞNAL
CHAIN
REPEAT
                            HILLER BERNER BE
```

ö

Gaps

;

1; Indels

Mismatches

3,

Conservative

Best Local Similarity

Matches

1 CFOWOKONMRKV 11 CYOWORRMRKL 48

ð g

38

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain genes.";
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
DYNEIN HAS APPASE ACTIVITY.
-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 1; Length 707; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        F26AE0340A4C19A8 CRC64;
                                                                                                                                                                                                                                                                                                     ANION (POTENTIAL).

N-LINKED (GLCNAC. .) (1
N-LINKED (GLCNAC. .) (1
N-LINKED (GLCNAC. .) (1
NR -> 1QG (IN REF. 1).

R -> Q (IN REF. 2).

M -> L (IN REF. 2).

S -> T (IN REF. 2).
                                                                                                                                                                                                      IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
   2.
BY SIMILARITY.
                                                                                                                                                                                 SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 4568 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                        77865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.4%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ODA4 OR ODA-4 OR SUPI
                                                                                                                                                                                                                                                                                                                                                                                                              449
629
707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQKNWRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 CLRWQNEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYHB CHLRE
Q39565;
REPEAT
DISULFID
                                                           DISULFID
DISULFID
                                                                                                                    DISULFID
                                                                                                                                                                  DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
SEQUENCE
                         DISULFID
                                               DISULFID
                                                                                 DISULFID
                                                                                            DISULFID
                                                                                                         DISULFID
                                                                                                                                            DISULFID
                                                                                                                                                         DISULFID
                                   DISULFID
                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                              METAL
METAL
METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                 BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYHB_CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

0;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Enropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resolution.";
J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99296631; PubMed=10366507;
Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eŭkaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus
                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
MICROTUBLIA-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                              EMBL; U02963; AAA19956.1; -.
InterPro; IPR004273; Dynein heavy.
Pfam; PF03028; Dynein heavy; 1.
Colled coil.
Microtubules; Dynein; ATP-binding; Flagella;
DOMAIN 277 293 COLLED COLL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.4%; Score 45; DB 1; Length 4568; 50.0%; Pred. No. 15;
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 50.0
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1650
1825
2045
2045
3162
3425
3425
3728
1926
2209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||| :| ::
1852 CFQWQSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2831
3106
3339
3648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISSUE=Milk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRFL HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  077811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
TRFL_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE OF THE SET OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                            PROSITE; PS00205, TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_3; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07BB84D50E1B165D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .)
(GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                           LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                IRON 1 (BY S IRON 1 (BY S IRON 1 (BY S IRON 1 (BY S IRON 2 (BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANION (BY N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANION
                                                                                                          InterPro; IPR01156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_EER; 2.
                                                                          EMBL; AJ010930; CAA09407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.30,
-20 7; Conservative
                                                                                                                                                                                                          PDB; 1B1X; 02-DEC-98.
PDB; 1B7U; 02-FEB-99.
PDB; 1B7Z; 02-FEB-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 CAKFORNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             695 AA;
                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                          DISULFID
DISULFID
                                                                                                                                                                                                                                                                                           DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
SEQUENCE
                                                                                                                                                                                        NON TER
SIGNAL
                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
BINDING
                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                               METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
                                                                                                                                                                                                                                                                                                   PAYCOCHLOROPHYLLIDE REDUCTASE.

PLACE RESPONSES.

PLOCHTON THE TREE REGIONARY PROTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ABSONBS MAXIMALLY IN THE RED REGION OF THE SPECTROM AND THE PER FORM THAT ABSONBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF RIN PER INDUCTS AN ARRIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF RIN PER INDUCTS AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBBANT OF RIBLIAGES BISPHOSPHATE CARBOXYLASE, CHLOROPHYLLI A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- PTM: CONTAINS ONE COVALENTY LINKED TETRAPYRROLE CHROMOPHORE.
-!- SIMILARITY: BELONGS TO THE PHYTOCHROWE FAMILY.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARMT-SIM) DIMERIZATION DOMAINS.
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOWAIN.
-!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                      MEDLINE=97198556; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.E.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAM; PRO1590; GAP; 1.

PEAM; PRO1518; HATPABGE C; 1.

PRINTS, PRO1033; PHYTOCHROME.

SMART; SM00065; GAF; 1.

SMART; SM00387; HATPABG C; 1.

SMART; SM00388; HisRA; I.

SMART; SM00091; PAS; 2.

TIGREAMS; TIGR00229; BENBOTY, box; 2.

PROSITE; PS50112; PAS; 2.
                                                                          Sorghum bicolor (Sorghum) (Sorghum vulgare)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, US6731, AAB41399.1, ...
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR0031018; GAF.
InterPro; IPR004359; HIS KIN sig.
InterPro; IPR003661; His Kin sig.
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR001294; PAS domain.
Pfam, PF00360; phytochrome.
Pfam, PF00360; phytochrome; 1.
Pfam; PF00369; phytochrome; 1.
Pfam; PF00989; PAS; 2.
                                                                                                                                           Panicoideae; Andropogoneae; Sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Multigene family.
DOMAIN 618 688
16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
Phytochrome C.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
```

HISTIDINE KINASE

PRT; 1135 AA.

PHYC_SORBI STANDARD; P93528; 16-OCT-2001 (Rel. 40, Created)

PHYC_SORBI

g

à

```
EMBL; AE004289; AAF95326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VC2181; -. Pro; IPR004565; Lolb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03550; LolB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FOWOKNIMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Nigg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 FOWOKSPOKL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCB1_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HISS OR TC0830
                                                                                                                                                                                                                                      cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MoPn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYH CHLMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HisRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYH_CHLMU
                           RAMANA BERNARA BERNARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21992816; PubMed=11997336; Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Mang J., Yu J., Yang H.; "A complete sequence of T. tengcongensis genome."; Genome Res. 12:689-700(2002).

-! SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                               Score 39; DB 1; Length 1135;
Pred. No. 41;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoanaerobacter tengcongensis,
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
  321 321 CHROMOPHORE (BY SIMILARITY).
1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.5%; Score 38; DB 1; Length 62; 60.0%; Pred. No. 3.3; Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         15-UUN-2002 (Rel. 41, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Sobsonal protein L28.
RPMB OR TIE1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOLB VIBCH STANDARD; PRT; 211 AA. 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) outer_membrane lipoprotein lolb precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=E1 Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE013107; AAM24713.1; -.
                                                                            54.98;
                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                 775 CLEWNKAMOKI 785
                                                                                                                                                                               1 CFQWOKNYMRKV 11
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|: |:|||
27 RWKPNIRKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOLB OR VC2181.
                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                    RL28 THETN
                           SEQUENCE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                        QBR9U1;
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOLB VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
```

AC DT DT DT DT DT DT DT DT DT RN RN RN RN RN RX

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Einla S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D. Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chaperone; Outer membrane; Lipoprotein; Transport; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                        Nature 406:477-483(2000).

-!- FUNCTION: PLAYS A CRITICAL ROLE IN THE INCORPORATION OF LIPOPROTEINS IN THE OUTER MEMBRANE AFTER THBY ARE RELEASED BY THE LOLA PROTEIN (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                          "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.

OUTER-MEMBRANE LIPOPROTEIN LOLB.

"TGT.YCERIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000)
-!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
diphosphate + L-histidy1-tRNA(His).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.5%; Score 38; DB 1; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 27 N-ACYL DIGLYCERIDE (BY SIN 211 AA; 24379 MW; F1EF70858484177E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anchor (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.0%; Pred. No. -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
```

TIGE;

SO WENT HERE AND THE COURT OF T

Matches

à d RESULT 11

HID DESCRIPTION OF COLOR OF THE SERVICE OF THE SERV

·-

Gaps

0;

1; Indels

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP).
                                                                                                                                                                                                                                                                                                   Flavoprotein; FMN; Transmembrane; Inner membrane; Complete proteome.
TRANSMEM 13 35 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87033683; Pubmed-3533924;
Portnoy D.A., Erickson A.H., Kochan J., Ravetch J.V., Unkeless J.C.;
"Cloning and characterization of a mouse cysteine proteinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Joseph L.J., Chang L.C., Stamenkovich D., Sukhatme V.P.; "Complete nucleotide and deduced amino acid sequences of human and turine preprocathepsin L. An abundant transcript induced by transformation of fibroblasts.", J. Clin. Invest. 81:1621-1629(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stearns N.A., Dong J., Pan J.X., Brenner D.A., Sahagian G.G.;
Comparison of cathepsin L synthesized by normal and transformed
cells at the gene, message, protein, and oligosaccharide levels.";
Arch. Biochem. Biophys. 283:447-457(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Denhardt D.T., Hamilton R.T., Parfett C.L.J., Edwards D.R., Pierre R.S., Materhouse P., Nilson-Hamilton M.; "Close relationship of the major excreted protein of transformed murine fibroblasts to thiol-dependent cathepsins.";
                                                                                                                                                                                                                                                                              Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88076849; PubMed=3689328;
Troen B.R., Gal S., Gottesman M.M.;
"Sequence and expression of the cDNA for MEP (major excreted protein), a transformation-regulated secreted cathepsin.";
Biochem. J. 246:731-735 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 316;
                                                                                                                                                                                                                                                                                                                                        35 POTENTIAL.
280 FMN (BY SIMILARITY).
34412 MW, 4AA9442245DE6250 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND CARBOHYDRATE-LINKAGE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 261:14697-14703(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=88213715; PubMed=2835398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91112761; PubMed=2275556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86271744; PubMed=3755373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-NOV-1990 (Rel. 16, Last sequ
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                EMBL; AE001300; AAC67872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 89-300 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                            316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 OWOKNER 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 OWOKONMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATL MOUSE
P06797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BNL;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATL MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALD DITAGE OF STATES OF ST
                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable Na(+)-translocation update)
(EC 1.6.5.-) (Na(+)-translocating NADH-quinone reductase subunit C (NG(*)-translocating NQU subunit C) (Na(+)-translocating NQU subunit C) (Na(+)-NQR subunit C)
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002106; AACRNA ligaseII.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR002314; HRNS.
InterPro; IPR002314; HRNS.
Fam; PF00587; TRNA-synt_2b; 1.
Pfam; PF00159; HGTP_anticodon; 1.
IIGRAMs; TIGR00442; hiss;
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA_synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO CLASS-11 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: NOR COMPLEX CATALYZES THE REDUCTION OF UBIQUINONB-1 TO UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT OF NA(+) IONS FROM THE CYPOPLASM TO THE PERIPLASM. NORA TO NORE ARE PROBABLY INVOLVED IN THE SECOND STEE, THE CONVERSION OF UBISEMIQUINONE TO UBIQUINOL (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFÂCTOR: FWN (BY SIMILARITY)
-!- SUBUNIT: COMPOSED OF SIX SUBUNITS; NORA, NORB, NORC, NORD, NORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 428; Pred. No. 23; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9CF859ED0E689DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND NORF (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Inner membrane (Potential).
-!- SIMILARITY: BELONGS TO THE NORC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis.
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 AA.
                                                                                                                                                                                                                                                                                        or send an email to license@igb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99000809; Pubmed=9784136;
                                                                                                                                                                                                                                                                                                                                                     EMBL; AE002349; AAF39630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48939 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              032422; 1QE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=D/UW-3/Cx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 CÉSWAKHLR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome
SEQUENCE 428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWOKNIMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NQRC CHI
O84281;
                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
```

```
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                           Katunuma N., Suzuki K.;
"Molecular cloning and sequencing of cDNA for rat cathepsin L.";
FEBS Lett. 223:69-73(1987)
                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
MEDLINE=90092543; PubMed=2599113;
IShidoh K., Kominami B., Suzuki K., Katunuma N.;
IGene structure and 5'-upstream sequence of rat cathepsin L.";
PEBS Lett. 259:71-74(1989).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-42 FROM N.A., TISSUE SPECIFICITY, AND INDUCTION
                                                                                                                                                         Ishidoh K., Towatari T., Imajoh S., Kawasaki H., Kominami
                                                                                                                     STRAIN=Wistar; TISSUE=Kidney;
MEDLINE=88030047; PubMed=3666143;
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
                                         Mammalia, Eutheria,
NCBI_TaxID=10116;
                                                                                               SEQUENCE FROM N.A.
                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mode by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                     CATALYTIC ACTIVITY: Specificity close to that of papain, As compared to cathepsin B, cathepsin L exhibits higher activity towards protein substrates, but has little activity on Z-Arg-Arg-NHMec, and no peptidyl-dipeptidase activity.
SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Cancer Res. 46:4590-4593(1986).
-!- FUNCTION: IMPORTANT FOR THE OVERALL DEGRADATION OF PROTEINS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.1%; Score 37; DB 1; Length 334; 55.6%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVATION PEPTIDE.
ACTIVATION PEPTIDE.
CATHERENIN, HEAVY CHAIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FE6747043307AD98 CRC64;
                                                                                                                                                                           -!- SÜBCELLULAR LOCATION: LyBOSOMA1.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0705; PAPAIN.

Probom; PD00015B; Peptidase C1; 1.

PROSITE; PS00139; THIOL PROTEASE CYS; 1.

PROSITE; PS00649; THIOL PROTEASE HIS; 1.

PROSITE; PS00640; THIOL PROTEASE HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000668; Peptidase Cl.
InterPro; IPR000169; SHprot acsite.
Pfam; PF00112; Peptidase Cl; 1.
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X06086; CAA29470.1; -.
EMBL; J02583; AAA37445.1; -.
EMBL; M20495; AAA39984.1; -.
EMBL; X04392; CAA27980.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37547 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; SO1177; KHMSL.
PIR; S13890; S13890.
HSSP; P07711; 1CJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:88564; Ctsl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P07711; 1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WOKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135
169
269
221
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
  ð
```

```
Zabludoff S.D., Charron M., Decerbo J.N., Simukova N., Wright W.W.; "Male germ cells regulate transcription of the cathepsin L gene by rat Sertoli cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawada A., Hara K., Kominami B., Tezuka T., Takahashi M., Takahara H.,
"Precursor of rat epidermal cathepsin L: purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L is lysosomal.

-I- TISSUE SPECIFICITY: Both mature cathepsin L and procathepsin L are found in the upper epidermis. The lower epidermis predominantly contains procathepsin L. In seminiferous tubules expression is greater at stages VI-VII than at stages IX-XII.
-INDUCTION: Expression in Sertoli cells is repressed by germ cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Procathepsin L is secreted. Mature cathepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papadopoulos \bar{\mathbf{v}}., "Identification of a stimulator of steroid hormone synthesis isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of steroidogenesis by TIMPI.
--- CATALYTIC ACTIVITY: Specificity close to that of papain. As compared to cathepsin B, cathepsin L exhibits higher activity towards protein substrates, but has little activity on Z-Arg-Arg-
                                                                                                                                                                                                                                                                                  MEDLINE=92168015, PubMed=1791830;
Erickson-Lawrence M., Zabludoff S.D., Wright W.W.;
Erickson-Lawrence M., Zabludoff S.D., Wright W.W.;
Eryclic protein-2, a secretory product of rat Sertoli cells, is the proenzyme form of cathepsin L.";
Mol. Endocrinol. 5:1789-1798(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NHMec, and no peptidyl-dipeptidase activity.
SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Towateri T., Katunuma N.,
"Amino acid sequence of rat liver cathepsin L.",
FEBS Lett. 236:57-61(1998).
-!- FUNCTION: Important for the overall degradation of proteins in
lysosomes. Procathepsin L is required for maximal stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boujrad N., Ogwuegbu S.O., Garnier M., Lee C.-H., Martin B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 18-37, FUNCTION, AND SUBCELLULAR LOCATION. STRAIN-Sprague-Dawley; TISSUE-Sertoli cells; MEDLINE-95296691; PubMed-7777858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 18-28, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley, TISSUE-Epidermis;
MEDLINE-20164186; PubMed=10699763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        localization.";
MEDLINE=21255611; PubMed=11356678;
                                                                                                                                           Endocrinology 142:2318-2327(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
MEDLINE=88296890; PubMed=3402618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dermatol. Sci. 23:36-45(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 114-288 AND 291-334.
                                                                                                                                                                                                            SEQUENCE OF 88-334 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ence 268:1609-1612(1995).
                                                                                                                                                                                                                                                           TISSUE=Sertoli cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunohistochemical
```

CATL RAT STANDARD; PRT; 334 AA.
P07154; Q9QV07;
01-APR-1988 [Rel. 07, Created)
01-FEB-1991 [Rel. 17, Last sequence update)
15-JUN-2002 [Rel. 41, Last annotation update)
Cathepain L precursor [EC 3.4.22.15) [Major excreted protein) (MEP)

|:|||| :: 52 WEKNMRMIQ 60

RESULT 13 CATL_RAT Rattus norvegicus (Rat).

Tue Dec

```
MSS1 SCHPO
Q9UTE7;
                                                                                                                                                       Matches
                                                                                                                                                                                                                                             SCHPO
                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                à
                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                   PRINTS; PR00705; PAPAIN.
PRODOM; PD000158; Peptidase C1; 1.
PROSITE; PS00139; THIOL_PROTEASE C7S; 1.
PROSITE; PS00649; THIOL_PROTEASE_NS; 1.
PROSITE; PS00640; THIOL_PROTEASE_NS; 1.
Hydrolase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                          CATHEPSIN L, HEAVY CHAIN.
CATHERSIN L, LIGHT CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
A SIMILARITY.
A LINKED (GLONG.).
A-P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                           52.1%; Score 37; DB 1; Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller N., Bradshaw H.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    37660 MW; AFFA997582E34AF6 CRC64;
                                                                                                                                                                                                                                                                                 ACTIVATION PEPTIDE
  -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein F30B5.4 in chromosome IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 27;
3; Mismatches
                                                                                                                                                                      InterPro; IPR000668; Peptidase C1.
InterPro; IPR000169; SHprot acsite.
Pfam; PF00112; Peptidase C1; 1.
                                                                                                                  EMBL, AF025476, AAB81616.1, -.
EMBL, S85184, AAB21516.1, -.
PIR, S07098, KHRTL.
                                                                                                         EMBL; Y00697; CAA68691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                    HSSP; 060911; 1FH0.
                                                                                                                                                                                                                                                                                                                                                                                                    334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WOKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 WEKNIMRMIQ 60
                                                                                                                                                             MEROPS; C01.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKYL CAEEL
219910;
                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                             DISTLFID
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKYL CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
à
```

```
the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAY MEDDINE=21848401; PubMed=11859360;

RA MEDDINE=21848401; PubMed=11859360;

RA Gouros U., Feat N., Hayles U., Bascham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gollins M., Connor R., Cronin A., Davis P., Hidagon G.,

RA Holroyd S., Hornsby T., Howarth S., Hunckle B.J., Hunt S., Jagels K.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Moorey P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Wellon J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Gabel C., Fuchs M., Fritzc C., Helzer B., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Decano S., Gloux S., Lelaure V., Mottier S.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Loas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Gerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RI Nature 415:91-880 (2002).

RI Mature 415:91-880 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: BELONGS TO THE BRA/TRME FAMILY OF GTP-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                          WormPep; F30B5.4; CE28552.
Hypothetical protein.
SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTPase MSS1 homolog, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.1%;
50.0%;
                                                                                                                                                                                                                                                                                   EMBL; U42437; AAA83493.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS. TRME SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 CIQWELNRER 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQKNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896
```

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       Ouery Match
Best Local Similarity 41.7%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 3; Indels
```

Search completed: February 21, 2003, 07:27:57 Job time : 6.6 secs

||:|:| 178 CFRWRKKLIEYR 189 1 CFOWOKNIMRKVR 12

g

ö

0; Gaps

Sequence:

Title:

Searched:

Database

```
QBuicz agrobacteri
Q92rhB rhizobium m
Q99fd19 mycoplasma
Q96fd19 mycoplasma
Q96fd2 arabidopsis
Q92kp4 helicobacte
Q97rg8 clostridium
Q97rg8 clostridium
Q97rg8 olostridium
Q97rg7 homo sapien
Q97977 homo sapien
Q92955 chlamydia p
Q99fh19 arabidopsis
Q19153 caenorhabdi
Q2230 arabidopsis
Q90863 human immun
Q90884 human immun
Q90884 human immun
Q92g16 rickettsia
Q86c55 strz conver
Q971n7 sulfolobus
Q72904 human immun
                                                              Q9sz87 arabidopsis
Q8r9ul thermoanaer
Q9xhpl sesamum ind
Q9apz3 vibrio chol
Q986a0 rhizobium l
      Q8yp77 anabaena sp
Q8rgt4 fusobacteri
Q8s013 oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28rmb8 cytophaga j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%; Score 63; DB 4; Length 711; ilarity 90.9%; Pred. No. 0.0041; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 AA.
                                                                                                                                                           Q8UHC2
Q92RH8
                                                                                                                                                                                                                  Q98Q19
Q9C6N2
                                                                                                                                                                                                                                                                                                                                                                                                                                       090863
090884
Q92GL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8SC55
Q971N7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBTCD2.
01-JUN-2002 (TEMBLrel. 21, Created)
01-JUN-2002 (TEMBLrel. 21, Last seq
01-JUN-2002 (TEMBLrel. 21, Last ann
Lactotransferrin.
                                                              Q9SZ87
                                                                                                                                          Q986A0
                                                                                                                                                                                                                                                                                097TQ8
                                                                                                                                                                                                                                                                                                                                                           Q9Z955
                                                                                                                                                                                                                                                                                                                                                                               Q9FHI9
                                                                                  Q8R9U1
                                                                                                                                                                                                    Q8YFK3
                                                                                                                                                                                                                                                            Q9ZKP4
                                                                                                                                                                                                                                                                                                 Q9NZW0
Q9NZW3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                          094937
    4
16
                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                         15
15
16
9
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQKNIMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 CFOWORNMRKV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
TISSUE-PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
\begin{array}{c} \mathbf{n} \\ \mathbf{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8TCD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UCY5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q88487 zea mays (m
Q9q910 human immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8xse2 ralstonia s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8z462 salmonella
Q9hpa3 halobacteri
Q93780 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               091tn4 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8tax2 homo sapien
Q9nus2 homo sapien
Q96m21 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8tcd2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q38115 bacteriopha
Q9xvd1 caenorhabdi
                                                                                                                 February 21, 2003, 07:25:55; Search time 20.8 Seconds (without alignments) 118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogucys homo sapien
Ogtr80 ovig aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9wyq1 thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q88487
    GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                        671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8TCD2
Q9UCY5
Q9TR80
Q8XSE2
Q38115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9Q9L0
Q9LTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96M21
Q9WYQ1
                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9HPA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8S487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8TAX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   093780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XVD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29NUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length; 200000000
                                                                                                                                                                                                  US-09-743-107B-81
                                                                                                                                                                                                                                     1 CPQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archeap:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp plant: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPTREMBL 21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_phage: *
                      Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bp mhc:*
                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
```

·,

Gapa

132 1132 1132 1133 1135 1144 115

No.

ö

```
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q38115
Q38115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9XVD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9XVD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORF29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 038115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9XVD1
                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCOUNT REPAREMENT OF THE SECOND SECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               83.1%; Score 59; DB 4; Length 38; 90.9%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.1%; Score 54; DB 6; Length 33; 72.7%; Pred. No. 0.007; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                       InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00405; transferrin, 1.
SEQUENCE 33 AA, 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ICC protein howolog.
ICC OR RSP0534 OR RS00414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                 seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A. STRAIN=GMI1000; MEDLINE=21681879; PubMed=11823852;
                                                                                                                    MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; 077698; ICE2.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 72.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FOWOKNIMIKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQKNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid megaplasmid
                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep)
                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biop
HSSP; 077698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8XSE2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O8XSE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         997R80

997R80

997R9

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
   AC OC OC OC OX EXP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
Aslanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico D., Chadler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

In Nature 415:497-502(2002)

R PMEL, AL646079; CAD17685.1; -.

InterPro; IPR004844; S/T_phosphtse.

InterPro; IPR004844; S/T_phosphtse.

R Pfan, PF00149; Metallophos; 1.

Plasmid; Complete proteome.

SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96332668; PubMed=8730874;
Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;
Inducible gene expression mediated by a repressor-operator system
isolated from Lactococous lactis bacteriophage rlt.";
Mol. Microbiol. 19:1331-1341(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis and molecular characterization of the temperate lactococcal bacteriophage {\rm rlt.}"_i, Mol. Microbiol. 19:1343-1355(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96332669; PubMed=8730875;
Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,
Venema G., Nauta A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                               60.6%; Score 43; DB 16; Length 279; 50.0%; Pred. No. 6.6; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.6%; Score 43; DB 9; Length 469; 60.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U38906; AAB18704.1; -.
SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              681 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20, C24H11.8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C24H11.8.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 CFOWEKGIRIAK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQKNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage rlt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 CYPWOKNILK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=43685;
```

0

m

```
MEDIANE-2050483; PubMed=11016950;

MEDIANE-205048 D.S., Weir D., Hall J.S., Well R., Goo Y.A.,

Meddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Meddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Meddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Meddocks D.G., Liang P., Riley M., Spudich J.L., Jung K.-H.,

A. A. Mam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Menome sequence of Halobacterium species RRC-1.",

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

MICEPPO: IPRO01646; Speptide repeat.

InterPro: IPR001646; Speptide repeat.

MICEPPO: IPR001646; Speptide repeat.

MICEPPO: PR001622; K-fannel Dore.

Menomial Prooteome.

Menomial Research M.M., 21BF5D5F0486CCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%; Score 42; DB 17; Length 584; 50.0%; Pred. No. 22;
                                                                                                         Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
               (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                 Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 63.6 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 CFTWRKDMERKR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F53H4.4 protein.
             01-MAR-2001 (
01-MAR-2001 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      093780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      093780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dobson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
Q93780
                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CT18,
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis B.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G.,
Whitehead S., Barrell B.G.,
"Complete genome sequence of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi.
Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                       "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                60.6%; Score 43; DB 5; Length 681; 70.0%; Pred. No. 17; 1.1ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.2%; Score 42; DB 16; Length 511; 58.3%; Pred. No. 19;
                                                                         Lloyd C.R.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                    Pfam; PF00520; ion_trans; 1. _ _ SEQUENCE 681 AA; 78178 MW; D36AC05C3FA029CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:848-852(2001).

EMBL, AL627276; CAD06049.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 19;
0; Mismatches
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81475; CABG3914.1;
InterPro; IPR001622; K+channel pore.
InterPro; IPR000636; M+channel nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                   MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity 70.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 58.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 RWOKNRRRVR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                          3 QWQKNIMRKVR 12
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 7; Conserv
                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                     CBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
```

Q8Z462

В

ö

Gaps

0;

```
ó
                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.7%; Score 41; DB 5; Length 275; 63.6%; Pred. No. 15; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                      Dobson k.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81089; CAB03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FPC704DB2 CRC64;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FOWOKINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

584 AA.

PRT;

PRELIMINARY;

Q9HPA3 ID Q9HPA3 AC Q9HPA3;

RESULT 8

```
OLOCT-2000 (TERMELREI. 15, Created)
01-OCT-2000 (TERMELREI. 15, Last sequence update)
01-OCT-2000 (TERMELREI. 15, Last annotation update)
01-OCT-2000 (TERMELREI. 15, Last annotation update)
64enomic DNA, chromosome 5, Pl clone:MSKI0.
Arabidopsis thaliana (Mouse-ear cress)
Rukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5, X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=COLUMBIA;
BADLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TM-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ11175 fis, clone PLACE1007375, weakly similar to phorbol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.3%; Score 40; DB 10; Length 121; 60.0%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.3%; Score 40; DB 4; Length 306; 55.6%; Pred. No. 26; cive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025708; AAH25708.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lecurations.";
clones.";
DNA Res. 7:31-63(2000).
EMBL; AB024037; BAA97406.1; -.
EMBL; AB024037; BAA97406.1; -.
"Antence 121 AA; 13798 MW; 3DEE6D4A539D2933 CRC64;
"Antence 121 AA; 13798 MW; 3DEE6D4A539D2933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBTAX2;,
QBTAX2;,
QBTAX2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last amnotation update)
Similar to hypothetical protein FLJ11175.
                                                              121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                              PRT;
                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWOKUMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||::|||:|
|82 CFRFQKNIRQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 CPÓWESTLR 277
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWOKNMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9NUS2;
                                                        Q9LTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TAX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NUS2
RESULT 12
Q9LTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
Q9NUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TAX2
                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCOCCOS DITENT OF THE STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRREARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                    Zea mays (Maize).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoli.ophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tanuri A., Machado E., Caride B., Costa L.J., Telles J.G.;
"Primary infections with HIV-1 of women and their offspring in Rio de Janeiro, Brazil: Finding of recombinant of HIV-1 subtypes B and F.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR000777; GP120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.7%; Score 41; DB 10; Length 570; 66.7%; Pred. No. 32; cive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.3%; Score 40; DB 15; Length 115; 60.0%; Pred. No. 9.1; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. B73;
Ramakrishna W., SanMiguel P., Emberton J., Bennetzen J.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. B73;
Llaca V., Linton B., Young S., Kovchok S., Messing J.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF466202, AAL75475.1; -.
SEQUENCE 570 AA, 63178 MW; AIBEF8390F0BA3F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 AA; 12832 MW; 86E509D6F6978127 CRC64;
                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) protative aldose reductase-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                             570 AA
                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
                                                                                                                             01-JUN-2002 (TrEMBLrel. 21,
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 ÓWPKNLRKI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QWEKTLRQVR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QWQKNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=VTRJ07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
9
                                                                                                                                                                                                                                           Z138B04.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                     QBS487;
                                                                    Q8S487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         076060
        RESULT 10
085487
AC 08548
AC 08548
DT 01-JUD
DT 01-JUD
DT 01-JUD
DE PLUAT
CO ENVARY
OC BUKARY
OC PADIC
OX NCBI
RN SEQUE
RC STRAI
RN SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEGUE
```

Matches

à

RESULT 11

ð

0;

Gaps

ö

ó;

Gaps

; 0

ester/diacylglycerol-binding protein UNC-13

```
||||: :| :|
66 CFQWRWGVRYLR 77
1 CFQWQKNMRKVR 12
ò
```

6; Conservative

Matches

ö

Gaps

; 0

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liboupa A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Warakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiyama A., Kawakami B., Suzuki Y., Nabohuman cDNA sequencing project.", Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

ENBL, AK057453; BAB71493.1; -- SEQUENCE 274 AA; 30083 MW; IDP43654D4135B2F CRC64;
                                                                                                                            TISSUB=PLACENTA,

IBOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.,

Ninomiya K., Iwayanagi T.,

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     036M21;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ32891 fis, clone TESTI2004929.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.3%; Score 40; DB 4; Length 466; 55.6%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%; Score 39; DB 4; Length 274; 50.0%; Pred. No. 35; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00499; C2 DOMAIN 1; UNKNOWN 1.
PROSITE; PS00049; C2 DOMAIN 2; 1.
PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
SEQUENCE 466 AA; 53192 MW; E4113A5062F58DGE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                 EMBL; AK002037; BAA92048.1; -...
HSSP; P21707; 1BYN.
InterPro; IPR000008; C2.
InterPro; IPR000504; RNA_rec_mot.
Pfan; PR00168; C2; 1.
PRINTS; PR00360; C2DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 CFÓWESTLR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQKNMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     096M21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
Search completed: February 21, 2003, 07:44:36 Job time : 21.8 secs
```

```
February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2. SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
4. SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
5. SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*
6. SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*
7. SIDS2/gcgdata/geneseqg-embl/AA1982.DAT:*
8. SIDS2/gcgdata/geneseqg-embl/AA1982.DAT:*
9. SIDS2/gcgdata/geneseqg-embl/AA1980.DAT:*
11. SIDS2/gcgdata/geneseqg-embl/AA1980.DAT:*
12. SIDS2/gcgdata/geneseqg-embl/AA1980.DAT:*
13. SIDS2/gcgdata/geneseqg-embl/AA1991.DAT:*
14. SIDS2/gcgdata/geneseqg-embl/AA1991.DAT:*
15. SIDS2/gcgdata/geneseqg-embl/AA1992.DAT:*
16. SIDS2/gcgdata/geneseqg/geneseqg-embl/AA1992.DAT:*
17. SIDS2/gcgdata/geneseqg/geneseqg-embl/AA1992.DAT:*
18. SIDS2/gcgdata/geneseqg/geneseqg-embl/AA1992.DAT:*
19. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
11. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
12. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
13. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
14. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
15. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
16. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
17. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
18. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
19. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
20. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
20. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
20. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
20. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
20. SIDS2/gcgdata/geneseqg/embl/AA1992.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |SIDS2/gcgdata/geneseg/genesegp-embl/AA1999.DAT:*
|SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT:*
|SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*
|SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Geneseq 101002:*
                                                                                                                                                                                                                                                                                                                     US-09-743-107B-82
70
1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                            Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		, ake			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	70	1001			000000000000000000000000000000000000000	
•	2		71	7	AA1/8082	Human Jackoterrin
7	68	97.1	12	21	AAY78038	Human lactoformin
e	68	97.1	12	21	AAV7R046	Timen lactoformi
4	S.B.	47 1	1.0	ا ر د		
٠,	9 1	1 .	71	4	AMI 1004 /	Human Lactoterrin
v	89	97.1	13	21	AAY78037	
و	69	97.1	13	21	AAY78048	Himan lactoforwin
7	68	97.1	13	2	AAV78049	Timmen Jackettill
a	0		,	1	CTOOLSTE	numan ractorerrin
0	0	7.7	14	7.7	AAY78036	Human lactoferrin
σ	69	97.1	14	21	AAY78050	Human Jactofornin
10	68	97 1	14	,	1307706	Transa Taccoretiti
	j.		+	7	TCOD/ TWW	エコヨカコ ニカンドントロドナーカ

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

Dentide for entime	rot anti-			-	-	-	·	Jactoferri	-, ا	1 -	O	toferrin		lacto	_	ferrin-re	Lactoferrin derive				a				Peptide for anti-u	Lactoferrin-derive	Lactoferrin-derive	Lactoferrin derive	- 1	Lactoferrin-derive	Lactoferrin deriva	Anti-parasitic pen	Thrombus formation	Lactoferrin hydrol
15 17 AAR98554	21 AAY780	21 AAY7806	21	21	6 21 AAY7806	G	21 ,	7 21 AAY7806	7 21 AAY7806	3 15 AAR6935	m	2	3 21	2	13	14	15	15,	15	т (16	7		_	-	_	_	17	-	17	+	18	20 19 AAW70310	13
68 97.1	68 97.1	97.	8 97.	97.	8 97.1	8 97.1	8 97.1	8 97.1	8 97.1	97.1	8 97.1	8 97.1	8 97.1	97.1	3 97.1	8 97.1	9 97.1	3 97.1	3 97.1	3 97.1	9 97.1	3 97.1	3 97.1	3 97.1	3 97.1	3 97.1	3 97.1	3 97.1	97.1	97.1	97.1	97.1	.1	1 97.1
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39			42	43	44	45

ALIGNMENTS

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative Human lactoferrin derived peptide SEQ ID NO:82. AAY78082 standard; Peptide; 12 AA. 98SE-0002441. 98SE-0002562. 98SE-0004614. 99WO-SE01230. (first entry) (ASCI-) A+ SCI INVEST AB. WO200001730-A1. Homo sapiens. Synthetic. 06-JUL-1998; 17-JUL-1998; 29-DEC-1998; 06-JUL-1999; 25-APR-2000 13-JAN-2000. AAY78082; RESULT 1

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula sloo be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis based on lactoferrin would costs. Therefore, provision of peptides as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colltis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 70; DB 21; Length 12; 100.0%; Pred. No. 1.7e-05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                              Claim 22; Page 36; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78038 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 70; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98SE-0002441,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78038;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

AAY78001 to AAY78100 represent peptides having sequences based on human

ò

Gaps

```
·.
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Bven though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, collitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                        97.1%; Score 68; DB 21; Length 12;
91.7%; Pred. No. 3.7e-05;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78046 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78046;
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78046
     à
                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

12 AA;

Sequence

X S

Query Match

0

Gaps

. 0

ö

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (auch as urinary tract infections, colitis, and Candida infections (auch as membrane), inflammations and/or tunours. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives.
fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; uninary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                           Score 68; DB 21; Length 12;
Pred. No. 3.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltzer L, Dolphin GT
                                                                                                                                                                                                                                                                                                                                                                                                                      Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                           AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 73; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mattsby-Baltzer I,
                                                                                                                                                         97.1%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                     Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                    1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                 1 CFÓWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                            12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson LA,
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                            AAY78047;
                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                              RESULT 4
   જે
```

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment urnary tract infections. A medicinal product of the peptide or fragment urnary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bacteriofial and may also be used then them them there is a successful to the colitis.
                                                                                                                                                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                          ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
97.1%; Score 68; DB 21; Length 12
91.7%; Pred. No. 3.7e-05;
...marches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 97.1%; Score 68; DB 21; Length 13; 1. Similarity 91.7%; Pred, No. 4e-05; 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dolphin GT;
                                                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltzer L,
                                                                                                                                                                                                     AAY78037 standard, Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                              bactericidal; preservative.
                                                                                                                                                                                                                                                                         (first entry)
                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASCI-) A+ SCI INVEST AB.
                                                                                   1 CFOWORNLRKVR 12
                                                                                                                   1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1998;
                                                                                                                                                                                                                                                                          25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                       AAY78037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                Matches
                                                                                                                                                                   RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COBt.
                                                                                                                                                                                                                                       ò
                                                                                                                g
```

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

cost.

AAY78049 standard; Peptide; 13 AA.

```
ARY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. Cumpicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; collitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                    AAY78048 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB.
   CFQWQRNLRKVR 12
                                     2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                        AAY78048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
ч
                                                                                                                                                                         RESULT 6
AAY78048
AAY78048
AAX78048
AAX
à
                                                            셤
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tunnours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                     Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.1%; Score 68; DB 21; Length 13; 91.7%; Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dolphin GT;
                                                                                            Human lactoferrin derived peptide SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:36
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78036 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                     98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                         99WO-SE01230.
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AA;
                                                                                                                                                                                                                                                       WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                       (ASCI-) A+ SCI
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                       06-JUL-1999;
                                                              25-APR-2000
                                                                                                                                                                                                                                                                                                                                                       06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                       29-DEC-1998;
                                                                                                                                                                                                                                                                                         13-JAN-2000
                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78036
ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         田城北城田城田
```

..

Gaps . 0

0; Indels

1; Mismatches

11; Conservative

Matches

1 CFQWQRNLRKVR 12

à 엄

2 CFÓWORNMRKVR 13

AAY78049 RESULT

Score 68; DB 21; Length 13; Pred. No. 4e-05;

97.1%; 91.7%;

Query Match Best Local Similarity

98SE-0002562. 98SE-0004614. 98SE-0002441. 99WO-SE01230

> 17-JUL-1998; 06-JUL-1998; 29-DEC-1998;

WO200001730-A1

Synthetic.

06-JUL-1999;

13-JAN-2000

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicial and bactericidal and may also be used as preservatives.
               Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-miorobial; anti-tumour;
urinary tract infection; colltis; Candida infection; fungicidal;
bactericidal; presexvative.
                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                      Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                        98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                            99WO-SE01230.
                                                                                                                                                                                                                                                                                                    (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                          WO200001730-A1.
                                                                                               Homo sapiens
                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                        29-DEC-1998;
                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                          17-JUL-1998;
                                                                                                                                                                            13-JAN-2000
                                                                                                              Synthetic.
```

```
ô
Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                         14 AA;
                                                                                                                                                                                                                                                                         Seguence
```

0; 97.1%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 4.4e-05; ive 1; Mismatches 0; Indels 11; Conservative 1 CFQWQRNLRKVR 12 Query Match Matches

3 CFQWQRNMRKVR 14

AAY78050 standard; Peptide; 14 AA. (first entry) 25-APR-2000 AAY78050; RESULT 9 AAY78050

Human lactoferrin derived peptide SEQ ID NO:50.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

99WO-SE01230.

06-JUL-1999;

13-JAN-2000.

Homo sapiens

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammantions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula so be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 4.4e-05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000 (first entry)
                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                              WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78051
δ
```

·;

Baltzer L,

The agent is low on. It can be

AAR98531-54 are peptides used in an anti-ulcer agent. The agin toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.

```
New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 75; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MORG ) MORINAGA MILK IND CO LTD
                                                                                                                                                                                                Mattsby-Baltzer I,
                       98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94JP-0283869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1996 (first entry)
                                                                                                                                        (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-ulcer agent contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                      WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-318857/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AA;
                                                        17-JUL-1998;
29-DEC-1998;
                             06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP08143468-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUN-1996.
                                                                                                                                                                                             Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR98554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
AAR98554
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE SECTION OF THE SE
```

```
.
0
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as withary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 4.4e-05; ive 1; Mismatches 0; Indels
```

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumourse. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

15 AA;

Sequence

peptide - has low toxicity, is heat-resistant and water-soluble

Claim 1; Page 11; 11pp; Japanese

```
ö
                                                                                                                                                                                                                              Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                             Gaps
                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                          Score 68; DB 17; Length 15
Pred. No. 4.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Dolphin GT;
                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                           AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Mattsby-Baltzer I,
                                                           97.1%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                   98SE-0002562.
98SE-0004614.
                                                                                                                                                                                             (first entry)
                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                               1 CFQWQRNLRKVR 12
                                                                                                               2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-147388/13.
                                                           Query Match
Best Local Similarity
                                           15 AA;
                                                                                                                                                                                                                                                                                                      WO200001730-A1.
                                                                                                                                                                                                                                                                              sapiena.
                                                                                                                                                                                             25-APR-2000
                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                        13-JAN-2000.
                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                           AAY78035;
                                           Sequence
                                                                             Matches
                                                                                                                                          RESULT 12
                                                                                                                                                $$$$$$$
                                                                                                               q
                                                                                               ò
```

AAY78063 standard; Peptide; 15 AA.

RESULT 14 AAY78063 25-APR-2000 (first entry)

AAY78063;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                   Gaps
                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68; DB 21; Length 15;
Pred. No. 4.7e-05;
1; Mismatches 0; Indels
     Length 15;
 Score 68; DB 21; Length 15
Pred. No. 4.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dolphin GT;
                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baltzer L,
                                                                                                                                                                         AAY78062 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.1%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0002562.
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB.
                                                              1 CFOWORNLRKVR 12
                                                                                            4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                         25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                          AAY78062;
                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                        qq
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides have a lactoferring and infammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.1%; Score 68; DB 21; Length 15; larity 91.7%; Pred. No. 4.7e-05; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dolphin GT;
                                                                                 Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78031 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                 99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                  98SE-0002441
                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 11, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 AA;
                                                                                                                                                                                                                                                            WO200001730-A1
                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                    7-JUL-1998;
                                                                                                                                                                                                                                                                                               13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanson LA,
                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SX B
ઠે
```

· 0

Gaps

·,

Local Similarity 91.7 nes 11; Conservative

g à

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as urinary tract infections and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula sloop used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower capbe them to be used for the same purposes as lactoferrin at lower
                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                       Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 68; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                     98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                  99WO-SE01230.
                25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 AA;
                                                                                                                                                                                                                                                     WO200001730-A1.
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                  06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                            13-JAN-2000
                                                                                                                                                                                                                  Synthetic.
```

Query Match 97.1%; Score 68; DB 21; Length 16; Best Local Similarity 91.7%; Pred. No. 5e-05; Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CFQWQRNLRKVR 12

5 CFQWQRNMRKVR 16

P &

Search completed: February 21, 2003, 07:37:14 Job time : 28.35 secs

```
NAME/KEY: Peptide
LOCATION: 1.18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN FEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: BOSTC
STATE: MA
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02109
                                                                                                                                                                                                                                                                                                             US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 24, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4, Appli
6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                          (without alignments)
40.818 Million cell updates/sec
                                                                            February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7
Sequence 8
Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                        1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/FB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-475-055-8

US-07-75-161A-3

US-07-95-161A-3

US-08-26-771-24

US-08-26-771-25

US-08-381-984-25

US-08-381-984-25

US-09-508-734-4

US-09-508-734-6

US-07-891-174-10

US-07-891-174-10

US-07-95-161A-8

US-07-95-161A-8

US-07-95-161A-8

US-07-95-161A-8

US-08-256-771-30

US-08-381-984-29

US-08-381-984-29

US-08-256-771-30

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-017-043A-3
US-08-464-182A-5
US-08-406-271-5
                                                                                                                                                                                                                          262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                           US-09-743-107B-82
70
                                                                                                                                                          1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                           Sequence:
                                                                                                                                                                                                                          Searched:
                                                                            Run on:
```

Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1:	App1	App]	App1:
Sequence 2,	Sequence 2,	Sequence 2,	Sequence 2,	Sequence 2,	Sequence 4,	Sequence 2,	Sequence 2,	Sequence 2,	Seguence 2,	Sequence 2.	Sequence 2,					
US-08-464-182A-2	US-08-408-271-2 US-08-724-586-2	US-09-421-632-2	US-09-932-190-2	US-08-655-640-2	US-08-655-640-4	US-08-154-019-4	US-08-461-333-4	US-08-464-167-4	US-09-158-313-4	US-08-476-798-4	US-08-145-681-2	US-08-250-308-2	US-08-453-703-2	US-08-456-106-2	US-08-456-108-2	US-09-265-577-2
0,0	4 M	4	4	7	7	Н	Н	m	m	4	Н	Н	н	~	m	4
54	694	694	694	705	708	711	711	711	711	711	711	711	711	711	711	711
97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	92.9	92.9	92.9	92.9	92.9	92.9
8 8	989	89	68	68	68	68	68	68	68	68	9	65	65	65	9	65
0 7 70 0 00	0 0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

역성보험적적적적적적적적적적

ALIGNMENTS

```
APPLICANT: YARAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MATARU
APPLICANT: MATARU
APPLICANT: TANAKA, SHIGERAL
APPLICANT: TANAKA, SHIGERAL
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UTHIDA, TOSHIAKI
TITLE OF INVENTION: UNIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: PATERT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSE: PATERT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSE: ATHIBEAULT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 02-MAR.1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, FAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: 5JN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
Sequence 3, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
```

```
US-08-628-380-8
                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                 ·.
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                           Sequence 8, Application US/08485948

Patent No. 2855882

GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
                                                                                                 .`
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                     Score 68; DB 1; Length 10; Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 4.3e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
PRIOR APPLICATION DATA:
PUBLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRN: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klauber & Jackson
OTHER INFORMATION: (20-37)"
                                                 97.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                             Query Match
Best Local Similarity 91.79
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.1
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                              1 CFQWQRNLRKVR 12
                                                                                                                                                                1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
   ;
US-08-204-487-3
                                                                                                                                                                                                                          RESULT 2
US-08-485-948-8
```

```
APPLICANT: LI, YONG MING
APPLICANT: VLASSARA, HELEN
APPLICANT: VLASSARA, HELEN
APPLICANT: CERMI, ANTHONY
ITILE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08475055;
Patent No. 5962245
GENERAL INFORMATION:
APPLICANT: YOUR MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 4.3e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
APPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackan Eeq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008 CIP
TELECHONNUNICATION INFORMATION:
TELEFEHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
Sequence 8, Application US/08628380
Patent No. 5891341
GENERAL INFORMATION:
                                                                                                                                                                                                                                       STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                   ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                      07601
```

; 0

```
97.1%; Score 68; DB 1;
                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: WATEEN NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                             ٠<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: modified site
LOCATION: 2
LIDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys re
OTHER INFORMATION: thiol
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
                                                                                                                                                                                                                                                                                                                                           TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 4.3e-05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esg., David A.
REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE: 070BER: 08/488,217
FILING DATE: 070BER: 08/418,642
FILING DATE: 070BER: 08/418,642
FILING DATE: APRIL 7,1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackbon Ebg., David A.
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
JADDRESS:
JALL Hauber & Jackson
SET: 411 Hackensack Avenue
Hackensack
New Jersey
'Y: USA
7760'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/07755161A Patent No. 5304633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide DESCRIPTION: LF-C1, 8-25 HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.1
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRAGMENT TYPE: internal US-08-475-055-8
                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
FEATURE:

NAME/KEY: modified site

LOCATION: 19

IDENTIFICATION METHOD:

OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cyber InfoRMATION: AUTHOR INFORMATION: La sesidue at location 2"

AUTHORS:
/note= "thiol group of
Cys residue at location 2 connected by disulfide bond with
thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOCUMENT NUMBER:
FILING DATE:
PRILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
```

Length 20;

```
LOCATION: 19
IDEMTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
                                             /note= "thiol group of Cys residue at location 2 connected by disulfide bond with thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TOSAKO, SHUN'ICHI
APPLICANT: TOSAKO, SHUN'ICHI
APPLICANT: KAMASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIAKI
ITILE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
ITILE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
CORRESPONDENCES: SOSTON
STREET: 53 STATE STREET
CONTY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 1; Length 2v, Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE TOWNER: PIN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
                                             OTHER INFORMATION: /note=
OTHER INFORMATION: Cyg re:
OTHER INFORMATION: thiol
FEATURE:
NAME/KEY: modified site
LOCATION: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 97.1%;
1 Similarity 91.7%;
11; Conservative
                           IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                   DATE:
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02109
        LOCATION:
                                                                                                                                                                                                                                                                                                                 JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MJ
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                           ..
                           Gaps
Best Local Similarity 91.7%; Pred. No. 4.8e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                       VS-07-891-174-3

i Sequence 3, Application US/07891174

i Patent No. 5317084

GENERAL INFORMATION:

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Rifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SRP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acid TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                              1 CFQWQRNLRKVR 12
                                                                                                     2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Com
OPERATING SYSTEM:
SOFTWARE: Display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
TISSUB TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY:
                                                                                                                                                                 RESULT 6
                                                              à
```

```
STATE: D.C. COUNTRY: U.S.A.
            US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-08-381-984-24
                                                                                                                                                                                                                         RESULT 9
                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
APPLICANT: MAMORU TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ABOS Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                           97.1%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 4.8e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                 /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IDBN Compatible
OFBRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRICR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/08256771 Patent No. 5656591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNAY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLLOGY: linear
MOLECULE TYPE: peptide
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                  single
                                                                                                                                    MOLECULE TYPE: peptide PEATURE:
                                                                                                                                                                                         CTHER INFORMATION: 1.20
COTHER INFORMATION: COTHER INFORMATION: US-08-204-487-1
                                                                                                                                                                           NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                        1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                2 CFQWQRNMRKVR 13
                                                                        TYPE: amino acid
STRANDEDNESS: Bir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                       US-08-256-771-25

Sequence 25, Application US/08256771

Patent No. 5656591

CENNERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTINICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
97.1%; Score 68; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.8e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.1%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.8e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                           1 CFOWORNLRKVR 12
                                                                                                                                   2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CFOWORINMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
```

9 06:51:41 2003

Tue Dec

```
OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6433509
TITLE OF INVENTION: was production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/O0139
CURRENT PILING DATE: 2000-66-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR PELING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.1%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 4.8e-05; Live 1; Mismatches 0; Indels
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
      805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                US/08/381,984
                                                                                                                                                  COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381
FILING DATE: April 11, 1995
CLASSIFICATION 25.2
PRIOR APPLICATION 25.2
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acide TYPE: amino acide STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CFQWQRNMRKVR 13
                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                    U.S.A.
                                                                                         20005
                                             STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment theree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD: OTHER INFORMATION: /note= "cysteine residues at positions 2 OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB 1; Length 20;
Pred. No. 4.8e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFRCATION: 252
PRICR APPLICATION: 252
PRICR APPLICATION NUMBER:
                                                                                                                                                ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08381984
FALENT NO. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
Sequence 24, Application US/08381984
                Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGIETRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: 20 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                     STREET: 805 FILLE CITY: Washington
                                                                                                                                                                                           CITY:
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                              20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
```

ö

```
PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                                  REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: AMINO ACID
    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
                                                                                                                                              TELEFAX: 202-371-8856
TELEX:
                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                     TOPOLOGY: line
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

GENERAL INPERMATION:

AGNIFAL INPERMATION:

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: US/09/508,734

PRIOR APPLICATION NUMBER: KR1999-07-14

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR SILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71
                                                                                                                                                o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                Gaps
                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                               97.1%; Score 68; DB 4; Length 22; 91.7%; Pred. No. 5.3e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 4; Length 24;
Pred. No. 5.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Discrete, 5.25 inch, 500XD
COMPUTER: Discrete, 5.25 inch, 500XD
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.1%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                       Matches 11; Conservative
              TYPE: PRT
CRGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                1 CFQWQRNLRKVR 12
                                                                                                                                                                                                     2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 805 Fiftee CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFÓWORNMRKVR 14
                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 RESULT 13
US-09-508-734-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 6
LENGIH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-508-734-6
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

```
OTHER INFORMATION: (note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" PUBLICATION INFORMATION:
AUTHORS:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 97.1%; Score 68; DB 1; 1 Similarity 91.7%; Pred. No. 6e-05; 11; Conservative 1; Mismatches
```

```
/note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
                                                                        APPLICANT: Manoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
WUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                               CITY: WASBILINGCON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
OURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION NUMBER: US/07/85,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN NUMBER: 33,367
REFERENCE/DOCKET UNBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRA: 202-371-8856
TELEFRA: 202-371-8856
                   ; Sequence 10, Application US/07891174; Patent No. 5317084; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys re-
OTHER INFORMATION: thiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified site
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
LOCATION:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
```

```
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
               Copyright
```

OM protein - protein search, using sw model

February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec Run on:

US-09-743-107B-82 1 CFQWQRNLRKVR 12 Perfect score: Seguence:

Scoring table:

Gapop 10.0 , Gapext 0.5 **BLOSUM62**

156504 segs, 31069816 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgr2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgr2_6/ptodata/2/pubpaa/PUSOB_NEW_PUB.pep:*
3: /cgr2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
4: /cgr2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
5: /cgr2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
6: /cgr2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
7: /cgr2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
8: /cgr2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
9: /cgr2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
10: /cgr2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
11: /cgr2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
12: /cgr2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
11: /cgr2_6/ptodata/2/pubpaa/USIO_PUBCOMB.pep:*
11: /cgr2_6/ptodata/2/pubpaa/USIO_PUBCOMB.pep:*
13: /cgr2_6/ptodata/2/pubpaa/USIO_PUBCOMB.pep:*
14: /cgr2_6/ptodata/2/pubpaa/USIO_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	*	>		SOMPLAKLES		
Score Matc		Match Length DB	DB	ID	Description	
68 97.		1 15	9	US-09-798-869-2	Land C and a mark	1
68 97		1 25	σ	US-09-798-869-20		1.5
68 97		1 694	σ	US-10-023-096-2	Semience 2 Ann	٠. ١٠.
60 85		7 15	σ	0S-09-798-869-6	Semience 6 App	1 ·r
51 72.9		9 15	σ	US-09-798-869-3	Sedience 3 Appl	√ √
51 72.9		9 25	9	US-09-798-869-23		17
43 61.4		4 15	0	US-09-798-869-7	, 4	4
42 60.0		0 15	σ	US-09-798-869-4	Segmence 4 appli-	7:-
42 60.0		0 25	6	US-09-798-869-22		1 -
39 55	٠	7 15	9	US-09-798-869-8	2	,
39 55		7 15	6	US-09-798-869-29	0	1.5
39 55	•	7 15	0	US-09-798-869-30	0	1.0
38 54	•	3 86	9	US-09-738-626-5715	57.7	1 (2
38 54		3 607	6	US-09-881-579-10	ord of englandings).
38 54		3 688	σ	US-09-881-579-15	April 151 Porter Res	1.5
37 52	•	9 21	10	US-09-864-761-47985	Semience 47985	4 4
37 52	٠	9 846	σ	US-10-051-409-4	Segmence 4 Juni	۲.
36 51	•	4 62	10	US-09-815-242-12129	Appropriate Section of the Section o	4
36 51	•	4 62	10	US-09-815-242-13026	Sequence 12129	¢ 4
						:

്യമയും തെയെപ്പ്പ്പ്പ്പ്പ് പോൾ	Sequence 1, Appli Sequence 119, App Sequence 119, App Sequence 119, App Sequence 119, App Sequence 119, App
US-10-066-500-58 US-10-066-58 US-10-066-58 US-10-066-494-58 US-10-066-494-58 US-10-066-494-58 US-09-904-536-11 US-09-904-536-11 US-09-904-536-14 US-09-904-536-14 US-09-904-536-14 US-09-904-536-14 US-09-904-536-14 US-09-904-536-17 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18 US-09-904-536-18	US-09-904-536-1 US-09-978-295A-119 US-09-978-192A-119 US-09-99-832A-119 US-09-99-832A-119 US-09-978-189-119
	n an an an an an H an an an an an
444444000000000000000000000000000000000	50.00 50.00 50.00 50.00
0 1 2 2 2 3 2 3 2 3 2 3 2 3 3 3 3 3 3 3 3	1 4 4 4 4 4 3 4 6 6 6 6

ALIGNMENTS

```
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.1%; Score 68; DB 9; Length 15; 91.7%; Pred. No. 2.7e-05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                     FILE REFERENCE: A34049-PCT-USA-A
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,863
FILORENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
                                           Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; CENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: HOMO SAPIENS
RESULT 1
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-798-869-2
```

3 CFOWORNMRKVR 14 d

1 CFOWORNLRKVR 12

à

0

Gaps

Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN; APPLICANT: (YSTEIN REKRAL); APPLICANT: BALDUR SVEINBJ (RNSSON) RESULT 2 US-09-798-869-20

```
SEQ ID NO 6
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell U.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                               Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
COMPUTER: IRM PC COMPATIBLE
COMPUTER: PC PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                        97.1%; Score 68; DB 9; I
91.7%; Pred. No. 4.4e-05;
tive 1; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELEPHONE: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERROE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/796,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1996-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSESEQ for Windows Version 4.0
SED ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10023096
Patent No. US20020160941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Kruzel, Marian L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 694 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.1
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                     CRGANISM: Homo Sapiens US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-023-096-2
                                                                                                                                                                                                                                                                                                  TYPE: PRT
```

```
ó
                                                      ·.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens OTHER INFORMATION: sequence)
                                                      ò.
  97.1%; Score 68; DB 9; Length 694; 91.7%; Pred. No. 0.0011; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.9%; Score 51; DB 9; Length 15; 63.6%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%; Score 60; DB 9; Length 15; 83.3%; Pred. No. 0.00054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                         APPLICANT: (YSTEIN REMAL
APPLICANT: (YSTEIN REMAL
APPLICANT: (YSTEIN REMAL
APPLICANT: (YSTEIN REMAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
SOFTWARE: FRRENSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PLING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO S: SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                         Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: (YSTEIN REKDAL APPLICANT: BALDUR SVEINBJ (RNSSON APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                1 CFQWQRNLRKVR 12
                                                                                                                                          22 CFÓWORNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CFOWOWNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: CAPRINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-798-869-3
                                                                                                                                                                                                                                        9-698-863-00-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-09-798-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-798-869-3
```

ò

Gaps

. 0

1; Indels

Mismatches

7; Conservative

Matches

```
60.0%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.47; 1.ve 2; Mismatches 3; Indels
                                                                                                                                                                                                         APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN RENDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                               ; Sequence 4, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
1 CFQWQRNLRKV 11
                                        3 CYÓWÓWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQRNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ČLRWONEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-22
                                                                                                                             US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens; OTHER INFORMATION: sequence)
US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.9%; Score 51; DB 9; Length 25; 63.6%; Pred. No. 0.026; Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.4%; Score 43; DB 9; Length 15; 54.5%; Pred. No. 0.32; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                  FILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1090-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JAPELICANT: O'GHIN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVERNBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                         Sequence 23, Application US/09798869
PUDLICACTION NO. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: RECDAL
APPLICANT: BALDUR SYBINBJ (RNSSON
APPLICANT: ALARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity F
                                                     3 CYQWQRRMRKL 13
                             1 CFOWORNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQRNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: CAPRINE
                                                                                                                                                 US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
```

o;

;0

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0%; Score 42; DB 9; Length 25; Best Local Similarity 54.5%; Pred. No. 0.76; Matches 6; Conservative 2; Mismatches 3; Indels
Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OCHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVERING/RNSSON
APPLICANT: LARS VORLAND
ITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CPT/GB99/02851
PRIOR APPLICATION NUMBER: CPT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
PRIOR PLING DATE: 1999-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.7%; Score 39; DB 9; Length 15; 54.5%; Pred. No. 1.4; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.7%; Score 39; DB 9; Length 15; 45.5%; Pred. No. 1.4; ive 4; Mismatches 2; Indels
                                                                                                                 APPLICANT: 1312LTM AEMOLIA
APPLICANT: BALDUR SYBINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PELING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOHN SIGGED SYNDSEN
APPLICANT: JOHN SIGGED SYNDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: ABALDUR SYNEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A4649-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US/09/799, 869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAESEQ for Windows Version 4.0
; Sequence 8, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                         APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQRNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CLRWOWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQRNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CFRWÓWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

RESULT 12 US-09-798-869-30

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.7%; Score 39; DB 9; Length 15; 45.5%; Pred. No. 1.4; 2; Indels tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.3%; Score 38; DB 9; Length 86; 54.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                       APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBAUGRSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB981838.4
PRIOR APPLICATION NUMBER: GB981838.4
PRIOR APPLICATION NUMBER: GB981838.4
PRIOR PILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FABELSEQ for Windows Version 4.0
SSOFTWARE: EASELSEQ for Windows Version 4.0
SSOFTWARE: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPELICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PRICATION NUMBER: UP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5715, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWORNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFRWQWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 FOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:::| |||:|
73 FEYRROLRKIR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-738-626-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-738-626-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                             Sequence 10, Application US/0981579;
Sequence 10, Application US/0981579;
Publication No. US2030028904A1
Seneral INFORMATION:
APPLICANT: Tina L. Gumienny
APPLICANT: Annie-Carole Tosello-Trampont
APPLICANT: Jason M. Kinchen
APPLICANT: Michael O. Hengartner
APPLICANT: Michael O. Hengartner
APPLICANT: Michael O. Hengartner
TITLE OF INVENTION: Genes Involved In Engulfment of Dying
TITLE OF INVENTION: Cells and Cell Migration
FILE REFERENCE: 1314.2008-001
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/285,469
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-15
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO: 15
LENGTH: 60
TYPE: PRT

ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-801-50-15)

Sequence 15, Application US/09881579

Publication No. US20030028904A1

SEQUENCE 15, Application US/09881579

Publication No. US20030028904A1

SEQUENCE INFORMATION:

APPLICANT: Enrico Bugnera

APPLICANT: Annie-Carole Tosello-Trampont

APPLICANT: Machael O. Hengartner

APPLICANT: Kodimangalam S. Ravichandran

APPLICANT: Kodimangalam S. Ravichandran

TITLE OF INVENTION: Cells and Cell Migration

FILE REFERENCE: 1314.2008-001

CURRENT APPLICATION NUMBER: US/09/881,579

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/285,469

FILM RELING DATE: 2001-06-14

PRIOR FILING DATE: 2001-04-19

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 15

LENGTH: 688

TYPE: PRT

ORGANISM: Murine

US-09-881-579-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.3%; Score 38; DB 9; Length 607; 66.7%; Pred. No. 76; cive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ||||||:
140 YLWQRNLRQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FOWORNLRK 10
RESULT 14
US-09-881-579-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-881-579-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-881-579-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
```

```
Gaps
              54.3%; Score 38; DB 9; Length 688; 66.7%; Pred. No. 86; 1; Indels tive 2; Mismatches 1; Indels
Query Match
Best Local Similarity 66 //
```

ò

Search completed: February 21, 2003, 08:08:08 Job time: 11.55 secs

: ||||||: 220 YLWQRNLRQ 228

2 FOWORNLRK 10

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 9.6 Seconds Run on:

(without alignments) 120.168 Million cell updates/sec

US-09-743-107B-82 70 1 CFQWQRNLRKVR 12 Title: Perfect score: Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	lactotransferrin p	_ rt	ı	he	\vdash	Ω	hypothetical prote		E	apolipoprotein B-1	hypothetical prote				-0	cytochrome P450 ho	trichohyalin like	carcinoembryonic a	hypothetical prote		(I)	cysteine synthase		MHC class I histoc	3-deoxy-manno-octu	histidyl-tRNA synt	cal p	ത	
RIES																														
SUMMARIES	ID	E	JC2323	S52107	T08030	AD2346	A28438	AB0858	T28820	E90094	B60950	F90580	T19429	T22597	T22879	T00510	T00513	B85431	D33876	AH3147	H70978	G86403	T47233	C82234	137477	D71876	F81660	T18633	T28852	A45687
	DB	. 4	7	7	N	7	1	7	N	C)	N	~	7	7	7	(7	C)	N	7	7	7	7	N	7	~	7	7	7	~	7
	Length	71	708	33	4568	298	707	511	932	205	274	282	681	275	357	515	543	3	114	$^{\circ}$	$^{\circ}$	æ	ч	C	9	σ	428	4	664	749
*	Query	7	72.9	œ.	65.7				58.6	57.1	57.1	55.7	55.7	54.3	54.3		54.3	54.3	52.9		52.9				52.9		52.9			
	Score	9	51	48	46	42	42	41	41	40	40	39	39	38	38	38	38	38	37	37	37	37			37	37	37	37	37	37
	Result No.		64	e	4	Ŋ	φ	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	ribosomal protein	ribosomal protein	ribosomal protein	50S ribosomal prot	pyridoxamine 5'-ph	pyridoxamine 5'-ph	probable pyridoxam	lipopeptide antibi	interleukin-2 rece	interleukin-2 rece	hypothetical prote	3-deoxy-manno-octu
G86506	G72115	867385	T04018	A48396	AH1301	AH1673	C89895	H97451	AB2670	AG3441	S74408	JC1113	S07442	T29571	E64639
7	7	7	7	~	N	7	7	7	0	7	N	Н	Н	N	N
759	759	962	1274	9	62	62	62	206	206	208	246	275	275	361	393
	6.	6.	6.5	4.	1.4	1.4	1.4	51.4	1.4	11.4	1.4	1.4	51.4	51.4	51.4
52.9	52	່ເດ	ທ່	S	Ņ	ហ	,	٠,	u,	uı	u)	L)	٠.		
37 52.9	37 52	37 52	37 5	36 53	36 5:	36 5	36	36	36	36	36	36 5	36	36	36

ALIGNMENTS

RESULT 1 TFHUL	
lactotransferrin precursor [validated] - human N.Alternate names: lactoferrin	
1. Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000 on: G01394; S11228; Ā45401; S10324; S15853; S20841; S07160; A61169; A31000; S7	4
R;Cho, Y. submitted to the EMBL Data Library, March 1994	
A;Reference number: G06820 A;Accession: G01394	
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA	
A; Residues: 1-711 < CHO.	
Aicloss-references: Embi-100/043/ NID:940/240; FIDN:AAB00324.1; FID:940/23/ R/Rey, WW.; Woloshuk, S.L.; Geboer, H.A.; Pieper, F.R.	
Nuclear Actus Res. 10, 2200, 1390 A;Title: Complete nucleotide sequence of human mammary gland lactoferrin.	
A; Reference number: S11228; MUID:90384839; PMID:2402455	
A, Molecule type: mRNA	_
A;Residues: 1-148,'T',150-422,'C',424-711 <rey></rey>	
A;Cross-references: EMBL:X53961; NID:g34415; FDIN:CAA77914.1; FID:g34416	
Mol. Endocrinol. 6, 1969-1981, 1992	
A; Title: Differential molecular mechanism of the estrogen action that regulates lactofer.	й
A. A. A. C. C. S. C.	
A; Molecule type: DNA	
A.Krebiculesi 1-15 o 11EN 5 o 12EN 7 A.Krebiculesi 1-15 o 11EN 5 o 12EN 5 o	
A; Note: sequence extracted from NCBI backbone (NCBIP:122202)	
K. POWELL, M.J. Ogden, J.E. Nivelein Noise Dear 10, 1011 1000	
Naciet, Aturs Res. 10, *11, *11, *13,00 N. A. Title: Nucleotide sequence of human lactoferrin cDNA.	
A;Reference number: S10324; MUID:90326549; PMID:2374734	
A.A.Cression: S103.24 A.Molerile tvne mRNA	
A.Residues: 3-711 -POW-	
A; Cross-references: BMBL: X52941; NID: g34411; PIDN: CAA37116.1; PID: g34412	
R)SCOWBLI, N.M.; KROOG, 1.A.; FUIK, W.U.; IWEEQIE, U.W. Riochem II 276 348-255, 1991	
Arities Expression of cloned human lactoferrin in baby-hamster kidney cells.	
A;Reference number: S15853; MUID:91264786; PMID:2049066	
A; Status: nucleic acid sequence not shown; not compared with conceptual translation	
A;Molecule type: mRNA A;Residues: 20-31 <st1></st1>	
A;Accession: S20841	
A. Molecule type: protein. A. Desidine. 20.28 / v. 20.21 / cm2.	

```
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain 21qr
                                     72.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.7%;
58.3%;
                                         Query Match 72.9
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1852 CFÓWÓSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFOWORNLRKVR 12
                                                                                                                                                                                                                                                           38 CYOWORRMRKL 48
                                                                                                                                                                                    1 CFOWORNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQRNLRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 CYÓWOKKMIRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                        à
                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                   A; Accession: S07160
A; Molecule type: mRNA
A; Molecule type: mNA
A; Molecule type: mNA
A; Molecule type: mNA
A; Molecule type: mNA
A; Molecule type: morphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID: 91235214; PMID: 1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Map position: 3421-3423
C; Superfamily: transferrin; transferrin repeat homology
C; Superfamily: transferrin; transferrin in binding; milk
C; Keywords: duplication; glycoprotein; in binding; milk
F; I-19 Domain: signal sequence #status predicted < SIG>
F; 20-711/Product: lactotransferrin #status experimental < NAT>
F; 21-356/Domain: transferrin repeat homology < TRH1>
F; 20-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
F; 157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #statat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: UC2323
R;Le Provoet, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A;Reference number: UC2323; MUID:94380047; PMID:8093048
                                                                                  É
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: normal breast tissue
R; Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
R.; Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
A; Jitle: Biochem. 145, 659-666, 1984
A; Title: Human Lactobransferrin: amino acid sequence and structural comparisons with oth
A; Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purification by aminohexyl affir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A; Mote: this is the final paper in a series
R; Houen, G; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affix A; Reference number: S74119; MUID:97054624; PMID:8898921
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-708 <LEP>
C;Superfamily: transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68; DB 1; Length 711
Pred. No. 0.00049;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 3-701,'SWKPVN' <PAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:119368; OMIM:150210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 CFOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A61169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S74119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lactoferrin - goat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
Jactoferrin - sheep (fragment)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
R.Oian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
B.Oochim. Biophys. Acta 123, 1995
A.Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet in A.Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet in A.Status: S2107
A.Accession: S2107
A.Accession: S2107
A.Accession: S2107
A.Molecule type: protein
A.Status: I.33 colA.
A.Molecule type: protein
A.Status: I.33 colA.
C.Superfamily: transferrin, transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T08030
R;Mitchell, D.R.; Brown, K.S.
Cell Soci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes A;Reference number: 216302; MUID:94274778; PMID:8006077
A;Accession: T08030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dynein beta heavy chain - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-4568 <MIT>
A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 4568;
   DB 2; Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.6%; Score 48; DB 2; Length 33; 54.5%; Pred. No. 0.074;
                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:119-1926/Region: nucleotide-binding motif A (P-loop) F:2202-2209/Region: nucleotide-binding motif A (P-loop) F:2530-2537/Region: nucleotide-binding motif A (P-loop)
Score 51; DB 2; Pred. No. 0.48; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.07
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB
Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: dynein heavy chain, ciliary C;Keywords: nucleotide binding; P-loop
```

```
C;Accession: AB0858
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Connecton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy. A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit
Nature 410, 1091-1096, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Nap position: 5
A,Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AL513382; PIDN: CAD06049.1; PID: g16504016; GSPDB: GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <DOU>
A;Cross-references: GB:AF165818; NID:g13794510; PIDN:AAK39885.1; GSPDB:GN00150
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: T28820
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: CNA
A,Residues: 1-92 - FAV>
A,Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A,Experimental source: strain Bristol N2; clone F07C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F07C3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
        C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: The highly reduced genome of an enslaved algal nucleus. A,Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26S proteasome SU B5 [imported] - Guillardia theta nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Accession: T28820
R; Favello, A.; Gattung, S.
submitted to the BMBL Data library, March 1996
A; Description: The sequence of C. elegans cosmid F07C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 2;
Pred. No. 37;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z20528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||: | |:
579 FQWQRSARLVK 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 FOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA A; Residues: 1-511 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: F07C3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: E90094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: E90094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                         R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lactoferrin precursor - mouse

NyAlternate names: lactotransferrin

Syspeciaes: Mus musculus (house mouse)

Cybeces: Nus musculus (house mouse)

Cybecesion: A28438; A41205

CyAccession: A28438; A41205

Aylithe: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret and the mouse mouse uterine and the mouse uterine secret and the mouse uterine a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Species: Nostoc sp. A. Nostoc sp. (strain PCC 7120)
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: AD2346
B;Kaneko, T.; Nakamira v ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <KUR>
A;Cross-references: GB:BA000019; PIDN.BAB76022.1; PID:g17133459; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-707/Product: lactotransferrin #status predicted <MAT>
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 1; Length 707; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2; Length 298;
Pred. No. 7.7;
```

3; Indels

60.0%; Scor. 54.5%; Pred. No. 10, 7.7 2; Mismatches

6; Conservative

Matches

Query Match Best Local Similarity

ö

RESULT 7

A; Molecule type: DNA A; Residues: 1-15 cLIU> A; Cross-references: GB: M74778 C; Superfamily: transferrin; transferrin repeat homology C; Keywords: dupil.cation; Glycoprotein F:1-19/Domain: signal sequence #status predicted <NIG> F:20-707/Product: lactotransferrin #status predicted <NM

A;Cross-references: EMBL:J03298 R;Liu, Y.; Teng, C.T.

A; Accession: A41205

A; Molecule type: mRNA A; Residues: 3-707 < PEN>

A;Accession: A28438

2; Indels

0; Mismatches

7; Conservative

Matches

163 FHWORNYRK 171

RESULT 6

2 FOWORNLRK 10

ò 셤

60.0%;

Query Match Best Local Similarity

A, Experimental source: strain PCC 7120 C, Genetics: A, Gene: alr4323

56

ô

apolipoprotein B-100 - rat (fragment)

C;Accession: B60950

57.1%;

C; Keywords: nucleomorph Query Match Best Local Similarity

A,Gene: prsB5 A,Map position: 1 A,Genome: nucleomorph

6; Conservative

Matches

à

```
A;Map position: 3
A;Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2;
                                                                           A,Reference number: Z19123
A,Reference number: Z19123
A,Reference number: Z1923
A,Accession: T19429
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,References: EMBL: Z81475; PIDN: CAB03914.1; GSPDB:GN00021; CESP: C24H11.8
A,Experimental source: clone C24H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1557 - WIL>
A; Cross-references: EMBL: Z83231; PIDN: CAB05749.1; GSPDB: GN00020; CESP: F57G9.1
A; Experimental source: clone F57G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: Z81089; PIDN: CAB03137.1; GSFDB: GN00028; CESP: F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
R;Dobson, R.
Rs;Dobson, R.
Rs;Dobson, R.
A;Reference number: Z19587
A;Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F57G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22879
E;Steward, C.
Submitted to the EMBL Data Library, December 1996
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.3%; Score 38; DB 2; Length 275; ilarity 54.5%; Pred. No. 36; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.7%; Score 39; DB 2; Length 681; Best Local Similarity 60.0%; Pred. No. 60; Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F53H4.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: Z19631
A;Accession: T22879
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-275 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||: ::|| |
262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||:| |:||
192 RWQKNRRRVR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 6, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                  A, Gene: CESP:C24H11.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: CESP:F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: CESP:F57G9.1
                               C; Accession: T19429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rilaw, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
J. Lipid Res. 31, 1109-1120, 1990
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: B60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: F90580
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-274 <LAW>
A;Note: authors translated the codon ATA for residue 8 as Val
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein MYPU_5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-282 <KURA
A;Coss-references: GB:AL445566; PID:g14089965; PIDN:CAC13723.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.7%; Score 39; DB 2; Length 282; 50.0%; Pred. No. 25; indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%; Score 40; DB 2; Length 274; 77.8%; Pred. No. 16; 1.1ve 0; Mismatches 2; Indels
                                                                                                                                                         Length 205;
                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C24H11.8 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
                                                                                                                                                      Score 40; DB 2;
Pred. No. 12;
1; Mismatches
```

Conservative

g

à

Best Local Similarity

Matches

Query Match

Conservative

Best_Local Similarity Matches 5; Conserv

Query Match

A;Gene: MYPU 5500 A;Genetic code: SGC3

à В RESULT 12 T19429

ö

```
ö
                                                                                                              Gaps
                                                                                                           ·.
                                                Query Match 54.3%; Score 38; DB 2; Length 357; Best Local Similarity 54.5%; Pred. No. 47; Matches 6; Conservative 5; Mismatches 0; Indels
A; Introns: 155/2; 207/3; 248/3; 290/2
```

A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-515 < ROUS
A; Cross-references: EMBL: AC002391; NID: 92642427; PID: 92642441
A; Experimental source: cultivar Columbia
R; M; Kao, H; Moffat, S; Rounsley, S.D.; Anea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
W; Koo, H; Moffat, K.S.; Cronin, L.S.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197

A;Accession: A84622 A;Status: preliminary A;Molecule type: DNA

A, Residues: 1-515 <STO>

A, Cross-references: GB: AE002093; NID: 92642441; PIDN: AAB87109.1; GSPDB: GN00139

A; Gene: At2g23220; T20D16.15

A;Map position: 2 A;Introns: 182/3; 310/3 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C; Keywords: heme; iron; metalloprotein F;312-471/Domain: cytochrome P450 homology <P45> F;449/Binding site: heme iron (Cys) (axial ligand) #status predicted

Gaps , , Query Match 54.3%; Score 38; DB 2; Length 515; Best Local Similarity 83.3%; Pred. No. 68; Matches 5; Conservative 1; Mismatches 0; Indels

; 0

1 CFOWOR 6

469 CFEWOR 474

g

Search completed: February 21, 2003, 07:47:54 Job time : 10.65 secs

us-09-743-107b-82.rsp

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-82 70 1 CFQWQRNLRKVR 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ption	P0278B homo sapien O9tumO camelus dro Q29tumO camelus dro Q39565 chlamydomon O77811 equus cabal P08071 mus musculu Q9x218 drosophila Q8x218 drosophila Q8x218 thermoaner P41187 liberibacte P30453 homo sapien Q9215 chlamydia m Q04916 rotavirus (Q1539 homo sapien Q92012 listeria mo Q92014 staphylococ Q55185 synechocyst P12342 bos taurus P2689B ovis aries Q927D1 chlamydia p Q9000 dosophila Q19910 caenorhabdi Q9100 arabidopsis Q2198B caenorhabdi Q9100 arabidopsis Q24325 drosophila Q14573 homo sapien P4506B haemophilus P37589 salmonollus P37589 salmonollus Q58878 methanococc
SUMMARIES	TRFL HUMAN TRFL CAMDR TRFL CAMDR TRFL HORSE TRFL HORSE TRFL HORSE TRFL HORSE NLA DROME RL28 THETN SYH CHLMU SYH CHLLW SYH SYH SYN CHLLW SYH SYH SYN CHLLW SYH SYN CHLLW SYH SYN CHLLW SYH SYN CHLLW SYN CHLLW
DB	
Length	7111 708 4568 695 695 695 602 602 603 603 603 603 603 603 603 603 603 603
ery	1 1 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Score	а п п п п п п п п п п п п п п п п п п п
Result No.	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

P12505 simian immu P49771 homo sanien	Q9kdle bacillus ha 035186 rattus norv	Q02135 lactococcus Q13639 homo sapien	084547 chlamydia t P48629 spinacia ol	Q9fg65 arabidopsis O9ulc6 homo sapien	P14632 sus scrôfa P20806 drosophila
VIF SIVS4 FL3L HUMAN	CCDA_BACHD	HISB_LACLA 5H4 HUMAN	SYH_CHLTR FD6C SPIOL	C911_ARATH	TRFL_PIG 7LES_DROVI
નન	-			44	нн
214	238	360	428	502 663	704 2594
50.0	50.0	50.0	50.0	50.0	50.0
3 3 3 3	32	35	35	35	32 32
9.94 5.74	36	8 6 6 7	40 41	42 43	44

ALIGNMENTS

us-09-743-107b-82.rsp

```
SEQUENCE OF 237-711 FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Mhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

Ghoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,

Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,

Dragan Y., Giacalone J., Pae A., Powell B., Solinsky K.A., Desilva U.,

Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Gardia D.,

Sagripanti J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
MEDLINE=90064528; PubMed=258556;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                          "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of
                                                                                                                                                                                                                                                                                                          MEDLINE-82046817; Pubmed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Mutagenesis of the histidine ligand in human lactoferrin: iron
                                                                                                                                 SEQUENCE OF 20-711.

MEDLINE=85076667; PubMed=6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F., Metz-Boutigue M.-H., Jolles J., Jolles P.;
"Human lactorransferrin: amino acid sequence and structural comparisons with other transferrins.";
Eur. J. Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                            PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding properties and crystal structure of the histidine-
253-->methionine mutant.";
Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sagripanti J.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'An 88 amino acid long C-terminal sequence of human
                                                       Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 670:243-254(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). MEDLINE=99190892; PubMed=10089347;
                                                                                                Nucleic Acids Res. 18:4013-4013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crystallogr. D 51:629-646(1995)
                    TISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=82262043; PubMed=7049727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 142:107-110(1982).
                                                                                                                                                                                                                                                                                                                                                                                                               and C-terminal domains.";
  SEQUENCE OF 3-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blood 70:989-993 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 609-711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactotransferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resolution.
                                                                                                                                                                                                                                                                                                                                                        Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker E.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jolles
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
FUNCTION: LACTOFERROXINS A, B AND C HAVE OPICID ANTAGONIST ACTIVITY. LACTOFERROXIN A SHOWS PREFERRICE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
                                                                                                                                                                                                            MEDLINE-91166929; PubMed-1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
from human lactoferrin.";
                                                                                                                                                                                                                                                                                                                         Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Quesiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanaal A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
"Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.",
Mol. Vision 4:31-32(1998).
             Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                         Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.; "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
Sun X.I., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted.
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS
                                                                                 ANGSTROMS).
                                                                                                                                                                                                                                                                              Agric. Biol. Chem. 54:1803-1810(1990).
                                              Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                            CHARACTERIZATION OF LACTOFERROXINS.
                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTRC
MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, M93150; AAA36159.1; --
EMBL, M83202; AAAS9511.1; --
EMBL, M83202; AAAS656.1; --
EMBL, M18642; AAA86665.1; --
EMBL, M7832168; AAG48753.1; --
EMBL, BC015822; AAH15822.1; --
EMBL, BC015822; AAH1582.1; --
EMBL, BC015823; AAH1582.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73700; AAAS9479.1; -.
52941; CAA37116.1; -.
95626; AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X53961; CAA37914.1; -.
EMBL; U07643; AAB60324.1; -.
                                                                                                                                                                                                                                                                                                             VARIANTS THR-30 AND ARG-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-96.
12-MAR-97.
21-APR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1LCF; 31-AUG-94.
1LCT; 31-OCT-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X52941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1LCT;
1LFG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1LGC;
1BKA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1LGB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1LFH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1LFI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1DSN;
1HSE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
EMBL;
```

m

```
æ
DISULFID
DISULFID
DISULFID
                         DISULRID
DISULRID
DISULRID
DISULRID
DISULRID
                                                                                                                                                           BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                            CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                           METAL
METAL
METAL
                                                                                                                       METAL
METAL
                                                                                                                                         METAL
METAL
                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
à
                                                                                                                                                                                                                                                                                                                                                             셤
                           ö
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus
                                                                                                                                                                                                                                  STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486[1999].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BMBL; AJ131674; CAB53387.1; -.
BSMBL; AF165879; AAF82241.1; -.
HSSP; O77611; 1B1X.
InterPro; IPRO4155; Transferrin.
PFIGH, PRO045; Lransferrin, 2.
PRINTS; PRO0422; TRANSFERRIN.
SMART; SMO0049; TRANSFERRIN.
SMART; SO00205; TRANSFERRIN 1; 2.
PROSITE; PSO0206; TRANSFERRIN 1; 2.
PROSITE; PSO0206; TRANSFERRIN 3; 2.
PROSITE; PSO0207; TRANSFERRIN 3; 2.
                         .
 Query Match

97.1%; Score 68; DB 1; Length 711;
Best Local Similarity 91.7%; Pred. No. 0.00017;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                          Camelus dromedarius (Dromedary) (Arabian camel).
                                                                                                      TRFL CAMDR STANDARD; PRT; 708 AA. O9TUMO; Q9MZS5; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 41, Last annotation update) 15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
SIMILARITY
                                                                                                                                                       Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY
BY
BY
BY
BY
BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19
708
708
64
64
192
217
200
200
264
399
                                        1 CFOWORNIRKVR 12
                                                           39 CPOWORNMRKVR 50
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384
384
384
1134
1189
367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signaî.
SIGNAL
CHAIN
REPEAT
REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                 g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              le Provost F., Nocart M., Guerin G., Martin P.;
"Characterization of the goat lactoferrin cDNA. Assignment of the
relevant locus to bovine U12 synteny group.",
Biochem. Biophys. Res. Commun. 2031334-1333(1994).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TRY O ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER (BY SINILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cupra marcus (gode).

Bukaryota, Metasoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.9%; Score 51; DB 1; Length 708; llarity 66.7%; Pred. No. 0.17; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F -> S (IN REF. 2)

G -> A (IN REF. 2)

G -> PLK (IN REF. 2)

LLS -> PLK (IN REF. 2).

L -> F (IN REF. 2).

A -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                  IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 2 (BY SIMILARITY)
ANION (BY SIMILARITY)
ANION (BY SIMILARITY)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRFL_CAPHI STANDARD; PRT; 708 AA.
AC 029477; 029479;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DCC 1998 (Rel. 37, Last sequence update)
DT 15-DCC 1998 (Rel. 37, Last sequence update)
DT 15-DCC 1801 (Rel. 37, Last cannotation update)
DE Lactotransferrin precursor (Lactoferrin)
BY SIMILARITY.
BY SIMILARITY
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Mammary gland;
MEDLINE=94380647; PubMed=8093048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77211 MW;
                                                                                                                                                                                                        1111
2211
272
414
414
452
545
614
614
682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | | | | 38 CAQWQRRMKKVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642 6
708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capra hircus (Goat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9925;
```

STANDARD;

```
chain genes.";
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES
                                                                                                                                                                                                                         Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                             Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonae.
                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
Chlamydomonas reinhardtii.
                                                                                                                                                                                                      STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=3055;
                                                DYHB CHLRE
Q39565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
NP BIND
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                          RESULT 4
DYHB CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                   à
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
                                                                                                                         EMBL; U53857; AAA97958.1; -.
HSSP; 077698; 1CE2.
InterPro; IPR001156; Transferrin.
PFINITS; PR00422; TRANSFERRIN.
PRINITS; PR00494; TR FER, 2.
PROSTITE; PS00206; TRANSFERRIN.
PROSTITE; PS00206; TRANSFERRIN.
PROSTITE; PS00206; TRANSFERRIN.
PROSTITE; PS00206; TRANSFERRIN.
PROSTITE; PS00207; TRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.9%; Score 51; DB 1; Length 708; 63.6%; Pred. No. 0.17; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 -> V (IN REF. 2).

L -> R (IN REF. 2).

C -> K (IN REF. 2).

F -> P (IN REF. 2).

S -> R (IN REF. 2).

S -> R (IN REF. 2).

D -> G (IN REF. 2).

FZEDA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
ALINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .)
(GLCNAC. . .)
(GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .)
(GLCNAC. . .)
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                        2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
N-LINKED
N-LINKED
N-LINKED
I -> V (II
L -> R (II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         708 AA;
                                                                                                                                                                                                                                                                       1
20
20
364
28
134
176
                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
METAL
BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                     DISÜLFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                    SIGNAL
CHAIN
REPEAT
                                                                                                                                                                                                                                                        Signal.
                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
METAL
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
DYNEIN HAS ATPASE ACTIVITY.
-!- SUBURIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERNEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U02963; AAA19956.1; ...
Interpro: IPR004273; Dynein, heavy.
Pfam; PP03028; Dynein, heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.7%; Score 46; DB 1; Length 4568; 58.3%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519961 MW; 9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL)
ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0778<u>11;</u>
15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1852 CFÓWOSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4568 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11158
11372
11372
11514
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
11778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
TRFL HORSE
ID TRFL HORSE
```

0

Gaps

; 0

Conservative

Matches

Local Similarity

|:|||| :||: CYQWQRRMRKL 48 CFQWQRNLRKV 11

38

qq à

```
NCBI_TaxID=10090;
   98
198
259
401
439
532
601
127
143
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Uterus;
                                                                                              CARBOHYD
CARBOHYD
SEQUENCE
                                                                                      CARBOHYD
                                                                  BINDING
   METAL
METAL
METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                               TRFL MOUSE
                                                                                                                                                      Matches
                                                                                                                                                                                                                       RESULT
    Dp
                                                                                                                                                                         ਨੋ
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           resolution.";
J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                EMBL; AJ010930; CAA00407.1; -.

R PDB; 1B1X; 02-DEC-98.

R PDB; 1B1X; 02-DEC-99.

R PDB; 1B72; 02-FEB-99.

R InterPro; IPR001156; Transferxin.

R PRINTS; PR00422; TRANSFERRIN.

R PRINTS; PR00205; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN 1; 2.

R PROSITE; PS00206; TRANSFERRIN 2; 2.

R PROSITE; PS00207; TRANSFERRIN 3; 1.

R Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.

I NON TER 1 6
                                                                                                                                                          Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                  SEQUENCE FROM N.A.

Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
15-JUL-1999 (Rel. 38, hast sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON 1 (BY SIMILARITY).
                                                                                                                                                                                                                                    1- SUBCELLULAR LOCATION: Secreted.
1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LACTOTRANSFERRIN
                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                         TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354
364
411
4431
4431
4497
4631
508
631
6631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
REPEAT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-14 FROM N.A.
MEDILEP292042099; PubMed=1939212;
Liu Y., Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 266:21880-21885 (1991).
--I- FUNCTION: TRANSPERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pencecost B.T., Teng C.T., "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 1; Length 695;
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                          07BB84D50E1B165D CRC64;
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                             (GLCNAC. . .)
                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRFL_MOUSE STANDARD; PRT; 707 AA. P08071; P70690; Q61799; Q922P2; 01-AUG-1988 (Rel. 08, Created) 15-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                          N-LINKED (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 262:10134-10139(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                          75991 MW;
                                                                                                                                                                                                                                                                                                                                                             61.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
  98
1198
2259
2259
4401
4401
1127
1127
287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 CAKFORNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                          695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uterine secretions.
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
```

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Druseryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Peerygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)

SEQUENCE FROM N.A. ACCormick A.V., Goldberg M.L.; "Gene required for elongation of meiosis I spindle in Drosophila

McCormick A.V. SEQUENCE

females.

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132;

SEQUENCE FROM N.A.

ø

```
.) (POTENTIAL).
                                                                                                                                                                    !ransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 S -> T (IN REF. 2).

449 A -> D (IN REF. 1).

449 E -> G (IN REF. 2).

629 E -> V (IN REF. 2).

77865 MW, P26AE0340AAC19AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANION (POTENTIAL).

N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
MR -> IQG (IN REF. 1).
MR -> Q (IN REF. 2).
M -> L (IN REF. 2).
S -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                       BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                       2.
BY SIMILARITY.
or send an email to license@isb-sib.ch)
                                                                              MOD; MOISSON; LET.
INCEPED; IPRO01156; Transferrin.
Pfam; PR00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANION
                              EMBL; D88510; BAA13633.1; -.
EMBL; BC006904; AAH06904.1; -.
EMBL; M74778; AAA39427.1; -.
                    EMBL; J03298; AAA40525.1; -.
                                                                                                                                                                                        19
707
357
707
                                                                                                                                                                                                                                 63
216
1191
191
199
263
398
                                                                                                                                                                                                                                                                                                                                                                                                                                       271
413
451
544
613
139
139
118
118
                                                             PIR; A28438; A28438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   629
707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                       P02788; 1CB6
                                                                                                                                                                                                                                                                                                                                                                                                                                      271
413
451
613
613
1139
481
118
                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                             Signal.
SIGNAL
                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                             REPEAT
                                                                       HSSE;
                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
METAL
                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                         METAL
```

```
ô
                                                                                       Gaps.
                                                                                       .;
0
                                                                                       3; Indels
                                                                                     9.9
                                                                                       Mismatches
                                                                                    Score 42;
Pred. No.
                                                                                    60.0%;
54.5%;
                                                                                       6; Conservative
                                                                                          1 CFQWQRNLRKV 11
                                                                                            37 CLRWONEMRKV 47
```

292 AA.

NLA DROME STANDARD; Q9XZL8; Q9V391; 30-MAY-2000 (Rel. 39, Created)

NLA DROME
ID NLA D
AC Q9XZL
DT 30-MA

Matches

ö g

```
Adams N.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Levis S.E., Hichards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Halt G., Nelson C.R., Miklos G.L.G.,
RA Baridon R.C., Rogers Y.-H.C., Halt G., Nelson C.R., Miklos G.L.G.,
RA Baridon R.C., Rogers Y.-H.C., Halt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Cawley B.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck U., Brokstein P., Berottier P.,
Buttis K.C., Busam D.A., Dang E., Mays A.D., Dew I., Diez S.M.,
RA Grarry J.M., Cawley S., Daline C., Deverport L.B., Davis R.,
Ra Gablos B., Delicher A., Deng Z., Mays A.D., Dew II., Diez S. M.,
Ra Gablos B., Delicher A., Howlar C., Ferriaz C., Ferriac S., Pleichmann W.,
RA Harris N.L., Harvey D., Hernandez J.R., Houck J.,
Buttis N.G., Evangelista C.C., Ferraz C., Galbart W.M., Glasser K.,
Alalali M., Kalush F., Krapen G.H., Gu. S., Gulbart W., Glasser K.,
Jalali M., Kalush F., Krapen G.H., Wei M., Horner S., Fleichmann W.,
RA Merkingel B.L., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Ra Mount S.M., Wow, W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ra Mount S.M., Wow, W., Wirky B., Murphy L., Muzny D.M., Nelson D.L.,
Ra Milaina N.V., Mondary C., Moriay C., Scheler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Shen H.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Shen B.,
Ranger E., Spradling A.C., Stapleton M., Skupski M.P., Shen B.,
Ranger E., Kohler S., Walnelson E., Wall Shen D.,
Ranger E., Spradling A.C., Stapleton M., Skupski M.P., Shen B.,
Ranger E., Spradling A.C., Stapleton M., Skupski M.P., Shen B.,
Ranger E., Spradling A.C., Stapleton M., Skupski M.P., Shen B.,
Ranger E., Remington K., Sunders R., Wenter E., Wang G.L.,
Ranger E., Remington K., Sunders R., Wenter E., Shen B.,
Ranger E., Spradling 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF147700; AAD33987.1; -.
EMBL; AE003712; AAF55285.1; -.
FlyBase; FBgn0026629; nla.
SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
```

Tue Dec

```
g
                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEE-1995 (Rel. 31, Created)
10-FEE-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                          MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTBINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Planet P., Jagoueix S., Bove J.M., Garnier M.; "Detection and characterization of the African Citrus Greening
  DB 1; Length 292;
8.9;
                                                                                                                                                                                                                            Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.3%; Score 38; DB 1; Length 62; 60.0%; Pred. No. 2.7;
                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L28.
RPMB OR TTE1495.
                                                                                                                                                                                                                                       Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                 62 AA.
  Score 39; DB Pred. No. 8.9; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                             Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE013107; AAM24713.1; -.
           54.5%;
  55.7%;
                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=MB4 / JCM 11007;
                                                                    150 FOWLRSFREIR 160
                                              2 FOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|: |:||||
27 RWKPNIRKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 OWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=34020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Nelspruit;
                                                                                                                               RL28 THETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPOB LIBAF
P41187;
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                       Qar9U1:
                                                                                                        THETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPOB LIBAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                 rpoBC operon.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
Liberobacter by amplification, cloning and sequencing of the rplKAJL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93235211; PubMed=8475492; Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J., Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L., du Toit E.D., Parham P.; "Structural diversity in the HLA-A10 family of alleles: correlations
                                                                                                                                                                                                                                                 {RNA}(N).
-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=93056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HLA-A,B antigens of black populations formed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Antigens 41:72-80(1993).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMPUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P30455; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34 (A-10) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.3%; Score 38; DB 1; Length 146; 60.0%; Pred. No. 6.5; 4; Indels tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Transcription; DNA-directed RNA polymerase.
NON TER 146 146
SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001572; RNA pol_B.
Pfam; PF00562; RNA pol_B; 1.
PROSITE; PS01166; RNA_FOL_BETA; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (A*3401/A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U09675; AAA19557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 60.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interallelic conversion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWORNLRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 CVOWSRGARK 19
                                                                                                                                                                                                                                                                                                                                                               BETA' CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with serology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LA34 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1A34 HUMAN
```

ô

α

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                      POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TH CHIMU STANDARD; PRT; 428 AA.

ID SYH CHIMU STANDARD; PRT; 428 AA.

AC Q9PJJ9;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40) Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 1; Length 365; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      063BF63E6E6E01F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW-34 (A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR 004379.

K -> N (ITA A*3402).

FTId=VAR 004380.

F -I (IIA A*3402).

/FTId=VAR 004381.

P -> S (IIA A*3402).

/FTId=VAR 004382.

Q -> R (ITA A*3402).

FTId=VAR 004382.

W -> L (INA A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /AR 004384.
(IN A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> V (IN A*3402)
/FTId=VAR 004379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . -> I (IN A*340 /FTId=VAR 004385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V -> L (IN
FTId=VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 AA; 41055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.9%;
                                                                                                                                                                                                                                                                                                            EMBL; X61704; CAA43873.1; -. EMBL; X61705; CAA43874.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 142800; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
Pfam; PF0129; MHC I; 1.
ProDom; PD000050; MHC I; 1.
SMARI; SM00407; IGG1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity 66.7
Atches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
332
332
365
110
188
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                            PIR; S16767; S16767.
PIR; S16771; S16771.
                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; 019673; 1HSB.
  MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 WORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 WDRNTRKVK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
1115
207
299
309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
SO THE PERFERENCE OF THE PERFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              STRAIN=MOPD / Nigg;
MEDLINE=20150255, PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00587; FRNA-synt 2b; 1.
Pfam; PF0129; HGTP_anticodon; 1.
TIGRFAMS; TIGRO0442; hiss; 1.
PROSITE; PS50862; AA, TRNA LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mucleic Acids Res. 28:1397-1406(2000).
-!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
diphosphate + L-histidyl-ENA(His).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDILINE=9333340; PubMed=8386274; MEDILINE=9323340; PubMed=8386274; Mackow E.R., Nerner-Eckert R., Fay M.E., Tao H., Chen G.-M.; Identification and baculovirus expression of the VP4 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Outer layer protein VP4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
Viruses, dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 1; Length 428;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428 AA; 48939 MW; 9CF859ED0E689DDF CRC64;
                        HISS OR TC0830.
Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UUN-1994 (Rel. 29, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
01-UUN-1994 (Rel. 29, Last annotation update)
01-UUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            749 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002106; AAtRNA ligasell.
InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004516; HisS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002314; tRNA-synt_2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human group B rotavirus ADRV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE002349; AAF39630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; 032422; 1QE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 CFSWAKHLR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=12705;
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
                                                                                                                           NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWORNLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGR: TC0830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VP4 ROTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       004916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOW WENT TO THE PROPERTY OF TH
```

0

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Bone marrow;
MEDLINE=$6651387; PubMed=7584026;
MOMUNTA N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,
Nomunta N., Miyajima N., Bahikawa K.-I., Tabata S.;
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                                                                                               (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
          -!- SUBCELLULAR LOCATION: Outer capsid.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   D1223527DEAE0F21 CRC64;
                                                                                                                                                                                                                                                                                      (GLCNAC. . .)
(GLCNAC. . .)
                                                                                                                                                                                                                                                                            (GLCNAC. . .)
                                                                                                                                                                                                                                                               (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                       (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                     (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 765 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                    N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                           N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                      EMBL; M91434; AAA47338.1; ...
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                  84362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein KIAA0008
J. Virol. 67:2730-2738(1993)
                                                                                                                                                                                                                     Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                    29
109
133
407
527
568
620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 1:27-35(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 CFTWDMNCANVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Eye, and Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                               749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                     Coat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOOB HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIAA0008.
                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YOOR HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
```

```
·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A MCDINE-INSTANTION TO THE TRANSPACE OF THE PROPERTY OF THE PROPERTY TO THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                        52.9%; Score 37; DB 1; Length 765; 62.5%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
                                                                                                                                                                     Hypothetical protein.
SEQUENCE 765 AA; 85668 MW; 00AFF91A02387EA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Hypothetical protein (17D1.07c in chromosome II.
                                                                                                                                                                                                                                                                                                              1; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
                                             EMBL; D13633; BAA02797.1; -.
EMBL; BC010658; AAH10658.1; -.
EMBL; BC016276; AAH16276.1; -.
                                                                                                                        InterPro; IPR005026; GKAP.
Pfam; PF03359; GKAP; 1.
                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              367 CFEWDRKL 374
                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPBC17D1.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YBX7 SCHPO
Q10201;
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
YBX7_SCHPO
                                                                                                                                                                                                                                                                                                      Matches
SS ¥ ¥ ¥ ¥ ¥ ¥ 8
                                                                                                                                                                                                                                                                                                                                                              ð
```

```
| BMED. A0013121 CAACA0411.1; -
| BR | InterPro; IPR0(01755; CAACA0411.1; -
| BR | InterPro; IPR0(01755; CAACA041.1; -
| BR | InterPro; IPR0(01755; CAACA041.1; -
| BR | Prom; Pro; IPR0(01757; CAL Logion. )
| BR | Prom; Pro; IPR0(01757; CAL Logion. )
| BR | Prom; Pro; IPR0(01757; CAL Logion. )
| BR | Pro; IPR0(01757; CAL Logion. )
| BR | Pro; IPR0(01757; CAL Logion. )
| FT | Mondal, CAL Logion. | | | |
| FT | Mondal, FT | Mondal, CAL Logion. |
| FT | Mondal, FT | Mondal, CAL Logion. |
| FT | Mondal, FT | Mondal, CAL Logion. |
| FT | Mondal, FT | Mondal, CAL Logion. |
| FT | Mondal, FT | Mondal, FT | Mondal, FT |
| FT | Mondal, FT | Mondal, FT | Mondal, FT |
| FT | Mondal, FT | Mondal, FT | Mondal, FT |
| FT | Mondal, FT | Mondal, FT | Mondal, FT |
| FT | Mondal, FT | Mondal, FT | Mondal, FT |
| FT | Mondal, FT | Mondal, FT | Mondal, FT | Mondal, FT |
| FT | Mondal, FT | Monda
```

; 0

0; Gaps

Query Match

51.4%; Score 36; DB 1; Length 60;

Best Local Similarity 66.7%; Pred. No. 5.8;

Matches 6; Conservative 2; Mismatches 1; Indels

4 WQRNLRKVR 12 |: ||:||| 27 WKANLQKVR 35 Search completed: February 21, 2003, 07:27:57 Job time : 4.6 secs

us-09-743-107b-82.rspt

```
Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q19153 caenorhabdi
Q77855 human immun
Q77856 human immun
Q98rr2 guillardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8yp77 anabaena sp
Q38115 bacteriopha
O31090 rhizobium 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8s934 diospyros k
Q8z462 salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8tcd2 homo sapien
Q9ucy5 homo sapien
Q9tr80 ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9nus2 homo sapien
                                                                                                       February 21, 2003, 07:25:55; Search time 20.8 Seconds (without alignments) 118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8tax2
                                                                                                                                                                                                                                                                                                                                                                                      671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TCD2
Q9UCY5
Q9TR80
Q8YP77
Q38115
O31090
Q8TAX2
Q8UGX2
Q8S934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q77855
Q77856
                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_plant:*
sp_rodent:*
sp_virus:*
sp_vortebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98RR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ## property color of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
                                                                                                                                                                                          US-09-743-107B-82
70
                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                           1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110
115
115
115
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466
488
488
511
932
91
205
279
570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPTREMBL
                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0
84.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.
11.
11.
11.
11.
11.
11.
11.
11.
                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
```

	17 3	9 55	7.7	109	15	Q9YQC1 Q9YQC0		Q9yqc1 Q9yqc0	L human	immun immun
	יחת	י עס ע		109		O9 YOB9		;q5X6O 3q5X6O	human human	immun immun
	ጣ ጣ	თთ		109 109		Q9YJI7 Q9YIJ2		7. i (7.60)	human human	immun
	w w	ი თ	7.1	115		Q9Q9L0		0090310	human	immun
	nm	, o		179		Q9CZQ7		09czd)	mus	musculu
	m m	o o	7.7	233		Q9D4X5		09d4x	mus mu	musculu
	nm	, o		282		Q98Q19		Q98q19	mycoplasma	asma
	m m	0.0	r. 1	341		QBR2A4		QBr2a4	mus mu	sculu
	n m	ט ט		368 368		09D9X0		509090 0x609x0	mus mus	musculu
	mr	0.0	7:0	368		O9JITI		Q9jit1	SUM.	sculu
	n m	ח פע		5/2		OSIESS 9XVD1		. 081653 09xvd1	caenorb	call1 abdi
	en e	on a	7.5	504		97204		097204	leishmania	nia
	nm	o ao	n m	81		090863		Q61.9u. 090863	human	immun
	mr	6 0 0	۳ د	105		Q9XFD5		O9xfd5	oryza sati	
	nm	D 60	i w.	148		Q9LIN4 Q9XHP1		091tn4 09xhp1	arabidoj . Bebamum	opsis m ind
	mm	oo a	w	275	O L	93780		093780	caenorhabd	abdi
	ი ო	0 00	, m	515	າ 01 ດີ	022185		062266	caenornabdı arabidonsi	abdı
	i Mi M	ma		543	101	022188		022188		opsis
						ALIGNMENTS	MENTS			
RESULT Q8TCD2	ULT 1									
n c	Q8TCD2 PRELIM	PR	PRELIMINARY	ARY;		PRT;	711 AA.			
A F	08TCDZ;	7) 600	TEMBI.	د او	_	(Footbod)				
Į	01-JUN-20	002 (T	(TrEMBLrel			,	Ĭ'n	(e)		
E E	01-JUN-20)02 (T	rEMBLr in	_		Last ann	annotation updat	late)		
so	Homo sapiens	ens (
0	Eukaryota	a; Met	oa;	Chordata,	ata;		Craniata; Vertebrata;	щ	omi;	
88	Mammalia; Euther NCBI_TaxID=9606;	: Euth :D=960	i a :	Prima	tes;		hini, Homin	idae; Homo.		
S C	[1]	NO CO	۶ 2							
RG	TISSUE=PROSTATE;	FROM	Σ.Α. Έ							
RA T	Strausberg	'9 R.;	(000)	4	<u>ت</u> ک	MDT./Con	+ Fand Jacano / Tawa et+	(
E E	EMBL; BC0	1 (FED)22347	-2002/	347	1 : E	EMBL/Genu 		databases.		
85	SEQUENCE	711	AA;	8327	≊		1B9C7EE097C45FAF	CRC64;		
S & S	Query Match Best Local S	imi		ω ω .		Score Pred.	4;	Length 711;		
W.	atches 10		Conserva	tive	≓	Ä.	smatches 0	; Indels	0; Gaps	0
ð	1 CFON	CFOWORNLRKV	KV 11							
qq	39 CPÓW	CPOWORNMRKV	KV 49							
RESULT	LT 2		٠							
סאכט	7.75									

01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJW-2000 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Q8xse2_ralstonia s Q8s487 zea mays (m

Q8XSE2 Q8S487

PRT;

PRELIMINARY;

Q9UCYS

·.

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWORNLRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 CYPWOKNILK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                163 FHWORNYRK 171
                                                                                                                                                                                                                                                                                        Bacteriophage rlt.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                            2 FOWORNLRK 10
                                                                                                                                                                                                                                                                                                              NCBI TaxID=43685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                      Viruses
                                                                                                                                                                                                                                   038115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  031090
                                                                                                                                                                                                                       038115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       031090
SOW REPARA
                                                                                                                                                                g
                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps,
                                                                                                                                                                             Gaps
                                                    Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                             ;
0
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                   84.3%; Score 59; DB 4; Length 38; 90.9%; Pred. No. 0.0011; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Čyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                         InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Blophys. Acta 1243:25-32(1995).
HSSP; O77698; 1CE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAB15A73961 CRC64;
                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last Bequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.6%; Score 48; DB 6; 54.5%; Pred. No. 0.09; ive 4; Mismatches
                                                                                                                                                                                                                                                                              33 AA.
                                                                                  Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; IBKA.
                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21595285; PubMed=11759840;
                                           MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein Alr4323.
                                                                                                                                                               Local Similarity 90.3
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anabaena sp. (strain PCC
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                 Lactoferrin (Fragment).
                                                                                                                                                                                                 FOWORNIRKVR 12
                                                                                                                                                                                                            21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNLRKV 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep
                                                                            seminal plasma.";
          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                       Q9TR80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08YP77
                                                                                                                                                                                                                                                                            Q9TR80
                                                                                                                                                                           Matches
                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
유
                                                                                                                                                                                                 ð
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96332668; PubMed=8730874;
Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;
"Inducible gene expression mediated by a repressor-operator system
isolated from Lactococous lactis bacteriophage rlt.";
Mol. Microbiol. 19:1331-1341(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venema G., Nauta A.; "Sequence analysis and molecular characterization of the temperate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  031090;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 31.0 kDa protein.
Rhizobium leguminosarum (biovar viciae).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96332669; PubMed=8730875;
Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,
                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasauda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena gp. strain PCC 7120.";
                                                                                                                                                                                                                                                        Score 42; DB 16; Length 298; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=VF39;
Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 469;
                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lactococcal bacteriophage rlt.";
Mol. Microbiol. 19:1343-1355(1996).
EMBL; U38906; AAB18704.1;
SEQUENCE 469 AA; 53160 MW; 1F8E02D4325CGBB9 CRC64;
                                                                                                          DNA Res. 8:205-213(2001).
EMBL; AP003596; BAB76022.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 298 AA; 34513 MW; 64036E6B52299A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 AA
                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 42; DB 60.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                        60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobiaceae; Rhizobium
```

0;

Tue Dec

```
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 CFOWESTLR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWORNLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 OWORNIR 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QWQRNLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella.
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8S934
Q8S934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK-ACS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8Z462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                            datches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 088934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBZ462
           RATE SERVICE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=PLACENTA;
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nagatisuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                      Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G., Ksenzenko V.N.; Ksenzenko V.N.; Shortional organization of the exopolysaccharide biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39."; Mol. Biol. (Mosk) 32:797-804(1998). EMBL, ARCOS8010; AAB88891.1; -.. Hypothetical protein. SEQUENCE 273 AA, 30986 MW; F195D2FEF7AD44D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ1175 fis, clone PLACE1007375, weakly similar to phorbol ester/diacy1glycerol-binding protein UNC-13.
                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                            58.6%; Score 41; DB 2; Length 273; 70.0%; Pred. No. 16; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025708; AAH25708.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ11175.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                 MEDLINE=99113394; PubMed=9914965
                                                                                                                                                                                                                                                                                                                 Local Similarity 70.0 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      245 RWLRNLRKLR 254
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   3 OWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 CFOWESTLR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQRNLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TAX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9NUS2
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TAX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9NUS2
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   du
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Peprmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ebenaceae; Diospyros.
NCBI_TaxID=35925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. HIRATANENASHI;
Nakano R., Ogura E., Kubo Y., Inaba A.;
"Water stress induces ethylene biosynthesis in Japanese persimmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                 A Ninomiya K., Iwayanagi T.;

I Mabo human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

R RBL; AK002037; BAA92048.1; -..

R HSSP; P21707; IBYN.

R InterPro; IPR000008; C2.

InterPro; IPR000008; C2.

R InterPro; IPR000008; C2.

R PRINTS; PR00360; C2DOMAIN 1; UNKNOWN 1.

R PROSITE; PS00039; C2; 1.

R PROSITE; PS00039; RRM RNP 1; UNKNOWN 1.

R PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.

R PROSITE; PS000030; RRM RNP 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.6%; Score 41; DB 10; Length 488; Best Local Similarity 100.0%; Pred. No. 29; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.6%; Score 41; DB 4; Length 466; 66.7%; Pred. No. 28; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB073006; BAB89349.1; -. SEQUENCE 488 AA; 55238 MW; 81C38BE8F67C21AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TIEMBLrel. 21, Created)
01-JUN-2002 (TIEMBLrel. 21, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diospyros kaki (kaki persimmon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
```

; 0

```
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       3 QWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                              67 OWNRTLOKVR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QWQRNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                      NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         077856;
                                 Q77855
Q77855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           077856
          RESULT 12
Q77855
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 077856
                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
     MEDLINE=21534947; PubMed=11677608;
MEDLINE=21554947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Rethwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Mhitchead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella
""Complete genome sequence of a multiple drug resistant Salmonella
""Complete Serovar Typhi CT18";
"Mature 413:848-852(2001).
"REMBL, AL627276; CAD06049-1; -.
REMBL, AL627276; CAD06049-1; -.
WHypothetical protein; Complete proteome.
"WHypothetical protein; Complete proteome.
                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                         58.6%; Score 41; DB 16; Length 511; 58.3%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.6%; Score 41; DB 5; Length 932;
63.6%; Pred. No. 59;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BRISTOL N2;
Favello A., Gattung S.;
"The sequenc of C. elegans cosmid F07C3.";
"Theteque (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 105038, AAG24025.1; -.
InterPro; IPR000731; HMGCR/patch_5TM.
PROSITE; PS50156; SSD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 105.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                              932 AA.
                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                      Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                  350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                          1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 FQWQRSARLVK 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                             019153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                ठे
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=95191002; PubMed=7884875;
MILDINE=95191002; PubMed=7884875;
MILDINE=95191002; PubMed=7884875;
MILDINE=95191002; PubMed=7884875;
Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;
Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;
"Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is unrelated to time of HIV-1 RNA positivity in the child.";
J. Virol. 69:2285-2296(1995).
EMBL; Z47867; CAA87881.1;
"InterPro; IPRO00777; GA120.
Pfam; PF00516; GP120.
ALDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95191002; PubMed=7884875; Maiken C.L., Dekker J., Medline=95191002; PubMed=7884875; Maiken C.L., Dekker J., Scherpbier H.J., de Perre P., Boer K., Goudsmit J.; Scherpbier H.J., de Perre P., Boer K., Goudsmit J.; Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is unrelated to time of HIV-1 RNA positivity in the child."; J. Virol. 69:2285-2296(1995).

BMBL, 247868; AA8882.1; -.

EIMEL: 247868; AA8882.1; -.

EIMEL: 247868; AA8882.1; -.

EIMEL: 747868; AA8882.1; -.

EIMEL: 747868; AA8882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%; Score 40; DB 15; Length 91; 70.0%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 15; Length 91;
Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AA; 10530 MW; BB10C62011F305D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AA; 10519 MW; EB20C63A22DA1288 CRC64;
                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                  Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Envelope protein (Fragment).
                                                                                                                                                                   Envelope protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
```

```
MEDINE-2123349; PubNed=11323671;
Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an enslaved algal nucleus.";
Mature 410:1091-1096(2001).

EMBL; AF165818; AAK39885.1;
InterPro; IPR001243; Proteasome_B.
InterPro; IPR001353; Protsme_protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=GMI1000;

MEDLINE=21681879; PubMed=11823852;
Salanoubar M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Biguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid megaplasmid.
Bacteria, Proteobacteria, beta subdivision, Ralstonia group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.1%; Score 40; DB 8; Length 205; 75.0%; Pred. No. 18; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 AA; 22691 MW; D30F5289CBC85049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31541 MW; ABB38818004B2EDA CRC64;
                                                                                                                                                                                                                 Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia
NCBI_TaxID=55529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03XSE2;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ICC protein homolog.
ICC OR RSP0534 OR RS00414.
                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                              205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL646079; CAD17685.1; -.
InterPro; IPR004843; M-ppestrase.
InterPro; IPR004844; S/T phosphtse.
Pfam: PF00149; Metallophos; 1.
Plasmid; Complete proteome.
SEQUENCE 279 AA; 31541 MW; ABB3
                                                                                                                                                                                   Guillardia theta (Cryptomonas phi).
                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00227; proteasome; 1
PRINTS; PR00141; PROTEASOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                            PRELIMINARY;
                                                                                                                                                         26S proteasome SU B5.
67 QWDRTLQKVR 76
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 CFFWERNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWORNL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=305;
                                                                                                                                                                                                    Nucleomorph.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteasome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ralstonia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                           Q98RR2;
                                                                            098RR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8XSE2
                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                              Q98RR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8XSE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
엄
```

ó

```
..
0
                          Gaps
                          ó
  Score 40; DB 16; Length 279;
Pred. No. 25;
                        4; Indels
                        3; Mismatches
 57.1%;
Query Match
Best Local Similarity 41.74
Matches 5; Conservative
                                                1 CFQWQRNLRKVR 12
                                                à
```

244 CFÓWEKGTRTAK 255

Search completed: February 21, 2003, 07:44:36 Job time: 20.8 secs

```
February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1984.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1990.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1990.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1990.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1990.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1990.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1990.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | SIDS2/gcddata/geneseq/geneseqp_embl/AA1992.DAT:
| SIDS2/gcddata/geneseqy_embseqp_embl/AA1992.DAT:
| SIDS2/gcgdata/geneseqy_embseqp_embl/AA1993.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA1994.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA1996.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA2000.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA2000.DAT:
| SIDS2/gcgdata/geneseqy_geneseqp_embl/AA2000.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-743-107B-83
71
1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::222::2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                               Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human lactoferrin									
SUMMARIES			ΩI	AAY78083	AAY78038	AAY78046	AAY78047	AAY78037	AAY78048	AAY78049	AAY78036	AAY78050	AAY78051
			DB	21	21	21	21	21	21	21	21	21	21
			e Match Length DB I	12	12	12	12	13	13	13	14	14	14
	ф	Query	Match	100.0	95.8	95.8	95.8	95.8	95.8	95.8	95.8	95.8	95.8
			Score	7.1	68	68	69	68	68	68	68	68	68
		Result	No.	1	7	٣	4	Ŋ	9	7	80	σ	10

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

Peptide for anti-u Human lactoferrin Human lactoferrin Human lactoferrin Human lactoferrin Human lactoferrin	4444 B4 44	Human lactoferrin Anti microbial pep Lactoferrin-relate Lactoferrin derive Lactoferrin derive	וו ענטס	Lactoferrin derive Lactoferrin-derive Lactoferrin derive Lactoferrin deriva Anti-parasitic pep Thrombus formation Lactoferrin hydrol
5 21 AAR9855 5 21 AAY7806 5 21 AAY7806 6 21 AAY7806 6 21 AAY7806 6 21 AAY7806	7 21 AAY7806 7 21 AAY7806 8 15 AAX6935 8 17 AAW1339 8 21 AAY7803 9 21 AAY7803	9 21 AAY7803 0 13 AAR2181 0 14 AAR4484 0 15 AAR4853 0 15 AAR4853 0 15 AAR74853	20 15 AARX)462 20 16 AAR84698 20 16 AAR86263 20 16 AAR80264 20 17 AAR98553 20 17 AAR01852 20 17 AAR03045	0000000
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
11 11 11 11 11 11 11 11 11 11 11 11 11	1 1 2 2 2 2 2 2 2 2 3 2 4 3 3 4 3 4 3 4 3 4	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	и с с с с с с с с с с с с с с с с с с с	8 4 4 4 4 4 4 9 0 11 13 16 4 13

ALIGNMENTS

```
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                              Human lactoferrin derived peptide SEQ ID NO:83.
                    AAY78083 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                           98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                         99WO-SE01230.
                                                         25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                   (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                WO200001730-A1.
                                                                                                                                                  Homo sapiens.
Synthetic.
                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                      17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                            06-JUL-1998;
                                                                                                                                                                                                  13-JAN-2000.
                                      AAY78083;
RESULT 1
          AAY78083
```

```
lattoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                               AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 71; DB 21;
100.0%; Pred. No. 8.3e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltzer L,
                                                                 Claim 22; Page 36; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78038 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                            12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78038;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

Gaps 0;

Length 12; Indels AAY78001 to AAY78100 represent peptides having sequences based on human

Dolphin GT;

```
;
0
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary fract infections, collifs, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                          95.8%; Score 68; DB 21; Length 12; 91.7%; Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78046 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQRNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNMKKVR
                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic,
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78046;
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
     ð
                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
```

m

Ŗ.

12

Sequence

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and Candida infection on a mucosal membrane), inflammarions and/or tunmours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tunmoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
                                                                                                                                                                                                                     ö
fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                     ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                 Length 12;
                                                                                                                                                                               Score 68; DB 21; Length 12
Pred. No. 2.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mattsby-Baltzer I, Baltzer L, Dolphin GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                            AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 73; 102pp; English
                                                                                                                                                                                                               1,
                                                                                                                                                                               95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                   1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                    1 CPOWORNMRKVR 12
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                            12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                              Seguence
                                                                                                            cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ношо
à
                                                                                                                                                                                                                                                                                g
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through peptide are taken up in the intestine through peptide lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammantions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and a contact of the costs. Therefore, provision of peptides as lactoferrin at lower and a contact of the costs.
                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                              Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-miorobial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
95.8%; Score 68; DB 21; Length 12; 91.7%; Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 95.8%; Score 68; DB 21; Length 13; 1 Similarity 91.7%; Pred. No. 3e-05; 11; Conservative 1; Mismatches 0; Indele
                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dolphin GT;
                                                                                                                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:37.
                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                          AAY78037 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                       bactericidal; preservative.
                                                                                                                                                                                                                                                              (first entry)
                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASCI-) A+ SCI INVEST AB
                                                                     1 CFQWQRNMKKVR 12
                                                                                                    1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 11; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-147388/13.
                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                          Ното варіепв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1998;
                                                                                                                                                                                                                                                              25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                             AAY78037;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                  Matches
                                                                                                                                                        RESULT 5
                                                                                                                                                                          AAY78037
```

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

98SE-0002441. 99WO-SE01230.

06-JUL-1999; 06-JUL-1998;

13-JAN-2000

WO200001730-A1.

Homo sapiens.

Synthetic.

Human lactoferrin derived peptide SEQ ID NO:49.

25-APR-2000

AAY78049 standard; Peptide; 13

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                     Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides used for treatment and prevention of infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.8%; Score 68; DB 21; Length 13; 91.7%; Pred. No. 3e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 74; 102pp; English.
                                                                                             AAY78048 standard; Peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-SE01230.
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB
   2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AA;
                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1.
                                                                                                                                                                 25-APR-2000
                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson LA,
                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                              AAY78048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                        셤
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides he used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower mable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68, DB 21, Length 13;
Pred. No. 3e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78036 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.8%;
                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78036
田林本本は田
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

ö

Gaps

ö

11; Conservative

Best Local Similarity

Matches

RESULT 7

IJ

us-09-743-107b-83.rag

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also for fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
                Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                        98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                     98SE-0002441.
                                                                                                                                                                                                                                                                99WO-SE01230.
                                                                             bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                   (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 AA;
                                                                                                                                                                                WO200001730-A1.
                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                                                                                     06-JUL-1998;
                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                        13-JAN-2000
                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
```

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for tracting and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 15; Page 75; 102pp; English.

Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13

(ASCI-) A+ SCI INVEST AB

29-DEC-1998;

17-JUL-1998; 06-JUL-1998;

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230

06-JUL-1999;

13-JAN-2000

WO200001730-A1

Synthetic.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

14 AA;

Sequence

```
Human, lactoferrin, modification, infection, inflammation, tumour;
food, infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis, Candida infection; fungicidal;
                        0;
95.8%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 3.2e-05;
                        0; Indels
                                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:51.
                        1; Mismatches
                                                                                                                                     AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                           bactericidal; preservative
                                                                                                                                                                                       25-APR-2000 (first entry)
                        11; Conservative
                                                 1 CFQWQRNMKKVR 12
                                                                        3 CFOWORNMRKVR 14
           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000.
                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                             AAY78051;
Query Match
                        Matches
                                                                                                            RESULT 10
                                                                                                                       AAY78051
ID AAY
                                                   à
                                                                                                                                                 ö
```

Gaps

. 0

Query Match 95.8%; Score 68; DB 21; Length 14; Best Local Similarity 91.7%; Pred. No. 3.2e-05; Matches 11; Conservative 1; Mismatches 0; Indels

12

CFOWORNMKKVR

à

3 CFOWORNMRKVR 14

99WO-SE01230.

06-JUL-1999;

Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;

bactericidal; preservative.

Homo sapiens

Human lactoferrin derived peptide SEQ ID NO:50.

25-APR-2000 (first entry)

AAY78050;

AAY78050 standard; Peptide; 14 AA.

RESULT 9 AAY78050

0

Gaps

The agent is low

```
AAR98531-54 are peptides used in an anti-ulcer agent. The at
in toxicity, is heat-resistant and stable in aqueous soln..
administered orally and be produced in large amounts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 AA;
                                                                                                                                                                                                                                                                                                                                                                                            13-JAN-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson LA,
                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                  AAY78035;
                                                     Sequence
                                                                                                                                                                        RESULT 12
                                                                                                                                                                                   AAY78035
ð
                                                                                                                                                                                               ·
0
                                                                                                                                                                     AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                      Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                      Score 68; DB 21; Length 14;
Pred. No. 3.2e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                          Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - has low toxicity, is
                                                                          Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                   Claim 18; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MORG ) MORINAGA MILK IND CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 11; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-ulcer agent contg. peptide
         98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                                                        95.8%;
                                                                                                                                                                                                                                                                                                                                                                                  91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                     (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                   1 CECWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CFOWORNMRKVR 14
                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                    14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP08143468-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1994;
            06-JUL-1998;
                    17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUN-1996.
                                                                           Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR98554;
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptidges based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                           Gaps
                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                            Length 15;
                                                 Score 68; DB 17; Length 15
Pred. No. 3.5e-05;
1; Mismatches. 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mattsby-Baltzer I,
                                                            95.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                               Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                               1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                  2 CFOWORNMRKVR
15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1998;
```

us-09-743-107b-83.rag

AAY78063 standard; Peptide; 15 AA.

RESULT 14

AAY78063

25-APR-2000

AAY78063;

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides the laso and including native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                           ö
                                                                                                                                                                                                                                                                                                                                                      Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                           Gaps
                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.8%; Score 68; DB 21; Length 15; ilarity 91.7%; Pred. No. 3.5e-05; Conservative 1; Mismatches 0; Indels
                  Score 68; DB 21; Length 15; Pred. No. 3.5e-05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dolphin GT;
                                                                                                                                                                                                                                                                                                                          Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer L,
                                                                                                                                                                                                                    AAY78062 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002441.
98SE-0002562.
98SE-0004614.
                      95.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-SE01230.
Query Match
Best Local Similarity >1...
Local 11; Conservative
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                               4 CFQWQRNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                                                                                         25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                       AAY78062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                   AAY78062
                                                                                                                                                                                                                                     ð
                                                                                                                            g
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tunours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also and informula have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                             Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 21;
Pred. No. 3.5e-05;
                                                                 Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78031 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%;
                                                                                                                                                                                                                                                                                                                                         98SE-0002441.
                                                                                                                                                                                                                                                                                                       99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                        98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 AA;
                                                                                                                                                                                                                                    WO200001730-A1.
                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                     06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                         17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                        29-DEC-1998;
                                                                                                                                                                                                                                                                      13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78031
ID AAY
XX
AC AAY
à
```

6

Gaps

; 0

1 CFOWORNMKKVR 12

Matches

4 CFOWORNMRKVR 15

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an inactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                   Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 68; 102pp; English.
                 25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-147388/13.
                                                                                                                                                                                                                                    WO200001730-A1.
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                  17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
                                                                                                                                                                                                                                                                          13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanson LA,
                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
```

Dolphin GT;

Mattsby-Baltzer I, Baltzer L,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

95.8%; Score 68; DB 21; Length 16; 91.7%; Pred. No. 3.7e-05; tive 1; Mismatches 0; Indels Best Local Similarity 91.7 Matches 11; Conservative 16 AA; Query Match

1 CFQWQRNMKKVR 12

ð g Search completed: February 21, 2003, 07:37:14 Job time : 28.35 secs

0

Gaps ; 0

5 CFOWORNMRKVR 16

```
CONTROL 1.18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 24, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4, Appl
5, Appl
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Appl
Appli
Appli
Appli
Appli
Appli
                                                                                                                 February 21, 2003, 07:25:59; Search time 8.65 Seconds (without alignments) 40.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Agreence 8, Agreence 8, Agreence 8, Agreence 29, Sequence 29, Sequence 6, Agreence 6, Agre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7,
Sequence 3,
Sequence 5,
Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    262574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
  5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-755-161A-3
US-07-891-174-3
US-08-256-771-24
US-08-256-771-24
US-08-381-984-24
US-09-508-734-4
US-09-508-734-6
US-07-55-161A-10
US-07-55-161A-10
US-07-55-161A-10
US-07-9508-734-8
US-07-951-174-10
US-07-9508-734-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-693-274A-7
US-09-017-043A-3
US-08-464-182A-5
US-08-406-271-5
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents AA:*
                                                                                                                                                                                                        US-09-743-107B-83
                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                    1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                      Sequence:
                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
```

8 9 0 1 2 2 2 4 4 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RESULT 1 US-08-204-487-3 Sequence 3, Application US/08204487; Patent No. 5565425 GENERAL INFORMATION: APPLICANT: YAMAMOTO, NAOKI APPLICANT: TANAKA, HIDEKI APPLICANT: TANAKA, SHIGEKI APPLICANT: TANAKA, SHIGEKI APPLICANT: DOSAKO, SHUN'ICHI APPLICANT: UCHIDA, TOSHIHIRO TITLE OF INVENTION: VIRAL INFEC TITLE OF INVENTION: INHIBITORS NUMBER OF SEQUENCES: 8	CORRES ADDR ADDR ADDR ADDR ADDR ADDR ADDR ADD	OPERATING SYSTEM: PC-DOS/MS- SOFTWARE: Patentin Release # CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/20 FILING DATE: 02-MAR-1994 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: CAMPBELL, PAULA A. REGISTRATION NUMBER: 32.503 REFERENCE/DOCKET NUMBER: FJN: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000	TELEFAX TENDERATION SEQUENCE LENGTH: TYPE: STRANDE TOPOLOG MOLECULE FEATURE: FEATURE: MAME/KE
9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	87-3 3, Ap. 556 INFOR ANT: ANT: ANT: ANT: ANT: OF IN	ADDRESSER: ADDRESSER: ADDRESSER: STREET: BOS CITY: BOS STATE: MA COUNTRY: COUNTRY: ADDRESSER: ADDRE	WARE: WARE: T APP LICATI NG DA SIFIC EY/AG STRAT STRAT STRAT RENCE MMMUNI	TELEFAX: RMATION F QUENCE CH LENGTH: am STRANDEDN TOPOLOGY: LECULE TY ATURE:
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	197-3 3, Application US/0820448 10. 5565425 INFORMATION: SANT: YAMAMOTO, NAOKI CANT: NAKASHIMA, HIDEKI CANT: NAKASHIMA, HIDEKI CANT: TANAKA, SHIGEKXI CANT: TANAKA, SHIGEAXI CANT: DOSAKO, SHUN'ICHI CANT: UCHIDA, TOSHIHRO OF INVENTION: VIRAL INFE OF INVENTION: VIRAL INFE OF INVENTION: NHIBITORS R OF SEQUENCES: 8	CORRESPONDENCE ADDRESS: ADDRESSE: PATENT ADM ADDRESSE: THIBEAULT STREET: 53 STATE STRE CITY: BOSTON STATE: MA COUNTRY: USA ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER: INP PC COMP	OPERATING SYSTEM: PC-DOS/MS-DO OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: DSTENTIN Release #1 CURSENT APPLICATION DATA: APPLICATION NUMBER: US/08/204 FILING DATE: 02-MR-1994 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: CAMPBELL, PAULA A. REGISTRATION NUMBER: 32,503 REFERENCE/DOCKET NUMBER: PJN-TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000	TELEFAK: (617) 248-71 TELEFAK: (617) 248-71 SEQUENCE CHARACTERISTICS LENGTH: 18 amino acid TYPE: amino acid STRANDENNESS: single STRANDENNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide NAME/KRY: Peptide
54 694 694 694 694 701 711 711 711 711 711 711 711	n US/08204 O, NAOKI MA, HIDEKI MA, HIDEKI SHIGEAKI SHUGEAKI SHUGEAKI TOSHIAKI VISHILIN VIRAL IN INHIBITO	ESS: T ADMIN AULT STREET STREET ORM: DPY dis	PC-I In Re- In Re- IR: UR S14 SRMATIC PAULA BER: NUMBEI NFORMI) 248-71(O ID NO: PERISTICS Lino acidi cid single lear peptide
000044001H004H1H004	DRI DRI DBI SAU CAK	INI ST Lisk	DOS/MS 11ease 15'08/2 994 ON: A: FJ ATION:	00 . s
US-08-464-182A-2 US-08-724-211-2 US-09-724-163-2 US-09-921-63-2 US-08-655-640-4 US-08-655-640-4 US-08-655-640-4 US-08-655-640-4 US-08-655-640-4 US-08-655-640-4 US-08-661-33-4 US-08-464-167-4 US-08-451-708-4 US-08-451-708-2 US-08-451-703-2 US-08-451-703-2 US-08-451-703-2 US-08-451-703-2 US-08-451-703-2 US-08-451-703-2 US-08-451-703-2 US-08-451-703-2 US-08-451-703-2	US/08204487 NAOKI , HIDEKI WATARU HIGBAKI HOGBAKI YOCHIHIRO OSHIAKI INHIBITORS	CORRESPONDENCE ADDRESS: ADDRESSE: PATENT ADMINISTRATOR, TEST ADDRESSE: THIBEAULT STREET: 53 STATE STREET CITY: BOSTON STATE: MA COUNTRY: USA ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: INP PC COMPALIBLE	DOS 1.0, 4,487	
71-22 71-22 72-2 72-2 72-2 73-4 73-4 73-4 73-4 73-2 74-2 74-2 75-2 76-2 77-2	US/08204487 NAOKI , HIDEKI WATARU HIGBAKI HIGBAKI YOCHIHRO OSHIAKI VIRAL INFECTION AND PROLIFERATION INHIBITORS	TESTA, HURWITZ &	Version #1.25	
epanence ged				
0,000,004,44,44,400,000,000				
APPPI APPPI APPPI APPPI APPPI APPPI APPPI APPPI APPPI APPPI APPPI APPPI				

```
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                        US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                ;
0
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 0
                                                                                                  .<u>`</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.8%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 2.2e-05; tive 1; Mismatches 0; Indels
                                                        95.8%; Score 68; DB 1; Length 18; 91.7%; Pred. No. 2.2e-05;
                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

PRICASSIFTCATION: 436

PRICA PARLICATION DATA:

APPLICATION NUMBER: 08/488,217

FILING DATE: JUNE 7, 1995

APPLICATION NUMBER: 08/418,642

FILING DATE: APRIL 7, 1995

CLASSIFTCATION 1436

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26/742

REFERENCE/DOCKET NUMBER: 26/742

REFERENCE/DOCKET NUMBER: 26/742

TELECOMMUNICATION INFORMATION:

TELECHOME: 201 487-580

TELEFAX: 201 343-1684

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               ; Sequence 8, Application US/08485948
; Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klauber & Jackson
OTHER INFORMATION: (20-37)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                             Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
STATE: New Jersey
                                                                                                                                       1 CFOWORNMKKVR 12
                                                                                                                                                                             1 CFOWORINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-485-948-8
                                                                                                                                                                                                                                       RESULT 2
US-08-485-948-8
      ; US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                         à
```

1 CFOWORNMRKVR 12

```
0;
                                                                                                        APPLICANT: LI, YONG MING
APPLICANT: VLASSARA, HELEN
APPLICANT: VLASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackengack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-475-055-8
Sequence 8, Application US/08475055
Patent No. 5962245
GENERAL INFORMATION:
APPLICANT: YOUR MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ABENTEONES:
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.8%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 2.2e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION DATA:
APPLICATION TOWAR: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
Sequence 8, Application US/08628380; Patent No. 5891341; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
```

```
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 2; Length 18;
Pred. No. 2.2e-05;
Ored. No. 2.2e-05;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/475,055
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                   TILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: UNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: UNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
NAME: JACKSON ESQ., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 347-1-008A
TELEPHONE: 201 487-5800
TELEPAN: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: How Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE: internal US-08-475-055-8
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                              07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-07-755-161A-3
```

```
LOCATION: 19
IDBNIFICATION METHOD:
OTHER INFORMATION: ()note= "thiol group of OTHER INFORMATION: (ys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICAMION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                   Э.
                                                                                                                                                                                NAME: Warren M. Cheek Jr
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN:
INDIVIDUAL ISOLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1i
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
```

DB 1; Length 20;

95.8%; Score 68;

```
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBBAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 95.8%; Score 68; DB 1; I Local Similarity 91.7%; Pred. No. 2.5e-05; Ne 11; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O2-MAR-1994
N. F.
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08204487; Patent No. 5565425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 53 STATE STREET
BOSTON
                     IDENTIFICATION METHOD:
OTHER INFORMATION: /nc
OTHER INFORMATION: Cye
OTHER INFORMATION: thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CFOWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
STREET: 53
CITY: BOST
                                                                                                                                                                                                                                                                                        JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                         ;
0
                         Gaps
                         0;
   91.7%; Pred. No. 2.5e-05; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IRM Compatible
OPERATING SYSTEM: Ms-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                       ; Sequence 3, Application US/07891174; Patent No. 5317084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
                                                         1 CFQWQRNMKKVR 12
                                                                                              2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                             STREET: 805 Fifte
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                    RESULT 6
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNITS:
                                                                                              g
```

```
FEATURE:
NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
/note= "thiol group of Cys residue at location 2 connected by disulfide bond with thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: MOSUCHI, WATARU
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: CHIDA, TOSHIAKI
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
```

us-09-743-107b-83.rai

```
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifeenth Street, N.W., #700 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALKEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                       1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                             2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.C.
U.S.A.
                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                            US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                             Query Match
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 2.5e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide
COCATION: 1..20
OTHER INPORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb computible computible operating system: Ms_008 software: In Compatible operating system: Ms_008 software: Wordperfect 5.1 current application Data:
Application Number: US/08/256,771 FILING DATE: July 22, 1994 PRIOR APPLICATION 1514 PRIOR APPLICATION TOWN. 514 PRIOR APPLICATION NUMBER:
FILING DATE: RILING DATE: RILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 20 amin -- ...
                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRY: U.S.A.
20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 2.5e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 2.5e-05; Matches 11; Conservative 1; Mismatches 0; Indels
```

us-09-743-107b-83.rai

```
Patent No. 6423509

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: useful microorganism thereof

FILE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT PILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR PILING DATE: 1998-07-13

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "cysteine residues at positions 2 OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 2.5e-05; tive 1; Mismatches 0; Indels
                                                                                       ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
805 Fifteenth Street, N.W., #700
                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELECOMMUNICATION: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                        Washington
                                                                      U.S.A.
                        CITY: Washi
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-508-734-4
                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
LIDBNITEICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 2.5e-05; vative 1; Mismatches 0; Indels
                                                                                                                                                        ADDRESSEE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
;
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
    Sequence 24, Application US/08381984
                        Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TILLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CFÓWÓRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                            D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                          20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION
                                                                                                                                                                                                                                                       COUNTRY:
```

us-09-743-107b-83.rai

```
UNITS:

UNITS:

NAME/KRY:

NAME/KRY:

NAME/KRY:

NOTHER INFORMATION:

OTHER INFORMATION:

COTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.8%; Score 68; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 3.1e-05; Matches 11; Conservative 1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
FUBLICATION DATE:
FEBRUART RESIDUES IN SEQ ID NO:
US-07-755-161A-10
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,387
REFREENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
FRAGMENT TYPE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CPOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                               FARENTAL INFORMATION:
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Wase production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT APPLICATION NUMBER: PCT/RR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-13
RIOR FILING DATE: 1996-07-13
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                     Gaps
                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.8%; Score 68; DB 4; Length 24; Best Local Similarity 91.7%; Pred. No. 3e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                  95.8%; Score 68; DB 4; Length 22; 91.7%; Pred. No. 2.7e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
ZIP: 2006 Exating to Discount of the Compatible COMPUTER READABLE FORM: MEDIUM TYPE: DISCOMPUTER: DISCOMPUTER: NS-DOS SOFTWARE: DISEDLAYING SYSTEM: MS-DOS SOFTWARE: DISEDLAYING SYSTEM: MS-DOS SOFTWARE: DISEDLAYING SYSTEM: WS-DOS SOFTWARE: DISEDLAYING SYSTEM: US/07/755,161A
                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-755-161A-10
; Sequence 10, Application US/07755161A
Petent No. 5304633
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09508734 Patent No. 6423509
                                                                                                             Query Match 95.8
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Kopatentin 1.71
SEQ ID NO 6
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWORNMKKVR 12
                                                                                                                                                                                                            1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                           2 CPÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CFOWORNMRKVR 14
                                                                      US-09-508-734-4
                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-508-734-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
```

```
1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                 DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                            US-07-891-174-10
                                                                                                               TITLE:
JOURNAL:
                                                                                                                                                   VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 4
LOCATION: 4
LIDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: (ys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                SCHWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION ADAR:
PRIOR APPLICATION BAR:
APPLICATION WHER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
RECISTRATION NUMBER: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified site 21
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
RESULT 15
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:
```

```
DEWTIFICATION METHOD:

OTHER INFORMATION: force= "thiol group of connected by disulfide bond with corner information: Cyg residue at location 4" CTHER INFORMATION: thiol group of Cyg residue at location 4" CTHER INFORMATION: thiol group of Cyg residue at location 4" CTHER INFORMATION: thiol group of Cyg residue at location 4" TITLE:

TITLE:

JUTHORS:

TITLE:

JUTHORS:

FILING DATE:

DACUMENT NUMBER:

FRIENDATE:

DATE:

DATE:
```

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:51:54 ; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec

US-09-743-107B-83 1 CFOWORNMKKVR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

156504 seqs, 31069816 residues Searched:

156504 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

1: ./cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: ./cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: ./cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

4: ./cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

5: ./cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: ./cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

7: ./cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

8: ./cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: ./cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

10: ./cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

10: ./cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

11: ./cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

12: ./cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

13: ./cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

14: ./cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

14: ./cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADITES

	Description	fland C appendix	5	2	9	m	Sequence 23, Appl	Sequence 29. Appl	3	7. A	4	22		11	Sequence 119, App	Sequence 119, App	Sequence 119, App	Sequence 119, App	14,	Sequence 6, Appli
SUMMAKIES	ID	US-09-798-869-2	US-09-798-869-20	US-10-023-096-2	9-698-861-60-SN	US-09-798-869-3	US-09-798-869-23	US-09-798-869-29	US-09-798-869-30	L-698-862-60-SD	US-09-798-869-4	US-09-798-869-22	8-698-862-60-SN	US-09-978-295A-119	US-09-978-697-119	US-09-978-192A-119	US-09-999-832A-119	US-09-978-189-119	US-09-796-753-14	US-09-981-649A-6
	DB	- 6	σ	σ	Q	σ	σ	σ	σ	σ	σ	σı	σ	6	6	σ	σ	σ	σ	10
	Query Match Length DB	15	25	694	15	15	25	15	15	15	15	25	15	338	338	338	338	338	553	553
	Query Match	5.8	95.8	95.8	84.5	71.8	71.8	63.4	63.4	9.09	59.2	59.2	6.4	4.9	54.9	54.9	54.9	54.9	4.9	6.4
o#c	O E	0	on	S	ω,		-	Ψ	w	Ψ	u)	пJ	S	Ŋ	u)	m	ம	L	ın	ĽΩ
	Score	89	99	68	9	51	51	45	45	43	42	42	39	39	39	39	39	39	39	39
	Result No.	1	2	m	4		9	7	8	σ	10	11	12	13	14	15	16	17	18	19

Sequence 24, Appl Sequence 30, Appl Sequence 28, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 25, Appl Sequence 27, Appl Sequence 28, Appl Sequence 28, Appl Sequence 21, Appl Sequence 16, Appl Sequence 18, Appl Sequence 1877, Appl Sequence 1	MO 15 M
US-09-981-649A-24 US-09-981-649A-30 US-09-981-649A-28 US-09-981-649A-28 US-09-98-6-753-26 US-09-98-869-25 US-09-798-869-10 US-09-798-869-10 US-09-798-869-10 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-798-869-24 US-09-917-34-16 US-09-917-34-16 US-09-917-34-16 US-09-510-332-68 US-09-510-332-68	US-09-888-320-2 US-09-815-242-12129 US-09-815-242-13026 US-09-764-864-1031 US-09-853-625B-16 US-10-066-500-58
01100000000000000000000000000000000000	9 1 1 1 0 9
8 8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	489 622 952 351 747
4444 8000000000000000000000000000000000000	24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
N N N Y P P P P P P P P P P P P P P P P	መመመመመው መቁጥተቀቀ
01000000000000000000000000000000000000	4 4 4 4 4 0 11 2 2 4 4 5

ALIGNMENTS

```
95.8%; Score 68; DB 9; Length 15; 91.7%; Pred. No. 2.5e-05; tive 1; Mismatches 0; Indels
              GENERAL INFORMATION

FUDLICATION NO. US20030022821A1

GENERAL INFORMATION

FAPPLICANT: OCHN SIGURD SVENDSEN

APPLICANT: OCHN SIGURD SVENDSEN

APPLICANT: BALDUR SVEINBJ (RNSSON

APPLICANT: LARS VORLAND

TITLE OF INVENTION: BICACTIVE PEPTIDES

FILE REFREENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 1999-08-31

PRIOR PILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

SOFTWARE: FSEQ ID NOS: 30

SOFTWARE: FSEXEQ FOR WINGONS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
```

; Sequence 20, Application US/09798869 ; Publication No. US20030022821A1 ; GENERAL INFORMATION: 3 CFOWORNMRKVR 14 US-09-798-869-20 RESULT 2 d

; 0

Gaps

.,

11; Conservative

1 CFQWQRNMKKVR 12

à

APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTEIN REKDAL APPLICANT: BALDUR SVEINBJ(RNSSON

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz.
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human IIILE OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                           95.8%; Score 68; DB 9; Length 25; 91.7%; Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
         TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 2.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10505/P58185C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEV/AGENT INPORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REPERRORS/DOCKET NUMBER: 10505/F5818
TELECOMUNICATION INPORMATION:
TELEPHONE: (202) 638-6666
TELEFRAX: (202) 393-5350
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
LARS VORLAND
                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CFÓWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-10-023-096-2
                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens; OTHER INFORMATION: Bequence)
US-09-798-869-6
                                             ..
95.8%; Score 68; DB 9; Length 694; 91.7%; Pred. No. 0.00088; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 9; Length 15;
Pred. No. 0.00051;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 9; Length 15;
Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: A34040-PCT-USA-A
FILE REFERENCE: A34040-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1990-08-13
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PLING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-28
NUMBER: OF SEQ ID NOS: 30
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURREAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PASTSEQ for Windows Version 4.0
SSOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                   Sequence 6, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN; APPLICANT: (YSTEIN REKOAL); APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09798869; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 91.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 10; Conservative
                                                                                     1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNMKKVR 12
                                                                                                                              22 CFOWORNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CFOWOWNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3
                                                                                                                                                                                                RESULT 4
US-09-798-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

ó

Gaps

..

Indele

1;

3; Mismatches

7; Conservative

Matches

```
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: BOVINE
US-09-798-869-30
                     US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7-698-867-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.4%; Score 45; DB 9; Length 15; 63.6%; Pred. No. 0.15; 2; Indels tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.8%; Score 51; DB 9; Length 25; 63.6%; Pred. No. 0.024; ive 3; Mismatches 1; Indels
                                                                                                   VEGOUTE 69-798-869-23

Sequence 23, Application US/09798669
Publication No. US20030022821A1
SERERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: STREADL
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A44049-PCT-USA-A
CURRENT FILING DATE: 2011-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB818938-4
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSELSEQ for Windows Version 4.0
SEG ID NOS: 23
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INDRIVATION:
GENERAL INDRIVATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GENERAL INSENDAL
APPLICANT: BALDUR SVEINBG (RNSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GE99818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRASEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 63.6
1 CFQWQRNMKKV 11
                                   3 CYOWORRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CYOWORRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic peptide (modified form of homo sapiens OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.4%; Score 45; DB 9; Length 15; 63.6%; Pred. No. 0.15; 1ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.6%; Score 43; DB 9;
54.5%; Pred. No. 0.31;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
TOPPLICANT: HALDING SVENDSEN
APPLICANT: HARS VORLAND
TITLE OF INVENTION: HICACITUR PEPTIDES
TITLE REPEBRICE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: CB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: HALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCE: A34049-PCT-USA-A
CURRENT PELLICATION NUMBER: US/09/798,869
CURRENT PELLING DATE: 2001-02-27
PRIOR PILLING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: ECT/GB99/02851
PRIOR APPLICATION NUMBER: G89918938.4
PRIOR FILLING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
```

```
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.9%; Score 39; DB 9; Length 15; 54.5%; Pred. No. 1.4; tive 2; Mismatches 3; Indels
                                                   APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PELING DATE: 1999-00-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 119, Application US/09978295A Patent No. US20020156006A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILLING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PELING TOWN NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
                 (YSTEIN REKDAL
BALDUR SVEINBJ (RNSSON
LARS VORLAND
APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan, James;
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker Kevin P.
Botstein, David
Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CLRWOWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-978-295A-119
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-798-869-8
                                                                                                                                                                                                                                                                                                                  LENGTH: 15
                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.2%; Score 42; DB 9; Length 25; 54.5%; Pred. No. 0.73; 1ve 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.2%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.45; ive 2; Mismatches 3; Indels
                                                                                                          APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYSINBU (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIO-BCTIVE PEPTIDES
FILE REFERENCE: A34049-FCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1990-08-31
PRIOR SEQ ID NOS: 30
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYZINBJ(RNSSON
APPLICANT: BALDUR SYZINBJ(RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 22, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                               ; Sequence 4, Application US/09798869; Publication No. US20030022821A1; Publication INFORMATION: APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.20,
Lhas 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CLRWONEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: MURINE
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-798-869-8
           US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

.; 0

Gaps ..

```
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630F1011 CURRENT APPLICATION NUMBER: US/09/978,295A CURRENT FILING DATE: 2001-10-15
```

PRIOR FILING DATE: 1998-04-15
PRIOR PRICING DATE: 1998-04-15
PRICH APPLICATION UNMERR: 60/081819
PRICH APPLICATION UNMERR: 60/081952
PRICH APPLICATION NUMBER: 60/081952
PRICH APPLICATION NUMBER: 60/081952
PRICH PLING DATE: 1998-04-15
PRICH PLING DATE: 1998-04-21
PRICH PLING DATE: 1998-04-21
PRICH PLING DATE: 1998-04-21
PRICH PLING DATE: 1998-04-21
PRICH PRICH PLING DATE: 1998-04-21
PRICH PLING DATE: 1998-04-21
PRICH PLING DATE: 1998-04-21
PRICH PLING DATE: 1998-04-22
PRICH APPLICATION NUMBER: 60/08269
PRICH APPLICATION NUMBER: 60/08269
PRICH APPLICATION NUMBER: 60/08276
PRICH APPLICATION NUMBER: 60/08332
PRICH APPLICATION NUMBER: 60/08336
PRICH APPLICATION NUMBER: 60/08336
PRICH APPLICATION NUMBER: 60/08346
PRICH APPLICATION NUMBER: 60/08346
PRICH PRICH DATE: 1998-04-29
PRICH PRICH DATE: 1998-05-07
PRICH PRICH DATE: 1998-

```
PRILICAR PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 54.9%; Score 39; DB 9; Length 338; Best Local Similarity 54.5%; Pred. No. 26; Matches 6; Conservative 2; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR PAPLICATION NUMBER: 60/08550
PRIOR PLILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/085573
PRIOR PILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Khjavin, Ivar J.
Kno, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06534
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-978-697-119

. Sequence 119, Application US/09978697

. Patent No. US20020169284A1

. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan, James;
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 CYGWRRNSKGV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
R FILING DATE: 1998-03-25
R APPLICATION NUMBER: 60/079656
R PILING DATE: 1998-03-26
R RPLING DATE: 1998-03-27
R FILING DATE: 1998-03-27
R RAPLICATION NUMBER: 60/079689
R PALING DATE: 1998-03-27
R PAPLICATION NUMBER: 60/079663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079728
R FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/079923
R APPLICATION NUMBER: 60/080105
R APPLICATION NUMBER: 60/080105
R FILING DATE: 1998-03-31
R FILING DATE: 1998-03-31
R FILING DATE: 1998-03-31
R FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080194

R APLICATION NUMBER: 60/080327

R APLING DATE: 1998-04-01

R APLICATION NUMBER: 60/080328

R FILING DATE: 1998-04-01

R PILING DATE: 1998-04-01

R PILING DATE: 1998-04-01

R FILING DATE: 1998-04-01

R PILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081195
R FILING DATE: 1998-04-08
R FILING DATE: 1998-04-09
R FILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/081203
FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
                                                                                                   FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/07791
                                                                                                                                                                                                         FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/07886
FILING DATE: 1998-03-20
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
APPLICATION NUMBER: 60/078939
APPLICATION NUMBER: 60/078939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-04-01
APPLICATION UNDRER: 60/081070
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
FILING DATE: 1998-04-15
                                                                                APPLICATION NUMBER: 60/077641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/078936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
```

us-09-743-107b-83.rapb

```
R APPLICATION NUMBER: 60/084640
R FILING DATE: 1998-05-07
R PAPLICATION NUMBER: 60/084598
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-5-07
                   FILING DATE: 1998-04-15
APPLICATION UNDHER: 60/082568
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
                                                                                                                                                            FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082700
                                                                                                                                                                                                                                                             FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
ELING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27
APPLICATION NUMBER: 60/083322
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
RILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083545
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/081838
                                                                                                               FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/083496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/083554
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
FILING DATE: 1998-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084411
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LICATION NUMBER: 60/083500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084639
FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085689
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/084627
FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/085338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/085323
                                                                                                                                                                                                                                                                                                                                                       ILING DATE: 1998-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1998-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILING DATE: 1998-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-05-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILING DATE:
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                         ·
0
                                                                                                                                                                                     h
Similarity 54.5%; Score 39; DB 9; Length 338;
6; Conservative 2; Mismathhee 7 - 7 - 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 119, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR PILING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-13
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PAPLICATION NUMBER: 60/065364
PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077630
PRIOR PILING DATE: 1998-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desnoyers, Luc
Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P2630P1C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan, James;
                                                                                                                                                                                                                                                                                            1 CFOWORNMKKV 11
                                                                                                                                                                                                                                                                                                                                   50 CYGWRRNSKGV 60
                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-978-192A-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                              à
```

NUMBER 1998-1 1998-1 1998-1 NUMBER 1998-1 NUMBER 1998-1 NUMBER 1998-1	1998-03- 1998-03- NUMBER: 6 1998-04-	1998- 1998- 1998- NUMBER 1998- 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER
PPLICATION ILING DATE PPLICATION ILING DATE PPLICATION ILING DATE PPLICATION ILING DATE ILING DATE ILING DATE PPLICATION ILING DATE PPLICATION ILING DATE PPLICATION ILING DATE	DATE DATE DATE DATE DATE DATE DATE DATE	ATION DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: ATION DATE: ATION DATE: ATION DATE: DATE: ATION DATE: DATE: ATION
PRIOR		PRIOR

PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/08200
PRIOR APPLICATION NUMBER: 60/08270
PRIOR APPLICATION NUMBER: 60/08279
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
PRIOR PRILING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-06
PRIOR PLING DATE: 1998-05-07
PRIOR PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PRIOR DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PRIOR DATE: 1998-05-13
PRIOR PRIOR DATE: 1998-05-13
PRIOR PRIOR DATE: 1998-05-13
PRIOR PRILICATION NUMBER: 60/08559
PRIOR PRINCATION NUMBER: 60/08559
PRIOR PRILICATION NUMBER: 60/08559
PRIOR PRILICATION NUMBER: 60/08559
PRIOR PRI

; PRIOR APPLICATION NUMBER: 60/085697

0; Gaps Query Match 54.9%; Score 39; DB 9; Length 338; Best Local Similarity 54.5%; Pred. No. 26; Matches 6; Conservative 2; Mismatches 3; Indels

0;

1 CFQWQRNMKKV 11 |: |:| | | 50 CYGWRRNSKGV 60 qq ò

Search completed: February 21, 2003, 08:08:08 Job time : 10.55 secs

THIS PAGE BLANK (USPTO)

```
5.1.3
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
```

OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-83 71 1 CFQWQRNMKKVR 12 Perfect score: Title:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	lactotransferrin n	600	- (1 D	precu		dynein beta heavy		interleukin-2 rece	Ω	265 proteasome SU	hypothetical prote	T)		probable peroxisom			conserved hypothet	hypothetical prote	3-deoxy-manno-octu	probable cytochrom	cytochrome P450 ho	hypothetical prote	conserved hypothet	hypothetical profe	Sugar ABC transpor	hypothetical profe	3-deoxy-manno-octu	hypothetical prote
SUMMARIES	ΙD	TFHUL	JC2323	S52107	AB0858	A28438	F90580	T08030	JC1113	S07442	C84325	E90094	AD2346	A84471	T17324	T37974	T40568	T22597	C82234	T33211	D71876	T00510	T00513	T28820	F86904	C97838	D72378	S67085	E64639	AI2343
	DB	į			7																			~	~	7	~	~	N	7
	Length	711	708	33	511	707	282	4568	275	275	584	205	298	531	558	223	238	275	323	335	393	515	543	932	1436	99	283	376	393	464
æ	Query Match	95.8	ä	۲.	59.2	ė,	Ċ.	57.7	ė	ė	6	4	4.	4	4	m.	٠ ص	Э.	53.5	₩.	m.	щ.	щ.	m.	ω.	ď.	52.1	ď	ď	52.1
	Score	89	51	48	42	42	41	41	40	40	40	39	39	39	39	38	38	38	. 38	38	38	38	38	38	38	37	37.	37	37	37
	Result No.	1	7	m	4	υ.	9	7	80	o	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical sh3-c probable cytochrom	diphosphate-fructo hypothetical prote	outer capsid prote	cell division prof	probable C-factor	ornithine decarbox	probable protein k	T14P4.7 protein -	CPE-binding protei	hypothetical prote	hypothetical prote	lactotransferrin n	hypothetical prote
T39801 B84514	T01470 T19429	A45687	H64185	C82155	S52784	B96547	E86156	A55377	E64464	T34079	TFBOL	T25415
0 0	7 7	9.0	1 (1	~	N	N	~	Н	~1	N	Н	7
501 518	583 681	749	425	235	435	476	513	268	602	665	708	742
52.1	н.	4-	4	. 7	7	. 7	۲.		۲.	۲.	۲.	.7
52	52 22	52.0	213	50	50	20	20	20	20	50	50	20
37	37	37	36.5	36	36	36	36	36	36	36	36	36
30	33 33	34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

THAT
lactotransferrin precursor [validated] - human
N'Alternate names: lactoferrin
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C; Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74
R;Cho, Y.
submitted to the EMBL Data Library, March 1994
A;Reference number: G06820
A;Accession: G01394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-711 <cho></cho>
A; Cross-references: EMBL: U07643; NID: q467236; PIDN: AAB60324.1: PID: q467237
R; Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990

Nucleic Actas Kes. 18, 2288, 1990 A,Title: Complete nucleotide sequence of human mammary gland lactoferrin. A,Reference number: S11228, MUID:90384839; PMID:2402455

A; Accession: S11228

A Molecule type: mRNA
A;Residues: 1-148, T.,150-422, C',424-711 <REY>
A;Residues: 1-148, T.,150-422, C',424-711 <REY>
A;Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:934416
A;Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A;Title: Differential molecular mechanism of the estrogen action that regulates lactofer:
A;Reference number: A45401; MUID:93125571; PMID:1480183

A, Accession: A45401
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Cross-references: 1.5 cTEN.
A, Esperimental source: placenta
A, Experimental source: placenta
A, Note: sequence extracted from NCBI backbone (NCBIP:122202)
B, Powell, M.J.; Ogden, J.B.
Nucleic Acids Res. 18, 4013, 1990
A, Title: Nucleotide sequence of human lactoferrin CDNA.
A, Reference number: S10324; MUID:90326549; PMID:2374734

A; Accession: S10324

A; Molecule type: mRNA A; Residues: 3-711 < POW>

A,Cross-references: EMBL:X52941, NID:g34411, PIDN:CAA37116.1, PID:g34412
R,Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Bjochem. J. 276, 349-355, 1991
A;Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066

A; Accession: S15853

A, Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: mRNA A; Residues: 20-31 <ST1>

A,Accession: \$20841 A,Molecule type: protein A,Residues: 20-28,'X',30-31 <ST2>

. 0

Gaps

; 0

```
lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 14-Unl-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession. S2107
R;Gian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet & A;Reference number: S52107; WUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0858
B;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Althors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Residues: 1-511 <PAR>
A)Cross-references: GB:AL513382, PIDN:CAD06049.1, PID:g16504016, GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NiAlternate names: lactotransferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                               Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.6%; Score 48; DB 2; Length 33; 54.5%; Pred. No. 0.07;
                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-33 <QIA>
C:Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.2%; Score 42; DB 2; 58.3%; Pred. No. 13;
                                               Score 51; DB Pred. No. 0.443; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                            71.8%;
63.6%;
          Query Match
Best Local Similarity 63.0
Lng 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lactoferrin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQRNMKKVR 12
                                                                                                                                                                           1 CFOWORNMKKV 11
                                                                                                                                                                                                                                           38 CYOWORRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 CYÓWOKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
A28438
                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                              à
                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A; Note: this is the final paper in a series
R; Houen, G.; Hoegdall, Burkholt, V.; Norskov, L.
Bur. J. Blochem. 241, 303-308, 1996
A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A; Reference number: S74119; MUID:97054624; PMID:8898921
                                                                              Ë
                                                                                                                                                                                                                                                                                                                          A, Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 3-701, 'SWKEVN' <PAN>
A; Experimental Source: normal breast tissue
R; Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 659-666, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Human lactorransferrin: amino acid sequence and structural comparisons with oth A;Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rile Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A;Reference number: JC2323; MUID:94380047; PMID:89033048
                                                                              οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding Bite: carbohydrate (ABR) (covalent) #status predicted
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression
A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Recession: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                               A;Residues: 436-487,'A',489-711 <RAD>
A;Cross-references: EMBLA1, NID:g186815; PIDN:AAA86665.1; PID:g386855
R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; 22 - 28 Pred. No. 0.00043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Map position: 3q21-3q23
C; Superfamily: transferrin; transferrin repeat homology
C; Superfamily: transferrin; transferrin; binding; milk
F;1-19/Domain: signal sequence #status predicted <SiG>F;20-711/Product: lactotransferrin #status experimental <MAT>F;21-356/Domain: transferrin repeat homology <TRHI>
                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A61169; MUID:91235214; PMID:1674448
A;Accession: A61169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GDB:119368; OMIM:150210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 CPÓWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-708 < LEP>
                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S74119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: JC2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JC2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin - goat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: LTF
```

0;

· 0

ö

Gaps

. 0

RESULT 2

à

```
A;Map position: IX
A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 1
3334/3; 3686/3; 3882/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: 0vis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 22-Jun-1999
Cisacession: JC1113; S18899; S18910
R;Buldos, N.; Sargan, D.; Williamson, M.; McConnell, I.
Gene 113, 283-284, 1992
A;Title: Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa protein, CD2:
A;Reference number: JC1113; MUID:92241682; PMID:1572550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK ce C; Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology C; Superfamily: interleukin-2 receptor alpha chain; glycoprotein; T-cell proliferation; transmeml F; E; 1-21) Domain: signal sequence #status predict code csica code csica code csica chain status predicted csica chain #status predicted csica chain #status predicted cwars code csica code csica code csica code csica csi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, December 1991
A.Description: Molecular cloning, expression and characterisation of the ovine IL-2R alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-165,'S',167-275 <VER>
A;Cross-references: EMBL:Z11560; NID:g1275; PIDN:CAA77652.1; PID:g1276
C;Complex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                  A,Molecule type: DNA
A,Residues: 1-4568 «MIT>
A,Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X60149; NID:g1287; PIDN:CAA42723.1; PID:g1288 R;Verhagen, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;24-77/Domain: complement factor H repeat homology <FH1>
F;123-184/Domain: complement factor H repeat homology <FH2>
F;144-264/Domain: transmembrane #status predicted <TVM>
F;265-275/Domain: intracellular #status predicted <IVM>
F;265-275/Domain: intracellular #status predicted <INT>
F;24-64,51-77,123-168,152-184/Disuifide bonds: #status predicted
F;80/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.7%; Score 41; DB 2; Length 4568; 41.7%; Pred. No. 1.7e+02; Live 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.3%; Score 40; DB 1; Length 275; 58.3%; Pred. No. 15; 58.3%; Indels tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: nuclectide binding; P-loop
F;1919-1926(Region: nucleotide-binding motif A (P-loop)
F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-2 receptor alpha chain precursor - sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Description: receptor for interleukin-2
                         A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                       A; Experimental source: strain 21gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1852 CFOWOSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S18899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 CLTWORRWKKNR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-275 <BUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: CD25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S18899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: JC1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                               A; Gene: ODA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
C;Accession: A28438; A41205
Y:Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
A;Reference number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein MYPU_5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C.Species: Mycoplasma pulmonis
C.Species: Mycoplasma pulmonis
C.Species: Mycoplasma pulmonis
C.Accession: F90580
R.Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A.Fritle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A.Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R,Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: 216302; MUID:94274778; PMID:8006077
A;Accession: T08030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-282 <KUR>
A;Cross-references: GB:AL445566; PID:g14089965; PIDN:CAC13723.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                     A.Molecule type: mRNA
A.Residues: 3-707 <PEN>
A.Cross-references: EMBL:J03298
R.Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A.Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A.Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:20-707/Froduct: lactotransferrin #status predicted <MAT>
F:358-695/Domain: transferrin repeat homology <TRH2>
F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.2%; Score 42; DB 1; Length 707; 54.5%; Pred. No. 17; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.7%; Score 41; DB 2; Length 282; 60.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: GB:M74778
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dynein beta heavy chain - Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
```

6; Conservative

Query Match Best Local Similarity Matches 6, Conserva

A; Residues: 1-15 <LIU>

A; Accession: A41205

A;Accession: A28438

6; Conservative

Matches

Local Similarity

Query Match

A; Genetic code: SGC3

A; Gene: MYPU 5500

Genetics:

A, Status: preliminary A, Molecule type: DNA

à

C; Accession: T08030

```
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; WUID:21595285; PMID:11759840
                        C;Species: nucleomorph Guillardia there in the control of a cukaryotic endosymbiont binote: nucleomorph is the vestigial nucleus of a cukaryotic endosymbiont c;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001 C;Accession: E90094

R;Douglas, S; Zauner, S; Fraunholz, M; Beaton, M; Penny, S; Deng, L.T.; Wu, X.; Rei Mature 410, 1091-1096, 2001

A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          En/Spm-like transposon protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84471
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402, 761-768, 1999
A;Itle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AD2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AF165818; NID: g13794510; PIDN: AAK39885.1; GSPDB: GN00150
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%; Score 39; DB 2; Length 298; llarity 66.7%; Pred. No. 25; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 2; Length 205;
Pred. No. 17;
3; Mismatches 3; Indels
26S proteasome SU BS [imported] - Guillardia theta nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || |:||:
63 CFFWERNLSSL 73
                                                                                                                                                                                                                                                                                                     A; Status: preliminary A; Molecule type: DNA A; Residues: 1-205 < DOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Genome: nucleomorph
C; Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-298 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 FHWÖRNYRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FOWORNMKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: AD2346
                                                                                                                                                                                                                                                                               A; Accession: E90094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: alr4323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: prsB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A84471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
```

```
hypotherical protein Vng1732c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84325
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
                                                             C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 22-Jun-1999
C;Accession: S07442
R;Weinberg, A.D.; Shaw, J.; Paetkau, V.; Bleackley, R.C.; Magnuson, N.S.; Reeves, R.; Mamunology 63, 603-610, 1988
A;Title: Cloning of CDNA for the bovine IL-2 receptor (bovine Tac antigen).
A;Reference number: S07442; MUID:88212503; PMID:2835311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A penciption: receptor for interleukin-2
A Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK checking interleukin-2 receptor alpha chain; complement factor H repeat homology cycuperfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology Cykeywords: cytokine receptor; duplication; glycoprotein; T-cell proliferation; transment F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-27/Product: interleukin-2 receptor alpha chain #status predicted <MAT>
F;2-43/Domain: extracellular #status predicted <ERT>
F;24-77/Domain: complement factor H repeat homology <FH1>
F;24-64/Domain: transmembrane #status predicted <IMT>
F;265-275/Domain: intracellular #status predicted <IMT>
F;265-275/Domain: intracellular #status predicted <IMT>
F;24-64,51-77,123-168,152-184/Disulfide bonds: #status predicted
F;80,109/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-275 <WEI>
A;Cross-references: EMBL:M20818; NID:g163208; PIDN:AAA51414.1; PID:g163209
C;Complex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-584 <STO>
A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.3%; Score 40; DB 2; Length 584; 41.7%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
interleukin-2 receptor alpha chain precursor - bovine N;Alternate names: CD25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || |:::|:: |
445 CFTWRKDMERKR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 CLIWORKWKKNR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                     A; Accession: S07442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: C84325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: VNG1732C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

à

Genetics

Matches

à

RESULT 11

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-223 <MUR>
A;Residues: 1-223 <MUR>
A;Cross-references: EMBL: Z69909; PIDN:CAA93785.1; GSPDB:GN00066; SPDB:SPAC19G10.03c
A;Experimental source: strain 972h-; cosmid c19G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable peroxisomal membrane protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                       A; Cross-references: GB: AE002093; NID: 94586022; PIDN: AAD25641.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein DKFZp564P2063.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17324
R;Duesterhodeft, A; Lauber, J; Mewes, H:W; Gassenhuber, J; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: 218727
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 1
A;Introns: 10/3; 170/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
C;Keywords: peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T37974

R; Murphy, L; Harris, D; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, March 1996
A; Reference number: Z21759
                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                               54.9%; Score 39; DB 2; Length 531; 87.5%; Pred. No. 44; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.5%; Score 38; DB 2; Length 223; Best Local Similarity 41.7%; Pred: No. 28; Matches 5; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%; Score 39; DB 2; Length 550;
54.5%; Pred. No. 46;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Accession: T17324
A, Status: preliminary
A, Molecule mRNA
A, Residues: 1-558 < DUE>
A, Cross-references: EMBL: AL117610
A; Cross-references: fetal brain; clone DKFZp564P2063
A; Note: DKFZp564P2063.1
                                                                                                                                                                                                            Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 CYELQQNSKKIK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: SPDB:SPAC19G10.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 CYGWRRNSKGV 65
                         A; Molecule type: DNA
A; Residues: 1-531 <STO>
                                                                                                                                                                                                                                                                                                                                                                              501 OWFRINKK 508
                                                                                                                                                                                                                                                                                                                           3 QWQRNMKK 10
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T37974
                                                                                                      C;Genetics:
A;Gene: At2g05650
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
Search completed: February 21, 2003, 07:47:55 Job time : 10.65 secs
```

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-83 71 1 CFQWQRNMKKVR 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	homo sapi	camel			P08071 mus musculu	Q39565 chlamydomon		P26898 ovis aries	Q10333 schizosacch	O77698 bubalus bub	Q9vnb3 drosophila		P45068 haemophilus		Q9xz18 drosophila		P49725 panagrellus		-	homo		P93528 sorghum bic			P55554 rhizobium B			Q9fg65 arabidopsis			50333	6929	57163
SUMMARIES		D	TRFL HUMAN	TRFL CAMDR	TRFL CAPHI	TRFL_HORSE	TRFL MOUSE	DYHB_CHLRE	IL2A_BOVIN	IL2A_SHEEP	YBM9 SCHPO	TRFL BUBBU	O83A_DROME	VP4 ROTGA	FTSA_HAEIN	VNS2 DSDNV	NLA DROME	CATK_RAT	DCOR_PANRE	YL14_CAEEL	TRFL_BOVIN	YOO8 HUMAN	T100_HUMAN	PHYC_SORBI	7LES_DROVI	RPOB_LIBAF	Y4LN RHISN	LOLB VIBCH	GLGA_BACST	C911_ARATH					RPSD_BUCAI
		ength DB	711 1	708 1	708 1	695 1	707	4568 1	275 1	275 1	238 1	708 1	453 1	749 1	425 1	275 1	292 1	329 1	435 1				989 1							502 1	528 1	530 1	269 1	573 1	612 1
٠	Query	Match Length	LO.	80.3	71.8	0.69	59.2	57.7	56.3	56.3	53.5	53.5	52.1	52.1	51.4	50.7	50.7	50.7	50.7	50.7	50.7	50.7		50.7	ο.	δ.	σ	თ	σ	σ		σ			49.3
		Score	68	57	51	49	42	41	40	40	38	38	37	m	36.5	36	36	36	36	36	36	36	36	36	36	35	35	32	35	35	32	32	35	35	35
	Result	No.	1	7	e	4	2	9	7	80	σ	10	11	12	13	14	13	16	17	18	19	20	27	22	23	24	25	26	27	28	29	30	31	32	33

Q9ulc6 homo sapien	P32325 saccharomyc	Q39017 arabidopsis	Q9vm75 drosophila	O00763 homo sapien	P23374 bacillus st	Q92aj2 listeria mo	Q99up4 staphylococ	Q8r9ul thermoanaer	Q9z3q1 rhizobium m	Q58878 methanococc	Q55185 synechocyst
PDI1_HUMAN	DBF4 YEAST	KDG1 ARATH	BP28 DROME	COA2 HUMAN	RL28 BACST	RL28_LISMO	RL28_STAAM	RL28 THETN	SYB2 RHIME	YE83 METUA	Y495_SYNY3
н	Н	-	Н	Н	Н	Н	н	Н	Н	н	7
663	704	728	2096	2483	9	62	62	62	151	152	246
49.3	49.3	49.3	49.3	49.3	47.9	47.9	47.9	47.9	47.9	47.9	47.9
35	35	32	32	32	34	34	34	34	34	34	34
34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

N

```
from human lactoferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1LCF; 31-AUG-94
1LCT; 31-OCT-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96-NON-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S11228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1LFG;
1LFH;
1LFI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1LGB;
1LGC;
1BKA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1DSN;
                                            awamori."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 237-711 FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Mnan W., Parrell L., Dedhia N., Ansari A., Mardis B., Schutz K.,

Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,

Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,

Dragan Y., Giacalone J., Pae A., Powell B., Solinsky K.A., Desilva U.,

Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,

Sagripanti J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
MEDLINE=90064528! PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker B.N.;
"Structure of human lactoferin: crystallographic structure analysis
                                                                                                                                                                                                                                                                                                                                                "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of
                                                                                                                                                                                                                                                                                                             Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-82262043; PubMed-7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-253-->methionine mutant." Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rado T.A., Wei X., Benz E.J. \sigma x., "Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                         SEQUENCE OF 20-711.
MEDLINE=85076667; PubMed=6510420;
Metz-Boutigue M.-H., Jolles J., Marurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
Eur. J. Blochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                          PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sagripanti J.i., Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "An 88 amino acid long C-terminal sequence of human
                                                     Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA."; Nucleic Acids Res. 18:4013-4013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353
                                                                                                                                                                                                                                                                                                                                                                                      N- and C-terminal domains.";
Biochim. Biophys. Acta 670:243-254 (1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and refinement at 2.8-A resolution."; J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acta Crystallogr. D 51:629-646(1995)
                   TISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                              MEDLINE=82046817; PubMed=6794640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97156796; PubMed=9003186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ?EBS Lett. 142:107-110(1982).
 SEQUENCE OF 3-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blood 70:989-993 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 609-711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    actotransferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resolution.
                                                                                                                                                                                                                                                                                                                                  Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jolles
```

```
Miltoworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,

Musiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,

Sugar J., Kumaramanickavel G., Munier F., Schorderer D.F.,

B. Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayau K.,

Hejtmancik J.F., Teng C.T.;

"Ramilial subepithelial ornneal amyloidosis (gelatinous drop-like
"Corneal dystrophy): exclusion of linkage to lactoferrin gene.";

Mol. Vision 4:31-32(1998).

"Corneal dystrophy): exclusion of linkage to lactoferrin gene.";

Mol. Vision 4:31-32(1998).

"CAN BIND TWO ATONE TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATONE PERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUBLIY BICARBONATE.

"FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTACONIST

ACTIVITY: LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE

LACTOFERROXIN B AND C HAVE SOMEWHART HIGHER DEGREES OF PREFERENCE

FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                        CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N., "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                              Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1119-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                                                                                                                                                         Agric. Biol. Chem. 54:1803-1810(1990).
                                                         Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF332168; AAC48753 1; EMBL; BC015822; AAH15822.1; EMBL; BC015823; AAH15823 1; EMBL; M73700; AAA59479.1; EMBL; X52941; CAA37116.1; EMBL; Y95626; AAB57795.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U07643; AAB60324.1;
EMBL; M93150; AAA36159.1;
EMBL; M83202; AAA59511.1;
EMBL; M83205; AAA58656.1;
EMBL; M18642; AAA86665.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X53961; CAA37914.1; -.
                                                                                                                                                                                                                                                                                                                                                            VARIANTS THR-30 AND ARG-48.
PubMed=9873069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1HSE;
1VFD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIGURE FROM N.A.

TISSUE-Mammary gland;

Paramasivam M., Stindy A., Singh R., Sahani M.S., Singh T.D.;

Paramasivam M., Stindy B., Stindy B., Sahani M.S., Singh T.D.;

Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

-I FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE BY SIMILARITY).

-I SUBJUNT: MONOMER (BY SIMILARITY).

-I SUBJUNT: MONOMER (BY SIMILARITY).

-I SUBJUNT: COMPOSED OF TWO HOMOLOGUIS DOMAINS.

-I SUBJUNT: BELONGS TO THE TRANSFERRIN FAMILY.
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                    Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ131674; CAB53387.1; -.
HSRB; AF165879; AAF92241.1; -.
HSRP; O77911; ID10115.
LILEPTO: IPRO1156; Transferrin.
FRIMTS; PR00405; TRANSFERIN.
PRINTS; PR004054; TR FER, 2.
PRINTS; PR002064; TR FER, 2.
PROSITE; PS002065; TRANSFERRIN.
PROSITE; PS002066; TRANSFERRIN.
TRANSFORT; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                        6
              95.8%; Score 68; DB 1; Length 711; 91.7%; Pred. No. 0.00022;
                                                      0; Indels
                                                                                                                                                                                                                                                 O9TUMO; Q9MZSS;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY
BY
BY
BY
BY
BY
BY
                                                      11; Conservative
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
363
363
363
708
64
55
217
2192
200
264
399
                                                                                         1 CFQWQRNMKKVR 12
                                                                                                                               39 CFOWORNMRKVR 50
                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRFL CAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
REPEAT
REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
                                 Best Loca
Matches
                                                                                                                                                                                           RESULT
                                                                                                                               g
                                                                                                                                                                                                                                                        THE FEET THE FEET THE SERVICE COURSE SERVICE S
```

```
Capra hirous (Goat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.3%; Score 57; DB 1; Length 708; 83.3%; Pred. No. 0.018; 2; Indels iive 0; Mismatches 2; Indels
BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-Mammary gland;
Liee T., Yu.D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRFL_CAPHI STANDARD; PRT; 708 AA. 029477; 029479; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 CAOWORRMKKVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642 6
708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9925;
                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                             DISULFID
DISULFID
DISULFID
                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                       METAL
METAL
                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRFL_CAPHI
```

0

```
TRFL HORSE 077811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                        TRFL_HORSE
                                             RESULT 4
                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           HSSP; 077698; 1CE2.
InterPro; IRPO01156; Transferrin.
InterPro; IRPO01156; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.8%; Score 51; DB 1; Length 708; 63.6%; Pred. No. 0.2; cive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F2EDA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANION (BY SIMILARITY)
ANION (BY SIMILARITY)
TWO HOMOLOGOUS DOMAINS.
TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | - > V (IN REF. 2).
|- > R (IN REF. 2).
|- > R (IN REF. 2).
|- > P (IN REF. 2).
|- > P (IN REF. 2).
|- > G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
LACTOTRANSFERRIN.
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77358 MW;
                                                                                                                                                                                                                                                      EMBL; U53857; AAA97958.1; -.
EMBL; X78902; CAASS517.1; -.
HSSP; O77698; 1CE2.
  -!- DOMAIN: COMPOSED OF
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signaĵ.
SIGNAL
CHAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
METAL
METAL
METAL
METAL
  SPET THE PET T
```

.. 0

Gaps

.. 0

Conservative

Matches

|:|||| |:|: CYQWQRRMRKL 48 CFOWORNMKKV 11

g à

Н 38

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       resolution...;
J. Mol. Biol. 289:303-317(1999).
J. Mol. Biol. TRANSFERINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-!- FUNCTION: TRANSFERRINS ARE
CAN BIND TWO ATTOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ010930; CAA09407.1; -.

R PDB; 1BIX; 02-DEC-98

R PDB; 1BIX; 02-PEB-99.

R PDB; 1BY0; 02-PEB-99.

R PDB; 1BY0; 02-PEB-99.

R PETROUGUS; TRANSFERRIN.

R PRINTS; SRO0045; TRANSFERRIN.

R PROSITE; PS00205; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN.

R PROSITE; PS00207; TRANSFERRIN.

R TRANSPORTE;

R ON TER.

I ON TER.
                                                                                                                                                                                                                                                                                              Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                  Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                        Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.; "CDNA sequence of mare lactoferrin."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                        15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                   LACTOTRANSFERRIN
695 AA
                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                                                                                                  TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse)
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
```

us-09-743-107b-83.rsp

Ŋ

Page

```
·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92042099; PubMed=1939212;
Liu Y., Teng C.T.;
Liu Z., Teng C.T.;
Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991).
-I- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pentecost B.T., Teng C.T.; "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB 1; Length 695;
Pred. No. 0.44;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (APR-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07BB84D50E1B165D CRC64;
                                                                                                                                                                                        IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POROTI, P70690, Q61799; Q922P2; (1707) POROTI, P70690; Q61799; Q922P2; (1707) POROTION (1801. 01. Last sequence update) POROTION (1801. 01. Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 707 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 262:10134-10139(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Uterus;
MEDLINE=87280033; Pubmed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 69.0%;
Similarity 75.0%;
9; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                               66
98
198
259
                                                                                                                                                                                                                                                                                                                                                                                                                             601
127
469
143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAKFQRNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482
695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uterine secretions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
284463

6344483

6344483

64443

6443

6443

6443

6443

6443

6443

6443

6443

6443

6443

6443

6443

6443

6444

6443

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

6444

644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRFL MOUSE
                              DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                       METAL
METAL
METAL
METAL
METAL
METAL
METAL
METAL
BINDING
BINDING
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HID DAY BE SEED OF SEE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MR -> 10G (IN REF. 1).
MR -> 0 (IN REF. 2).
MR -> 1 (IN REF. 2).
S -> T (IN REF. 2).
S -> T (IN REF. 2).
L -> 0 (IN REF. 1).
E -> G (IN REF. 1).
MY -> 1 (IN REF. 1).
MY -> 1 (IN REF. 1).
MY -> 1 (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                 PROSITE; PS00265; TRANSFERIN 1; 1.
PROSITE; PS00206; TRANSFERIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 42; DB 1; Length 707; 54.5%; Pred. No. 7.3; 3; Indels iive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                   2.
BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
LACTOTRANSFERRIN.
                                                                                                         EMBL; J03298; AAA40525.1; ---
EMBL; D88510; BAA13633.1; --
EMBL; BC006904; AAH06904.1; ---
EMBL; M74778; AAA39427.1; ---
FTR; A28438; A28438
HSSP, P02788; LEE.
MGD; MGI:96837; LLE.
INTERPRO; IPRO01156; Transferrin.
FFAN, FF00405; transferrin, 2.
FFAN; FRO0422; TRANSFERRIN.
SWART; SM00094; TR_FER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629 6
707 AA;
                                                                                                                                                                                                                                                                                                                          CHAIN
REPEAT
REPEAT
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                     Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
METAL
METAL
```

à 용 01-OCT-1989 (Rel. 12, Last sequence update) 16-OCT-2001 (Rel. 40, Last amnotation update) Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PSS) (TAC antigen) (CD2S).

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and properties institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Cell Sci. 107:635-644 (1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                    Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U02963, AAA19956.1; -.
InterPro; IPR004273; Dynein_heavy.
Bram; PF05028; Dynein_heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 4568;
69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL)
                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) yayein beta chain, flagellar outer arm. ODA4 OR ODA-4 OR SUP1.
                                                   PRT; 4568 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYNEIN HAS ATPASE ACTIVITY.
                                                                                                   01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA; 519961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11175
1400
1650
1825
2045
20848
3162
3425
1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4568
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1158
1372
1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2831
3106
3339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3648
1919
2202
2530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain genes."
J. Cell Sci.
                                             DYHB CHLRE
Q39565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMAIN
                          OYHB CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
RESULT 6
                                                     STATE THE THE TENENCE OF COURTS AND THE STATE OF THE STAT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   MEDLINE=96116968; PubMed=6863178;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Inceptor alpha (IL-2R alpha) gene.";

Mamm. Genome 6.751-753(1995)

-!- FONGTION: RECEPTOR FOR INTERLEUKIN-2.

-!- SUBUNIT: NON COYALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R

EXIST IN 3 DIFFERENT FORMS: A HIGH AFPINITY DIMER, AN INTERMEDIATE

AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE

WITH A GAMMA CHAIN.
                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88212503; PubMed=2835311;
Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
Reeves R., Magnuson J.A.;
"Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
Immunology 63:603-610(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                   Bos taurus (Bovine).
Wakaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora, Bovoidea;
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERLEUKIN-2 RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
SIGNAL 1 21 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.3%; Score 40; DB 1; Length 275; 58.3%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LINKED (GLCNAC. . .) (PO 4901BBF9A4862390 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Type I membrane protein. -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000436; Sushi SCR_CCP.
Pfam; PF00084; sushi; 2.
SMART; SM00032; CCP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31238 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M20818; AAA51414.1; -. EMBL; U24226; AAC48487.1; -. PIR; S07442; HSSP; P01589; IIIM.
                                                                                                                                                                                                                                                                         SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275
243
262
275
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185
64
77
168
184
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 CLTWORKWKKNR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
152
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
à
```

ô

275 A.A.

PRT;

STANDARD;

IL2A BOVIN P12342;

IL2A_BOVIN

RESULT 7

1852 CFQWQSQLRYIQ 1863

1 CFQWQRNMKKVR 12

ਨੋ

01-OCT-1989 (Rel. 12, Created)

à d

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
-1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
-1- SUBDUKT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERREDIATE
EXIST IN 3 DIFFERENT CHAIN), AND A LOW AFFINITY MONOMER (BETA CHAIN), THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92241682; PubMed=1572550;
Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.;
"Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
                                                                                                                                                                                                                                                             Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-PEB-1996 (Rel. 33, Last annotation update)
11-PEB-1996 (Rel. 33, Last annotation update)
11-EB-1996 (Rel. 31)
11-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PS5) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Repeat; Signal; Sushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.3%; Score 40; DB 1; Length 275; 58.3%; Pred. No. 6.4; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-T-cell;
Verhagen A.A.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S -> T (IN REF. 2).
1101A2DE5AC5A088 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                            275 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUSHI 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z11560; CAA77652.1; -.
EMBL; X60149; CAA42723.1; -.
EMBL; A19167; CAA01447.1; -.
PIR; S18910; S18910.
PIR; S18899; S18899.
PIR; JC1113; JC1113.
HSSP; POISS9; ILM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 S
30904 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein;
                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                  Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 113:283-284 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00084; sushi; 2
SMART; SM00032; CCP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
243
262
275
78
185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166
275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
263
23
122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD25."
                                                         L2A SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                     P26898;
KESULT 8
IL2A SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THAIN
                                                                               SO THE THE THE THE TANK BRANCH BRANCH
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.5%; Score 38; DB 1; Length 238; 41.7%; Pred. No. 12; trive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL096788; CAB46672.1; -.
Hypothetical protein.
SEQUENCE 238 AA; 26479 MW; 58095AA8CD708180 CRC64;
                                                                                             Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                           01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
Hypothetical protein C582.09 in chromosome II.
SPBC582.09.
                                                                                 Schizosaccharomyces pombe (Fission yeast)
                   PRT;
                                                                                                                                                               MEDLINE=21848401; PubMed=11859360;
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 CYELQQNSKKIK 166
                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=4896;
                  YBM9 SCHPO
                          Q103<u>3</u>3;
SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
RESULT
YBM9_SC
                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

RESULT 10

ó

Gaps

.. 0

Conservative

us-09-743-107b-83.rsp

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                               Karthikeyan S., Paramasivam M., Yadav S., Srinivasan A., Singh T.P.; "Structure of buffalo lactofezrin at 2.5-A resolution using crystals grown at 303 K shows different orientations of the N and C lobes."; Acta Crystallogr. D 55:1805-1813(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
                                                                                                                  Bubalus bubalis (Domestic water buffalo).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidee; Bovinae; Bubalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001156; Transferrin.
Pfam; Pr00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
Paramasivam M., Thattaliyath B.D., Kumar A., Srinivasan A.,
Singh T.P.;
                                                                                                                                                                                                                                                     "CDNA sequence of Buffalo lactoferrin.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LACTOTRANSFERRIN
                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
               708 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    :- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                  MEDLINE=20003130; PubMed=10531476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ005203; CAA06441.1; -. PDB; 1CE2; 19-MAR-99.
               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; 3D-structure.
                                                                                                                                                                               NCBI_TaxID=89462;
               BUBBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
   TRFL
```

```
STRAINEBEXCELEY,

REDILINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Champen M., Henderson S.M.,

Barandon R.C., Rogers Y. T.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Bast B. B.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ranckova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,

Ranckova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,

Ranchors M., Cawley S. Dahlke C., Davenport L.B., Davies P.,

Ranchors M., Deup L.E., Downes M., Dangan-Rocha S., Dunkov B.C., Dunk

Ranchors M., Ganger J. Garrell J.H., Galbart W.M., Glasser K.,

Ranchors M., Ganger J., Heinander J., Hernander J.R., Houck J.,

Ranchors M., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,

Ranchors M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Ranko P., Liei Y. Leviteky A.A., Li J., Mizzi J., Moshrefi A.,

Ranko P., Liei Y., Leviteky A.A., Li J., Mizzi J., Moshrefi A.,

Ranko P., Liei Y., Leviteky A.A., Li J., Mizzi J., Moshrefi A.,

Ranchon J., Larvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Ranko P., Liei Y., Leviteky A.A., Li J., Mizzi J., Moshrefi A.,

Ranko P., Liei Y., Leviteky A.B., Nichley D., M., Halson D.L.,

Ranchout S.M., Moy M., Murphy B., Murphy L., Muzhy D., Murphy B., Markelov G., Milshina N.V., Nabarry C., Morise J., Parlach J.M.,

Reinert K., Remington K.A., Nixon K., Pubrish M., Palazolo M., Pittman G.S., Paller M., Stupski M.P., Spirlh T.,

Spier E., Spradling A.C., Standers R., Venter E., Wang A.H., Wang X.,

Spier E., Spradling A.C., Standers R., Venter B., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Perrygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophil, Drosophila.
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                   IRON 2.

ANION (POTENTIAL).

ANION (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                             53.5%; Score 38; DB 1; Length 708;
                                                                                                                                                                                                                                                      08D2600AAB2F9ACD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                      Pred. No.
IRON 1.
IRON 1.
IRON 2.
IRON 2.
IRON 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative odorant receptor 83a. OR83A OR CG10612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                          77729 MW;
                                                                                                                                                                                                                                                                                                                    54.5%;
                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                             1 CFOWORNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                    38 CHRWQWRMKKL 48
                                                                                                                                                                                                                                                        708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
  1111
2111
2211
2272
4114
4144
6144
140
252
252
3300
495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O83A DROME
                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                       BINDING
                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09 VNB3;
                                       METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                               à
```

Tue Dec

SEQUENCE FROM N.A.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Kel J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhu X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; science 287:2185-2195 (2000)
                                                                                                                                                Unpublished observations (MAY-2001).
-!- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
                                                                                                                                                                                                                                        -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annobation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02949; 7tm 6; 1.—
Pfam; PF02949; 7tm 6; 1.—
Hypothetical protein; Transmembrane; G-protein coupled receptor; Glycoprotein; Olfaction; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.1%; Score 37; DB 1; Length 453; 66.7%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LINKED (GLCNAC. . .) (PO
4B660B3380901192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=12705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003603; AAF52033.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0037322; Or83a.
InterPro; IPR004117; 7tm_6.
                                                                                                                                                                                                                                                      gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
85
106
148
                                                                                                                      CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 WQRHLKDVR 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
50
86
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381
409
430
249
                                                                                                                                    Robertson H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360
                                                                                                                                                                                                                           RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VP4 ROTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIÑ
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     004916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VP4 ROTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                          Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.; "Identification and baculovirus expression of the VP4 protein of the Unman group B rotavirus ADRV."; Uniol. 67:2730-2738(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
-!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN ANOMALOUS FILAMENT
GROWTH (BY SIMILARITY). MAY BE A COMPONENT OF THE SEPTUM. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                           J. Virol. 67:2730-2738(1993).
-!- SUBCELLULAR LOCATION: Outer capsid.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 749; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D1223527DEAE0F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Cell division protein ftsA.
FTSA OR HII142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
                      MEDLINE=93233240; PubMed=8386274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M91434; AAA47338.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
109
133
407
527
568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 CFTWDMNCANVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTSA HAEIN
P45068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTSA_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DP
STATE TETTER BRANKS SOLUTION OF THE TETTER SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeelffer B.D.,
RA Adams M.D., Devis B. R. Richards R.G., Champe M., Pfeelffer B.D.,
RA Ballew R.M., Basu A., Raxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y. Benco P.V., Barnan B.P., Bhandari D., Belshakov S.,
Roktova D., Botchan M.R., Boutler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Gabrielian A., Daller C., Ferraz C., Ferraz C.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Guan P., Harris M.J.,
R. Hostin D., Houston K.A., Hawland T.J., Hernandez C.R., Ketchum K.A.,
R. Hostin D., Houston K.A., Lawland T.J., Wel M.-H., Ibeewam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kemington D.,
R. Merkulov G., Milshima N.V., Moharry C., Morberson D.,
Multains N.M., Palland B., Murphy L., Muzny D.M., Nelson D.I.,
R. Nelson R., Pitteman G.S., Pan S., Pollard J., Puri V., Reenington K., Sauders R., Ventex S., Wook M., Strong R., Sha H.,
Rander K., Reinington K., Sauders R., Ventex S., Who J., Sha S., Tector C., Turner R., Ventex B., Wang Z.-Y., Wasarman D.A., Walsender J., Shang Z.-Y., Wasarman D.A., Walsender S., Zhan G., Zhan M., Strong R., San K., Shith H.O.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shu B.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shu B.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shu B.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shu B.,
Shue B.C., Stan-Kamos I., Sungers M., Stang S., Zhu X., Smith H.O.,
                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                           Nebula protein.
                                                                                                                                                                                                                                                                                                                    [emales
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMID outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boublik Y., Kouassi K.N., Cavallaro C., Bergoin M.; "Complete nucleotide sequence and genome organization of an infectious clone of Diatraea saccharalis densovirus (DSDNV)."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Densovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.4%; Score 36.5; DB 1; Length 425; 63.6%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                   Pfam; PF02491; Ft8A; 2.
TIGRFAMS; TIGR01174; ft8A; 1.
Cell division; Cell shape; Complete proteome.
SEQUENCE 425 AA; 45836 MW; AF5C4B808D73CE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 AA; 31154 MW; AA9B1B03D7718C71 CRC64;
  MAY INTERACT WITH FTSZ (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FTSA/MREB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 40;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diatraea saccharalis densovirus (DsDNV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF036333; AAC18000.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.78;
                                                                                                                                                                                                                                                                    EMBL; U32794; AAC22797.1; -.
                                                                                                                                                                                                                                                                                                                    InterPro; IPR003494; FtsA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nonstructural protein NS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 CHODWONNLKK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQ-WQRNMKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=72003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WORNMKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 WORNWKK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNS2 DSDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

RESULT 14 VNS2_DSDNV

Matches

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
-!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0026629; nla.
SEQUENCE 292 AA; 31423 MW; 64FlBBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF147700; AAD33987.1; -. EMBL; AE003712; AAF55285.1; -.
```

292 AA.

NIA DROME STANDARD; E Q9XZLB; Q9V391; 30-MAY-2000 (Rel. 39, Created)

ACH

RESULT 15 NLA DROME

g

Matches

Query Match 50.7%; Score 36; DB 1; Length 292; Best Local Similarity 45.5%; Pred. No. 34; Matches 5; Conservative 4; Mismatches 2; Indels

0;

0; Gaps

2 FQWQRNMKKVR 12 |||||:::| 150 FQWLRSFRLR 160

ò

Search completed: February 21, 2003, 07:27:58 Job time : 5.6 secs

į

Н

```
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSE DA PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOCO OCT BY SOCO O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q98rr2 guillardia
Q8yp77 anabaena sp
Q9daz8 mus musculu
Q91zd5 mus musculu
Q91z75 mus musculu
Q81z75 hemerocalli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q98q19 mycoplasma
Q8r2a4 mus musculu
Q38115 bacteriopha
Q9sp27 callistephu
Q9hpa3 halobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8tcd2 homo sapien
Q9ucy5 homo sapien
Q9tr80 ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         salmonella
                                                                                                                                 (without alignments)
118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           February 21, 2003, 07:25:55; Search time 20.8 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9xfd5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q82462
GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8Z462
Q98Q19
Q8R2A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8YP77
Q9DAZ8
Q91ZD5
Q91Z75
O81653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9TRB0
Q9XFD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q38115
Q9SP27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HPA3
                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8TCD2
Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q98RR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
7: sp_mtc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                                   US-09-743-107B-83
                                                                                                                                                                                                                       1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110
111
111
111
111
111
111
111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_plant: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
469
514
514
514
514
333
332
333
333
333
                 Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
```

```
Q8rgt4 fusobacteri
Q8rgt4 fusobacteri
Q91006 trypanosoma
Q77855 human immun
Q77855 human immun
Q8q454 human immun
Q8ytpl sesamum ind
Q9xtpl sesamum ind
Q9xrg ceenorhabdi
Q9xrg helicobacte
Q2xp4 helicobacte
Q2xp4 helicobacte
Q2x188 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                               O9jjz5 mus musculu
Q19153 caenorhabdi
Q9cdi2 lactococcus
                                                                                                                                                                     Q72904 human immun
Q8rmb8 cytophaga j
Q8tnf5 methanosarc
Q9rjp2 streptomyce
Q9sic0 arabidopsis
                                                                                                                                                     092gl6 rickettsia
09d4t5 mus musculu
                                                                                                                                                                                                   Q9wyq1 thermotoga
Q9j196 mus musculu
Q91zf3 mus musculu
                                                                                                                                                                                           ralstonia s
                     Ogufk6 homo sapien
Ogufk6 homo sapien
                O9nz17 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
0
                                                                                                                                                                                           Q8xse2
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63; DB 4; Length 711
Pred. No. 0.0033;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Straubberg R.; Straubberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                              711 AA
                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                061888
09ZKP4
022185
022188
09JUZ5
019153
09CDIZ
09ZGL6
                                                                                                                                                                                                                                                                                             Created)
Q9RJP2
Q9SIC0
Q9NZL7
                             Q9UFK6
Q8RGT4
Q9N906
                                                   Q77855
Q77856
Q8Q454
Q9XHP1
                                                                                 Q93780
Q9KSU3
                                                                                                                                                                     Q72904
Q8RMB8
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                    Q8TNF5
                                                                                                                                                                                           Q8XSE2
                                                                                                                                                                                                                 Q91ZF3
                      CONVEY
                                                                                                                                                                                                                                                                                                                                                                                                                     88.7%;
                                                    15
                                                                                          16
                                                                                                                       110
                                                                                                                                               16
                                                                                                                                                                                                                                                                                             21,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.9
hes 10; Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                     554
558
589
2186
                                                                                                                       543
550
932
1436
                                                                           148
275
323
335
335
515
                                                                                                                                                     99
122
122
248
270
                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 CFOWORNMRKV 49
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE PROM N.A.
TISSUE=PROSTATE;
Lactotransferrin
 Query Match
                                                                                                                                                                                                                                                                             Q8TCD2
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
```

38 AA

PRT;

PRELIMINARY;

0

Gaps

0;

```
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin W., Harden A., Hen T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitchead S., Barrell B.G., Jamonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi (T18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update) .
01-0CT-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
synthase (Pseudouridine synthase B (TRNA pseudouridine 55 synthase) (PSISS synthase) (Pseudouridylate synthase) (Uracil hydrolyase)
(EC 4.2.1.70).
genes that are differentially expressed at rice young panicle."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

-! SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL; AR140466; AAD29699.1; -.

Interpro; IR7001128; Cytochrome_P450.

Pfam; PR00067; P450; 1.

PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                              59.2%; Score 42; DB 10; Length 105; 70.0%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.2%; Score 42; DB 16; Length 511; 58.3%; Pred. No. 17; 5.1ve 0; Mismatches 5; Indels
                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein, Complete proteome.
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                  SEQUENCE 105 AA; 11912 MW; B0EEFCDD487E19F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STX3070.
                                                                                                                    PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                               511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 AA.
                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:848-852(2001).
EMBL; AL627276; CAD06049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                  Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                               1 CFQWQRNMKK 10
                                                                                                                                                                                                                                                                                             61 CFOWERLGKK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                    NON TER
                                                                                                                                                                                                                                                                                                                                                                                             Q8Z462;
                                                                                                                                                                                                                                                                                                                                                                            Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            098019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
Q98Q19
                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                             Q8Z462
          ð
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEEDTHAN
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                   Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzee, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu J., Yang J.; "Suppression subtractive hybridization (SSH) identified candidate
                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                          83.1%; Score 59; DB 4; Length 38; 90.9%; Pred. No. 0.00082; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.6%; Score 48; DB 6; Length 33; 54.5%; Pred. No. 0.074; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qian Z.Y., Jolles P., Migliore Samour D., Fiat A.M.; Biochim. Biophys. Acta 1243:25-32(1995).
HSSP, O77698; ICE2.
InterPro: IPRO01156; Transferrin.
Pfam; PPRO0405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                            0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 AA
                                                                                                               seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                   SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95127729; PubMed=7827104;
                                                                                                                                                              InterPro; IPR001156; Transferrin.
                                                                                                                                                                            Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytochrome P450 (Fragment).
                                                                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                            2 FOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                              21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 CYÓWOKKMRKL 29
                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9940;
                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PANICLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29XFD5;
                                                                                                                                                                                                                                                                                                                                                                                                          09TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9XFD5
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
Q9TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

0

Gaps

0;

```
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Flavone synthase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 CFEWNANDKEV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                    1 CFOWORNMKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                          39 CYPWOKNLLK 48
               Bacteriophage rlt.
                                 NCBI_TaxID=43685;
                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYP93B5
                                                                                                                                                                                                                                                                                                                                                                                 09SP27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09HPA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
Q9HPA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                    à
  셤
                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                       Gaps
                                                                           MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.; "Multiple new and isolated families within the mouse superfamily of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NOBI_TaxID=10090;
                                                                                                                         "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis."; Nucleic Acids Res. 29:2145-2153(2001).
                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
        Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.7%; Score 41; DB 11; Length 341; 66.7%; Pred. No. 17; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                               57.7%; Score 41; DB 16; Length 282; 60.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                         282 AA; 31961 MW; A598529F52B1EBEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 AA; 39632 MW; B3D8259F7AD11130 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Vomeronasal receptor VIRE6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 AA.
                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129X1/SVJ;
MEDLINE=21676859; PubMed=11802169;
                                                                                                                                                       EMBL, AL445565; CACC13723.1; -...
Mypulist; MYPU 5500; -..
InterPro; IRR004510; TruB.
InterPro; IRR005501; TruB.N.
Pfam; PR01509; TruB N; 1.
TIGRFAMS; TIGR00431; TruB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mat. Neurosci. 5:134-140(2002).
EMBL; AY065506; AAL47911.1; -.
                   Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vlr vomeronasal receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q38115
Q38115;
01-NOV-1996 (TEMBLE1. 01,
01-NOV-1996 (TEMBLE1. 01,
01-NOV-1998 (TEMBLE1. 09,
                                                                                                                                                                                                                                Lyase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
Mycoplasma pulmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                           Local Similarity
                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             2 FOWORNMEKV 11
                                                                                                                                                                                                                                                                                                                         20 FAWQNNIKKI 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 CFTWTRNIK 339
                                                                   STRAIN-UAB CTIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQRNMK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     OBR2A4;
                                                                                                                                                                                                                                                                                                                                                                                         QBR2A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              V1RE6
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
Q38115
                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                              Q8R2A4
ö
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
MEDLINE=96332668; PubMed=8730874;
MEDLINE=96332668; PubMed=8730874;
Mauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;
"Inducible gene expression mediated by a repressor-operator system isolated from Lactococcus lactis bacteriophage rit.";
Mol. Microbiol. 19:1331-1341(1996).
                                                                                                                                                                                                                                                                                                        Venema G., Nauta A.;
"Sequence analysis and molecular characterization of the temperate lactococcal bacteriophage rlt.";
Mol. Microbiol. 19:1343-1355 (1996).
EMBL; U38006; AAB18704.1; -.
SEQUENCE 469 AA; 53160 MW; 1F8E02D4325CGBB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Steridae; euasterida II; Asterales, Asteraceae; Asteroideae; Asteraceae; Callistephus.
NCBI_TaxID=13379;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-96332669; PubMed-8730875;
Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.3%; Score 40; DB 10; Length 514; 54.5%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.3%; Score 40; DB 9; Length 469; 50.0%; Pred. No. 36; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Martens S., Forkmann G.;

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL; AF188612; AAF04115.1; -.

EMBL; AF188612; AAF04115.1; -.

EMBL; PF00067; P450; -.

PROSTIE; PS000385; P450.

PROSTIE; PS00086; CYTOCHROME P450; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 514 AA; 58412 MW; 90B631B28952A5E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Callistephus chinensis (China aster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
```

```
163 FHWORNYRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             2 FQWQRNMKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                           01-MAR-2002
01-MAR-2002
                                                                                   01-MAR-2002
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                  Q8YP77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DAZ8;
                                   08YP77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9DAZ8
                                                                                                                                                                                                                                                                                                                                                                   Matches
            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DAZ8
                         08YP77
                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                MEDLINE=20504483; PubMed=11016950; Merquist B., Pan M., Mennedy S.P., Mahairas G.G., Thorseon V., Shorgna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorseon V., Shorgna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Jeck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]

MEDLINE=EROM N.A.
MEDLINE=21223349; PubMed=11323671;
MEDLINE=21223349; Sauner S., Fraunholz M., Beaton M., Penny S., Deng L.T., Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an englaved algal nucleus.";
Nature 410:1091-1096(2001).
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                      .`
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
                                                                                                                                                                                                                                                                                                                                           56.3%; Score 40; DB 17; Length 584; 41.7%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.9%; Score 39; DB 8; Length 205; llarity 45.5%; Pred. No. 23; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                            Halobacterium sp. (etrain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                  584 AA; 65151 MW; 21BF5D5F0486CCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 AA; 22691 MW; D30F5289CBC85049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_TaxID=55529;
01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
265 proteasome SU BS.
                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR000243; Proteasome B.
InterPro, IPR001353; Protsme protease.
Pfam; PF00227; proteasome; 1.
                                                                                                                                                                                                                                                              Interbro, IPR001646, Spectide repeat.
Interpro, IPR001622; K+channel pore.
Pfam, PF00805, Pentapeptide, 2.
Complete proteome.
SEQUENCE 584 AA, 65151 MW, 21BF5DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guillardia theta (Cryptomonas phi).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF165818; AAK39885.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00141; PROTEASOME.
                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                          445 CFTWRKDMERKR 456
                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNIMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CFFWERNLSSL 73
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
Les 5; Conserv
                                                                                                       SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleomorph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteasome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            098RR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              098RR2
                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q98RR2
6
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Arakwa T., Hara A., Shipata K., Yoshino M., Itoh M., Ishii Y., Rakwa T., Hara A., Shipata K., Yoshino M., Itoh M., Ishii Y., RA Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Xanawa K., Izawa M., Nishi Y., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kadota K., Matsuda H., Rikaido I., Rasika H., Kodina H., Ratil D., Lewis S., Matsuo Y., Kikaido I., Pesole G., Quackenbush J., Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furnon M., Anno H., Baldarelli R., Barsh G., Bakai K., Deffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Austone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Basaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Shashi R., Toyo-Ka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Masahizazi Y., Toyo-Wa K., Wang K.H., Weitz C., Whittaker C., Wilming L., Masahizazi Y., Toyo-Wa K., Wang K.H., Weitz C., Whittaker C., Wilming L., Masahizazi Y., Kawai H., Kohtsuki S., Hansahizazi Y., Kawai H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21595285; PubWed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 54.9%; Score 39; DB 16; Length 298; Local Similarity 66.7%; Pred. No. 34; Local Similarity 6 17 Mismatches 2; Indels 18 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003596; BAB76022.1;
Hypochetical protein; Complete proteome.
SEQUENCE 298 AA; 34513 MW; 64036E6B52299A9F CRC64;
                                                                              (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=PLACENTA;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120).
                                                                                                                                                                                                             Hypothetical protein Alr4323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17,
        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1600000123Rik protein.
1600000123RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
```

```
ð
                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=PLACENTA; Deussing J., Schwinde A., Peters C.; Deussing J., Kouadio M., Rehman S., Werber I., Schwinde A., Peters C.; "Identification and Characterization of a Dense Cluster of Placenta-specific Cysteine Peptidases and Related Genes on Mouse Chromosome
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                            Score 39; DB 11; Length 332;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.9%; Score 39; DB 11; Length 332; 55.6%; Pred. No. 38; tive 3; Mismatches 1; Indels
                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                               MEDOPS, COLLIST.

MED: MG1:1916256; 160000123R1K.

MGD: MG1:1916256; 160000123R1K.

MGD: MG1:1916256; 160000123R1K.

InterPro; IPR0001668; Peptidase C1.

PRINTS; PR007105; PAPAIN.

PROSITE; PS00039; THIOL, PROTEASE HIS; UNKNOWN 1.

SEQUENCE 332 AA; 37298 MW; 0804F1BA5B6538E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CATHEPSIN-3.
; 4184B90725B41C0D CRC64;
                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000668; Poptidase_C1.
InterPro; IPR00169; SHprot_acfite.
Pfam; PF00112; Peptidase_C1; 1.
ProDom; PD001158; Peptidase_C1; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                  54.9%; Scor.
55.6%; Pred. No. 30,
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 AA.
                                                                                                                                                                                                                                                                                                  332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
           EMBL; AK005389; BAB23995.1; -. HSSP; P07711; 1CJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY034574; AAK58450.1; -. MGD; MGI:2151929; Cts3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 17 P
114 332 C
332 AA; 37326 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91275;
01-DEC-2001 (TrEMBLrel. 19, C;
01-DEC-2001 (TrEMBLrel. 19, L;
01-MAR-2002 (TrEMBLrel. 20, L;
Cathepsin M.
                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                           Cathepsin-3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                            4 WORNMKKVR 12
                                                                                                                                                                                                                             52 WEENMKKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 WEENMKKIK 60
                                                                                                                                                                                                                                                                                                                        01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91Z75
                                                                                                                                                                                                                                                                                                 Q912D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                        RESULT 14
Q91ZD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
091275
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GE DI GE
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                            ò
```

```
OC BULARYOLIUS (Mouse).

OC BULARYOLIUS (Mouse).

OC MAMMALIA; Mutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBL_TaxID=10090;
RN NCBL_TaxID=10090;
RN SEQUENCE FROM N.A.

RC STRAIN=129/SVEVTACFER; TISSUE=SPLEEN;
RA REHMAN S., Peters C., Deussing J.;
RA REHMAN AV057446; AAL15416.1; -..

DR EMBL; AV057446; AAL15416.1; -..

DR InterPro; IPR0001669; SHprot acsite.

DR Prodom; PR000112; Peptidase C1; 1.

DR Prodom; PR000112; Peptidase C1; 1.

DR PROSTIE; PR000169; SHprot acsite.

DR PROSTIE; PR00039; THFOL PROTEASE HIS; UNKNOWN 1.

SQ SEQUENCE 333 AA, 37388 MW; 6DD0BEB91C033110 CRC64;

QUETY MATCH

SC COMBETVALIVE S5.6%; Pred. No. 38;

MATCHES 5; COMBETVALIVE 3; Mismatches 1; Indels 0; Gaps

QY 4 WQRNWKKUR 12

| | | | | | | :.

Db 52 WEBNWKKIR 60

Search completed: February 21, 2003, 07:44:37

Job time: 21.8 secs
```

·;

Peptide for anti-u Human lactoferrin Human lactoferrin

Human lactoferrin Advanced glycosyla Human lactoferrin Amino acid sequenc Human lactoferrin

AAY78063 AAY78031 AAY78064 AAY78065 AAY78034 AAY78034 AAY78066 AAY78067

Anti microbial pep Lactoferrin-relate

AAY78033 AAY68867 AAY78032 AAR21810 AAR4841 AAR48530

Lactoferrin derive Lactoferrin derive Lactoferrin derive Bovine lactoferrin Bovine lactoferrin

AAR57461 AAR57462 AAR84698

AAR84699 AAR80263 AAR80264 AAR98553

AAR91852 AAW03045 AAR90607

AAR87622 AAW26150 AAW14036 AAW70310

AAR87621

Anti-parasitic lac Anti-parasitic lac

Peptide for anti-u Lactoferrin-derive Lactoferrin-derive Lactoferrin-derive Lactoferrin-derive Lactoferrin deriva Anti-parasitic pep

Lactoferrin derive

Thrombus formation Lactoferrin hydrol

ALIGNMENTS

```
February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Geneseq 101002:*

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDS2/gcddata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDS2/gcddata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDS2/gcddata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDS2/gcddata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDS2/gcddata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to ha score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Descrip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
Human
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                              908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78038
AAY78046
AAY78047
AAY78037
AAY78048
AAY78048
AAY78050
AAY78050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78084
                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                US-09-743-107B-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                        1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211221122122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0
                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
68
68
68
68
68
68
                                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
```

WALSOU. DAT: *	KES	KENOTI. T	
AA1991.DAT:*	AAY7	PAY78084	
AA1992.DAT:*	qi	AAY78084 standard; Peptide; 12 AA.	
AA1993.DAT:*	X		
AA1994.DAT:*	AC	AAY78084;	
AA1995.DAT:*	X		
AA1996.DAT:*	DI	25-APR-2000 (first entry)	
AA1997.DAT:*	X		
AA1998.DAT:*	DE	Human lactoferrin derived peptide SEQ ID NO:84.	
AA1999.DAT:*	×		
AA2000.DAT:*	KW	Human, lactoferrin; modification; infection; inflammation; tumour;	n; tumour;
A2001.DAT:*	KW	food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;	anti-tumour;
AA2002.DAT:*	KW	urinary tract infection; colitis; Candida infection; fundicidal;	qicidal;
	MX.	bactericidal; preservative.	
te to have a	X		
t being printed,	SO	Homo sapiens.	
oution.	SO	Synthetic.	
	X		
	PN	WO200001730-A1.	
	×		
	PD	13-JAN-2000.	
Description	×		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PF	06-JUL-1999; 99WO-SE01230.	
Human lactoferrin	X		
Human lactoferrin	PR	06-JUL-1998; 98SE-0002441.	
Human lactoferrin	PR		
Human lactoferrin	PR	29-DEC-1998; 98SE-0004614.	
Human lactoferrin	X		
Human lactoferrin	PA	(ASCI-) A+ SCI INVEST AB.	
Human lactoferrin	X		
	ΡΙ	Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;	
	×		
Human lactoferrin	DR	WPI; 2000-147388/13.	

N

```
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                     AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                           Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 71; DB 21; Length 12; Local Similarity 100.0%; Pred. No. 1.3e-05; nes 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 70; 102pp; English.
                                                                Claim 22; Page 36; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78038 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                     12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              н
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
à
```

. 0

```
.,
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tunours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
                                                                                                                                                  Bven though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                       95.8%; Score 68; DB 21; Length 12; 91.7%; Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78046 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWORNMRKVR
                                                                                                                                                                                                                                                                                    12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78046;
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                            Matches
     à
                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
```

ö

; 0

Gaps .; 0

```
fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammantory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                            Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                            Length 12;
                                                                                                                         Score 68; DB 21; Length 12
Pred. No. 4.3e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                                                                                                                                                                             AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 73; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA, Mattsby-Baltzer I,
                                                                                                                         95.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                        1 CFQWERNMRKVR 12
                                                                                                                                                                                                 1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-147388/13.
                                                                                                                                      Local Similarity
                                                                                                  12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                             25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1998;
17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                  Sequence
                                                                                                                         Query Match
                                                                                                                                                Matches
                                                                                                                                                                                                                                     RESULT 4
   85888888%
                                                                                                                                                                                               d
                                                                                                                                                                          ð
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower cannot be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                    Score 68; DB 21; Length 12;
Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 95.8%; Score 68; DB 21; Length 13; l Similarity 91.7%; Pred. No. 4.7e-05; 11; Conservative 1; Mismatches 0; Indels
                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolphin GT;
                                                     4.3e-05;
                                                                                                                                                                                                                                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:37.
                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                   AAY78037 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mattsby-Baltzer I,
                                  95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0004614
                                                                                                                                                                                                                                                                                                           25-APR-2000 (first entry)
                                                 Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASCI-) A+ SCI INVEST AB.
                                                                                                        1 CFOWERNMRKVR 12
                                                                                                                                          1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Sequence
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                               RESULT 5
AAY78037
                                                                                                                                                                                                                                                      à
```

0

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also to fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower

Human lactoferrin derived peptide SEQ ID NO:49.

(first entry)

25-APR-2000

AAY78049;

AAY78049 standard; Peptide; 13 AA.

4

```
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through linding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candaid infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                           Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%; Score 68; DB 21; Length 13; 91.7%; Pred. No. 4.7e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baltzer L, Dolphin GT
                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 74; 102pp; English
                                                                                        AAY78048 standard; Peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                             99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0004614.
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASCI-) A+ SCI INVEST AB.
1 CFQWERNMRKVR 12
              2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AA;
                                                                                                                                                                                                                                                                                                       WO200001730-A1.
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                      36-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
                                                                                                                                            25-APR-2000
                                                                                                                                                                                                                                                                                                                                13-JAN-2000
                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                  AAY78048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                 d
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMY NOUL TO MAIN TABLO LEPPENENT PROPLICUES INVAINGE SECRETION. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as utinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78001 to AAY78100 represent peptides having sequences based on human
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 21; Length 13;
Pred. No. 4.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78036 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.8%;
                                                                                                                                                                                                                                                                                                                                                     99WO-SE01230
                                                                                         bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91...
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AA;
                                                                                                                                                                                                                                    WO200001730-A1
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                     06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
                                                                                                                                                                                                                                                                                             13-JAN-2000
                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXEXEX B
```

· 0

Gaps

; 0

11; Conservative

Matches

1 CFQWERNMRKVR 12

2 CPÓWORNMRKVR 13

g

8

RESULT 7

98SE-0002441. 98SE-0002562. 98SE-0004614.

(ASCI-) A+ SCI INVEST AB.

29-DEC-1998; 06-JUL-1998; 17-JUL-1998;

99WO-SE01230

06-JUL-1999;

13-JAN-2000

WO200001730-A1

Synthetic.

```
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                           Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                          Claim 12; Page 69; 102pp; English.
                                                                                                                                      98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                     99WO-SE01230,
                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                WO200001730-A1
                                                      sapiens,
                                                                                                                   06-JUL-1999;
                                                                                                                                     06-JUL-1998;
                                                                                                                                                      29-DEC-1998;
                                                                                                                                               17-JUL-1998;
                                                                                                  13-JAN-2000
                                                               Synthetic.
                                                      Ношо
```

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammatcins and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also tingicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-inflammatory and anti-i

14 AA; Sequence

Gaps . 0 95.8%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 5.1e-05; 1: Mismatches 0; Indels 11; Conservative Similarity Query Match Local Matches

0;

AAY78050 standard; Peptide; 14 AA. AAY78050; AAY78050

(first entry) 25-APR-2000

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative. Human lactoferrin derived peptide SEQ ID NO:50.

Homo sapiens

99WO-SE01230.

06-JUL-1999;

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin acceptors and are then transported through the opecific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.8%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 5.1e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                                                                                                                                            Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                              WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78051
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ö

The agent is low It can be .

Gaps

.

```
anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-ulcer agent contg. peptide - has low toxicity, is
                                                                                                Claim 18; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                           AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MORG ) MORINAGA MILK IND CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 11; 11pp; Japanese
                                                Mattsby-Baltzer I,
                                                                                                                                                                                                                                              95.8%;
91.7%;
      98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                     Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                            94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0283869
                                                                                                                                                                                                                                                                                                                                                      12-NOV-1996 (first entry)
                                  (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                          1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                        3 CFOWORNMRKVR 14
                                                              WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-318857/32
                                                                                                                                                                                                                                                    Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                14 AA;
      06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               JP08143468-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-1996.
                                                 Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                         AAR98554;
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                       g
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such and infant formula food. The peptides are also in food stuffs such and and also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                   AAR98531-54 are peptides used in an anti-ulcer agent. The a
in toxicity, is heat-resistant and stable in aqueous soln..
administered orally and be produced in large amounts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                               Length 15;
                                                                                                                                                          95.8%; Score 68; DB 17; Length 15
91.7%; Pred. No. 5.5e-05;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                         1 CPOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                      2 CFQWQRNMRKVR
                                                                                                                15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78035;
                                                                                                                  Sequence
                                                                                                                                                          Query Match
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                     AAY78035
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the individual constitution. A medical product of the peptide or fragment the circulation. A medical product of the peptide or fragment to be used for treating and/or prevention of infections (such as curnary tract infections, colitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower costs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68; DB 21; Length 14;
Pred. No. 5.1e-05;
1; Mismatches 0; Indels
                                                                                                                                                               Dolphin GT;
                                                                                                                                                          Baltzer L,
```

infections,

15 AA;

Sequence

AAY78063 standard; Peptide; 15 AA.

; 0

25-APR-2000 (first entry)

AAY78063;

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammartions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
                                                                                                                                                                                                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urrinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                Gaps
                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
        Score 68; DB 21; Length 15;
Pred. No. 5.5e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.8%; Score 68; DB 21; Length 15; 91.7%; Pred. No. 5.5e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dolphin GT;
                                                                                                                                                                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:62.
95.8%; Scc. 91.7%; Pred. No. 5...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                    AAY78062 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           danson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-SE01230.
                                                                                                                                                                                                                                                     (first entry)
                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB.
                                                                      1 CFOWERNMRKVR 12
                                                                                                      4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
        Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1998;
                                                                                                                                                                                                                                                    25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000,
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapie.
Synthetic.
                                                                                                                                                                                                                     AAY78062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                    à
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would costs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
0
                                                                                                                         Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 68; DB 21; Length 15;
Pred. No. 5.5e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolphin GT;
                                                                                          Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78031 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                   98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.8%;
                                                                                                                                                                                                                                                                                                                                                                                 98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yb.e.
Best Local Similarity 91.77
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AA;
                                                                                                                                                                                                                                                   WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                 06-JUL-1998;
                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson LA,
                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78031
ઠે
```

·

Gaps

.. 0

11; Conservative

Matches

4 CFOWORNMRKVR 15

CFOWERNMRKVR 12

à

```
25-APR-2000 (first entry)
```

Human lactoferrin derived peptide SEQ ID NO:31.

Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, utinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative

Homo sapiens. Synthetic. WO200001730-A1.

13-JAN-2000.

99WO-SE01230. 06-JUL-1999;

98SE-0002441. 98SE-0002562. 98SE-0004614. 17-JUL-1998; 29-DEC-1998; 06-JUL-1998;

(ASCI-) A+ SCI INVEST AB.

Baltzer L, Dolphin GT; Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 11; Page 68; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the spetide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammarions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower conts.

16 AA; Sequence

0; Gaps Query Match 95.8%; Score 68; DB 21; Length 16; Best Local Similarity 91.7%; Pred. No. 5.9e-05; Matches 11; Conservative 1; Mismatches 0; Indels

ö

1 CFQWERNMRKVR 12

d

Search completed: February 21, 2003, 07:37:15 Job time : 29.35 secs

Run on:

```
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl
Appli
Appli
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                         February 21, 2003, 07:25:59; Search time 8.65 Seconds (without alignments) 40.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, P
Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8,
Sequence 8,
Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25
Sequence 24
Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3
Sequence 2
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4
Sequence 6
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7
Sequence 8
Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-204-487-3

US-08-628-98-8

US-08-628-98-8

US-08-628-98-8

US-08-628-161A-3

US-07-081-174-3

US-08-204-487-1

US-08-216-487-1

US-08-216-487-1

US-08-216-487-1

US-08-217-24

US-08-21-984-25

US-09-508-734-4

US-09-508-734-4

US-09-508-734-8

US-07-755-161A-10

US-07-755-161A-10

US-07-91-174-8

US-07-91-174-8

US-07-91-174-8

US-08-26-771-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6
                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                           262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                    US-09-743-107B-84
71
                                                                                                                         1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein
                                                                                                                                                                                                                                                                                        Database :
                                                                                                                         Sequence:
                                                                                                                                                                         Searched:
```

Result

No.

LOCATION: 1.18 OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE

TOPOLOGY: linear MOLECULE TYPE: peptide NAME/KEY: Peptide

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HILLSSARA
APPLICANT: HILLSON VIASSARA
APPLICANT: ANTENN CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                              Score 68; DB 1; Length 18;
Pred. No. 4e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.8%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 4e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07601

ZIP: 07601

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATA:
FILING DATA:
CLASSIFICATION: 436
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APPLICATION: 436
APPLICATION NUMBER: 08/418,642
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAWE: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 947-1-008A
TELEPOME: 201 487-5800
TELEPHONE: 201 487-5800
TELEPOMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION OF 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08485948
Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
OTHER INFORMATION: (20-37)"
                                                                                                          Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FRAGMENT TYPE: internal US-08-485-948-8
                                                                                                                                                                                                                                                                                                          1 CFQWQRNMRKVR 12
                                                                                                                                                                                                                                                           1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
       ; US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

1 CFOWORNMRKVR 12

```
Sequence 8, Application US/08628380
Patent No. 5891341
GENERAL INFORMATION:
APPLICANT: ULASSARA, HELEN
APPLICANT: VLASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: ARGENTE FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 95.8%; Score 68; DB 2; Length 18; 1 Similarity 91.7%; Pred. No. 4e-05; 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER EADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
CLASSIFICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: JGCKEN NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELERDRANGICATION INFORMATION:
TELERDRANGICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-475-055-8; Sequence 8, Application US/08475055; Patent No. 596245; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide DESCRIPTION: LF-C1, 8-25 HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                            TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.8%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 4e-05; 0; Indels tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STRET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                            ZIP: 07601

MEDIUM TYPE: Floppy disk
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                     TILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PREDICATION NUMBER: 08/485,948
FILING DATE: 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
ATTORNEY/AGENT INPORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELEPHONE: 201 487-5800
TELEPAX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHRACATERISTICS:
                  E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.8
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FRAGMENT TYPE: internal US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
CORRESPONDENCE ADDRESS:
                                                       CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
OPERATION SYSTEMS

GOTTOMAR SYSTEMS

GOTTOMAR SYSTEMS

FALLY PRIZACTION DATA:

FATLY CATCON DATA:

FATLY C
```

95.8%; Score 68; DB 1; Length 20;

```
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
                                               /note= "thiol group of Cys residue at location 2 connected by disulfide bond with thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICERALI
APPLICANT: TANAKA, SHICERALI
APPLICANT: TANAKA, SHICERALI
APPLICANT: KAWASAKI, YOSHINIRO
APPLICANT: KAWASAKI, YOSHINIRO
APPLICANT: UNUBINA, TOSHINALI
TITLE OF INVENTION: URAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: IMHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURMITZ & ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER ZEBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Comparible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
TURRENT APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 1; I
Pred. No. 4.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CAMPBEL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08204487; Patent No. 5565425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                           FEATURE: NAME/KEY: modified site
                       IDENTIFICATION METHOD: OTHER INFORMATION: /mc OTHER INFORMATION: Cys OTHER INFORMATION: thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                       DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 02109
                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                            AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                        VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                              ö
                              Gaps
                         Indels
                                                                                                                                                                                                   Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
    Pred. No. 4.4e-05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAX-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION TOWNER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                              1 CFQWERNMRKVR 12
                                                                                     2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION IN GENOME:
CHROMOSOME/SEGMENT;
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                              RESULT 6
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
                                                            à
                                                                                                  qq
```

us-09-743-107b-84.rai

Page

```
Query Match

95.8%; Score 68; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.4e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                       1 CFQWERNMRKVR 12
                                                                                                                                                            2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                    US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                     ઠે
                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: MAMORY TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderocth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                  Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.4e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                 LOCATION: 1.20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IDEN COMPATIBLE COMPUTER: DISK COMPATIBLE COMPUTER: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
CLASSIPPICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/08256771
Patent No. 5656591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORREY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 amino acids
                                                                                                         single
                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                               NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                       2 CFQWQRNMRKVR 13
                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-256-771-24
                                                                                                                                                                                                                                                             US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                      RESULT 9
US-08-256-771-25
1 Sequence 25, Application US/08256771
2 Sequence 25, Application US/08256771
3 Fatent No. 5656591
3 GENERAL INFORMATION:
3 APPLICANT: Manoru TOMITA et al.
3 TITLE OF INVENTION: ANTINICROBIAL AGENTS AND METHOD FOR TREATING
3 TITLE OF INVENTION: PRODUCTS THEREWITH
3 TITLE OF INVENTION: PRODUCTS THEREWITH
3 TITLE OF INVENTION: ADDRESS: 32
3 CORRESPONDENCE ADDRESS: 32
4 CORRESPONDENCE ADDRESS: 4 Fifteenth Street, N.W., #700
5 CITY: Washington
5 STREET: U.S.A.
6 COUNTRY: U.S.A.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCATION:
DENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to other Information: prevent disulfide bond"
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
95.8%; Score 68; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.4e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OFFRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT AFPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: JUJY 22, 1994
CLASSIFICATION EATA:
APPLICATION NUMBER: APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
TELECOMMUNICATION NUMBER:
REGISTRATION NUMBER:
TELECOMMUNICATION NUMBER:
```

```
LOCATION:
DEBATIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PASSYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR PRIOR PELING DATE: 1999-07-14
PRIOR PELING DATE: 1998-07-14
PRIOR PELING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "cysteine residues at positions 2

OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.4e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                               MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYGTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFFCATION: 252
PRICE APPLICATION NUMBER:
APPLICATION NUMBER:
                805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
                                                                                                                                                                                                                                                                                                                                                                                                                            Cheek, Jr.
BER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek,
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                      20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                         STATE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /note= "cysteine residues at positions 2 OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 4.4e-05; ive 1; Mismatches 0; Indels
                                                           APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
CONTRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION: 272
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
Sequence 24, Application US/08381984 Patent No. 5804555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CFQWQRNMRKVR 13
                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                     .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
```

```
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 21

IDBNITICATION METHOD: 7

OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" sublication: AUTHORS: AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
95.8%; Score 68; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 5.5e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMOUNICATION INFORMATION:
TELEPHONE: 202-311-8850
TELEPAX: 202-371-8856
                                                                                                                                                                   TELEX:
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: modified gite
                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CPÓWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                       TOPOLOGY: 11;
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                   USCOURT OF APPLICATION US/09508734

Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

Setent No. 6425509

TITLE DF INVENTION: Wass production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: WASS production method of lactoferrin polypeptide from yeast and FILE REFRENCE: PA/S/G/00139

CURRENT APPLICATION NUMBER: US/09/508,734

PRIOR FILING DATE: 1990-07-14

PRIOR FILING DATE: 1990-07-14

PRIOR FILING DATE: 1990-07-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: KOPATEHINI 1.71

SEQ ID NO 6

LENGTH: 24
                                                                                                                                                  ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                Gaps
                                                                                                                                              .
0
                                                                                             Y Match 95.8%; Score 68; DB 4; Length 22; Local Similarity 91.7%; Pred. No. 4.9e-05; hes 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.8%; Score 68; DB 4; Length 24; 91.7%; Pred. No. 5.3e-05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER;
                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                       1 CFQWERNMRKVR 12
                                                                                                                                                                                               2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CFQWQRNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-07-755-161A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D
                                                         US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-508-734-6
LENGTH: 22
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

NAME/KEY: modified site LOCATION: 21

```
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                       / Match 95.8%; Score 68; DB 1; Length 25; Local Similarity 91.7%; Pred. No. 5.5e-05; les 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 21, 2003, 07:50:36 Job time: 8.7 secs
                                                                                                                                                                                                                                                             DOCUMENT NUMBER:
FILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                US-07-891-174-10
                                                                                                                                                              JOURNAL:
                                                                                                                                                                                 VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                      PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
```

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec

US-09-743-107B-84 71 1 CFQWERNMRKVR 12 Perfect score: Sednence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

156504 seqs, 31069816 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PuB.WW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Semience 2. Appli	20		Sequence 6. Appli	Sequence 3. Appli	Sequence 23. April	7.7	4	2	8	Segmence 29. Appl	30.	2, 4	4	Sequence 47985, A	Seguence 46393. A	Sequence 5715. An	Segmence 26 Appl	112	
I D	US-09-798-869-2	US-09-798-869-20	US-10-023-096-2	9-698-864-80-SD	US-09-798-869-3	US-09-798-869-23	US-09-798-869-7	US-09-798-869-4	US-09-798-869-22	US-09-798-869-8	US-09-798-869-29	US-09-798-869-30	US-09-888-320-2	US-10-051-409-4	US-09-864-761-47985	US-09-864-761-46393	US-09-738-626-5715	US-09-796-753-26	US-09-978-295A-119	
Query Match Length DB	15 9	25 9	694 9	15 9	15 9	25 9	15 9	15 9	25 9	15 9	15 9	15 9	489 9	846 9	21 10	40 10	86 9	333 9	338 9	
Query Match Le	95.8	95.8	95.8	84.5	71.8	71.8	9.09	59.2	59.2	54.9	54.9	54.9	53.5	52.1	50.7	50.7	49.3	49.3	49.3	
Score	69	68	68	9	51	51	43	42	42	39	39	39	38	37	36	36	35	35	35	
Result No.	H	7	ю	4	ហ	9	7	œ	σ'n	10	11	12	13	14	15	16	17	18	19	

	Sequence o, Appl. Sequence 14, Appl. Sequence 24, Appl. Sequence 24, Appl. Sequence 30, Appl. Sequence 30, Appl.	Sequence 22, Appli Sequence 2, Appli Sequence 2, Appli Sequence 46806, A Sequence 12129, A	Sequence 13026, A Sequence 320, App Sequence 320, App Sequence 1324, App Sequence 58, Appl Sequence 58, Appl	Sequence 58, Appl Sequence 41002, A Sequence 1200, Ap Sequence 1031, Ap Sequence 530, App
US-09-978-697-119 US-09-978-192A-119 US-09-999-832A-119 US-09-978-189-119	US-09-796-753-14 US-09-981-649A-6 US-09-981-649A-24 US-09-981-649A-30	Þ	US-09-9818-242-13026 UG-09-984-245-320 US-09-984-761-33619 US-09-925-300-1324 US-10-066-500-58 US-10-066-273-58	
00005	9 6 6 6 6 6	25055	010000	69999
	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	559 1701 50 62	246 63 747 744 744 744	747 77 88 95 168
4 4 4 4 4 0 0 0 0 0 6 6 6 6 6		24444 20444 2077 2007 2007	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	446.5 46.5 46.5 7.6
ម ម ម ម ម ម ម ម ម ម ម ម ម ម ម ម ម ម ម	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		ਆ ਦਾ ਦਾ ਦਾ ਦਾ ਸੰਨਾਨੀ ਨੀ ਨੀ ਨੀ ਨੀ	4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1 2 1 2 1 2 1 2 1 3 1 3 1 3 1 3 1 3 1		๚ ๚ ๚ ฅ ฅ ๗ ๗ ๚ ๚ ๚ Ի ๗ ๗ ๗	4 4 4 4 4 4 4 6 4 6 4 6 6 4 6

ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%; Score 68; DB 9; Length 15; 91.7%; Pred. No. 3.6e-05; Live 1; Mismatches 0; Indels
Sequence 2, Application US/09798869

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TYPEL OF INVENTION SUGNE SURING
APPLICANT:
BALON APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
FRIOR APPLICATION NUMBER: PCT/GB99/02851
FRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
BRIOR APPLICATION NUMBER:
APPLICANTON NUMBER:
BRIOR APPLICANTON NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-798-869-20
Sequence 20, Application US/09798669
Publication No. US20030022821A1
GENERAL INFORMATION
JAPPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: YSTEIN REKNAL
APPLICANT: APPLICANT: ABLDUR SVEINBJ (RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CFQWQRNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

ö

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Ogllnick, Paul D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoférrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.

ZIP: 20004

ZIP: 20004

COMPUTER FELDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/023,096

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A.
               TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSELSEQ for Windows Version 4.0
: LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REPERENCE JOCKET NUMBER: 10505/P58185C
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PADDLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION WUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                          Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
  LARS VORLAND
                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CFÓWQRINMRKVR 14
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-023-096-2
APPLICANT:
                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
·,
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens OTHER INFORMATION: sequence)
                                                            0;
             Length 694;
                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.5%; Score 60; DB 9; Length 15; 83.3%; Pred. No. 0.0007; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 9; Length 15; Pred. No. 0.02;
     95.8%; Score 68; DB 9;
91.7%; Pred. No. 0.0014;
iive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                               APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: ALALDY SVEINBAL (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BICACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1090-08-31
PRIOR APPLICATION NUMBER: PCT/GB09/02851
PRIOR APPLICATION NUMBER: GB0918938.4
PRIOR PLING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTHARE: FASTSEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09798869
Fublication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGHED SVENDSEN
APPLICANT: (YSTEIN REKNAL
APPLICANT: ARBY VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
FRICK APPLICATION NUMBER: PCT/GB99/02851
FRICK APPLICATION NUMBER: PCT/GB99/02851
FRICK APPLICATION NUMBER: GB9818938.4
FRICK FILING DATE: 1999-08-31
FRICK APPLICATION NUMBER: GB9818938.4
FRICK FILING DATE: 1999-08-31
FRICK APPLICATION NUMBER: GB9818938.4
FRICK FILING DATE: 1999-08-31
FRICK FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                             Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.8%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
Query Match
Best Local Similarity
                                                                                                      1 CFOWERNMRKVR 12
                                                                                                                                                       22 CFÓWORNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CFÓWOWNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3
                                                                                                                                                                                                                              RESULT 4
US-09-798-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
```

```
1 CFOWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: MURINE
US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 22
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                  à
                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens; OTHER INFORMATION: sequence)
US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.8%; Score 51; DB 9; Length 25; 63.6%; Pred. No. 0.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
60.6%; Score 43; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.38;
Matches 6; Conservative 3; Mismatches 2; Indels
      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                    Sequence 33, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OCHN SIGURD SVENDSEN
APPLICANT: ARS YORLAND
APPLICANT: ARS YORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRERENCE: A34649-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRANCE OF SEQ FOR WINDGRMS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-34
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 63.6
Matches 7; Conservative
                                       1 CFQWERNMRKV 11
                                                                            3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||:||:|
3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: CAPRINE
                                                                                                                                                      US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

. 0

Gaps

.,

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.2%; Score 42; DB 9; Length 25; 54.5%; Pred. No. 0.9; 1ve 2; Mismatches 3; Indels
                                                                               US-09-798-869-4

Sequence 4, Application US/09798869

Publication No. US20030022821A1

GENERAL INFORMATION:
APPLICANT: (GYTEIN RENDAL

APPLICANT: GYTEIN RENDAL

APPLICANT: HALDUR SVEINBJ(RNSSON

TITLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FRSEUEN WINDOWS Version 4.0

SEQ ID NO 4

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYBINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRACERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
3 CYÓWOWRMRKI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CLRWQNEMRKV 13
```

0

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine ; OTHER INFORMATION: sequence)
US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134.9%; Score 39; DB 9; Length 15; 13xity 54.5%; Pred. No. 1.7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.9%; Score 39; DB 9; Length 15; 45.5%; Pred. No. 1.7; tive 4; Mismatches 2; Indels
                                                                                            APPLICANT: INCUENTAL KEKDAL,
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE EFFTIDES
FILLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILLING DATE: 2001-02-27
FRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILLING DATE: 1999-08-31
PRIOR FILLING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09798869
Fublication No. US20030022821A1
GENERAL INPORMATION:
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-06-31
PRIOR APPLICATION NUMBER: PCT/G899/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
Sequence 8, Application US/09798869; Publication No. US20030022821A1
                                        GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
.....has 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CLRWQWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM; BOVINE
US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

3 CFRWQWRMKKL 13

RESULT 12 US-09-798-869-30

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barry III, Clifton E. APPLICANT: Barry III, Khisimuzi APPLICANT: Mdluli, Khisimuzi APPLICANT: Mdluli, Khisimuzi APPLICANT: Mdluli, Khisimuzi APPLICANT: Bekker, Linda-Gail APPLICANT: Bekker, Linda-Gail APPLICANT: The Government of the United States of America APPLICANT: as represented by The Secreteary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis FILE REPERENCE: 015280-413100US CURRENT APPLICATION NUMBER: US/09/888,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Mycobacterium tuberculosis
) OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.5%; Score 38; DB 9; Length 489; 54.5%; Pred. No. 67; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.9%; Score 39; DB 9; Length 15; 45.5%; Pred. No. 1.7; 2; Indels Live 4; Mismatches 2; Indels
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OF STEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-00-22
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 30
LENGTH: 15
LENGTH: 15
LENGTH: 15
RECORD NOS: 30
SEQ ID NO 30
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/0988320; Publication No. US20030013090A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-10-051-409-4
; Sequence 4, Application US/10051409
; Publication No. US20030027171A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.55
These 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CFRWQWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 COKWPRRMRKM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 CFÓWRR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWER 6
                                                                                                                                                                                                                                                  SEQ ID NO 47985
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 47985, Application US/09864761
SEREAL INCOMATION:
SECURIOR CONTROL SHARTON
SERVED TO USZOZOGO-0875A1
GENERAL INFORMATION:
APPLICANT: BRANK, DAVIG R.
APPLICANT: BRANK, DAVIG R.
APPLICANT: HANG, DAVIG R.
APPLICANT: HANG, DAVIG R.
APPLICANT: HANG, DAVIG R.
APPLICANT: HANG GENER EXPRESSION ANALYSIS BY MICRORERY
TITLE OF INVENTION: HUMAN GENORE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN ENGINE AND SHORT STATES AND SHORT STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.1%; Score 37; DB 9; Length 846; 50.0%; Pred. No. 1.6e+02; Live 3; Mismatches 1; Indels
                                                                                         APPLICANT: Fann, Ming-Ji
APPLICANT: Chou, Chen-Kung
TITLE OF INVENTION: CELL CYCLE REGULATOR PROTEIN
FILE REFERENCE: 12005-003001
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/051,409
CURRENT FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2001-01-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH: 846
Yang, Chu-Wen
Tsou, Ann-Ping
Chi, Chin-Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:|:| :
448 CFEWDRKL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWERNM 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-864-761-47985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-051-409-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

ö

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec Run on:

US-09-743-107B-84 1 CFQWERNMRKVR 12 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Andreas Andrea	lactoferrin - goat	ı	ا د	ייייייייייייייייייייייייייייייייייייייי	26S proteasome SII	מַ נְ	trichohvalin like		abolipoprotein B-1	33.3K hynothetical	hypothetical prote	hypothetical prote	MHC Class I histor	Oliter canaid arote	trimethylmether	3-deoxy-manno-octu	hypothetical prote	probable cytochrom					CVTOChrome P450 mo				hypothetical prote	1 0)
SUMMARIES		i 																												
SUMM	e e	TFHUL	JC2323	852107	AB0858	A28438	E90094	T22597	B85431	T08030	B60950	G86403	T29571	AD2346	137477	A45687	G82168	D71876	T32605	B96691	C70655	B85441	0473	C85441	17	C84325	H96515	T28820	m	H97451
	DB	н	~	~	7	-													~	7	C)	7		7	8	7	7			~
	Length	711	708	33	511	707	205	275	1432	4568	274	289	361	298	365	749	820	393	433	481	489	492	499	200	200	584	887	932	152	206
₩	Query Match	95.8	71.8	9.19	62.0	59.2	57.7	57.7	57.7	57.7	56.3	56.3	56.3	54.9	54.9	54.9	54.9	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	52.1	52.1
	Score	68	51	48	44	42	41	41	41	41	40	40							38											
	Result No.	н	7	Э	4	<u>د</u>	9	7	80	σn	10	11	12	13	14	15	16	17	18	19	20	21	22	73	24	25	26	27	28	29

A; Status: nucleic acid sequence not shown; not compared with conceptual translation

A,Molecule type: mRNA A,Residues: 20-31 <ST1> A,Accession: 820941 A,Molecule type: protein A,Residues: 20-28,'X',30-31 <ST2>

A; Molecule type: DNA
A; Residues: 1.15 < TEEN>
A; Cross-references: GB:852659; NID:9263311; PIDN:AAB24877.1; PID:9263312
A; Rote: Bequence extracted from NCBI backbone (NCBIP:122202)
B; Powell, M.J.; Ogden, J.B.
Nucleic Acids Res. 18, 4013, 1990
A; Title: Nucleotide sequence of human lactoferrin cDNA.
A; Reference number: 810324; MUID:90326549; PMID:2374734
A; Accession: 810324
A; Molecule type: mENA
A; Residues: 3-711 × POWA
A; Residues: 3-712 × Powell, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A; Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A; Recenter number: 815853; MUID:91264786; PMID:2049066
A; Coresina variation of cloned human lactoferrin in baby-hamster kidney cells.
A; Recenter number: 815853; MUID:91264786; PMID:2049066

A;Accession: A45401

dovamine 5.	probable novidovam	Signal Dentidace I	のathenain 1. (知り 2	Cathebair I. (E)	nrohable tyrosine	COTTOCHTOMP D450 (F	Cytochrome D450	himothorian rent	himothetical prote	himothotical proce	mypounetical proce	roll:22 limported	probable secreted	propagae oxidored	ds - gzills aring	hypothetical prote
AB2670	AG3441	E87515	KHRTL	KHWST	C71467	T10896	F71417	T24218	T19429	A96807	096582	B87162	E70848	T09017	0.11000	D20413
7	~	0	Н	Н	N	N	0	7	(7	0	10	l C	N	n	ı	4
206	208	255	334	334	415	505	517	536	681	720	124	134	303	339	00.0	0 1
52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	50.7	50.7	50.7	50.7	-	
37	37	37	37	37	37	37	37	37	37	37	36	36	36	36	75	2
3.0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4	•

ALIGNMENTS

RESULT 1

	TFHUL
	lactotransferrin precursor [validated] - human
	N;Alternate names: lactoferrin
	C;Species: Homo sapiens (man)
	C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
_	C; Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07760; A61169. A71000. S74
	R;Cho, Y,
	submitted to the EMBL Data Library, March 1994
	A; Reference number: G06820
_	A;Accession: G01394
	A;Status: preliminary; translated from GB/FMRI/DDB.T
	A; Molecule type: mRNA
	A;Residues: 1-711 <cho></cho>
	A; Cross-references: EMBL: U07643: NID: 9467236: PIDN: AABG0324 1. DID: 9467237
	R. Rey, M.W.; Woloshuk, S.L.; deBoer, H.A. Diener B.D.
	Nucleic Acids Res. 18, 5288, 1990
	A:Title: Complete nucleotide seminance of human mammary aland lanteformin
	A:Reference number: \$11228; MITD-90184839. DMITD-24024
	A:Accession: S11228
	A; Molecule type: mRNA
	A;Residues: 1-148,'T',150-422,'C',424-711 <rry></rry>
	A; Cross-references: EMBL: X53961: NID:034415; DIDN:02837914 1. DID:024416
	R; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella T.
	Mol. Endocrinol. 6, 1969-1981, 1992
	A:Title: Differential molecular mechanism of the estronen action that remulates lactoform
	A;Reference number: A45401; MIID:93125571; PMID:14801895 acciou icgulates factorell
	STATE OF THE PROPERTY OF THE P

ö

Gaps

.

1; Indels

Length 708;

```
Biochim. Biophys. Acta 1243, 25-32, 1995
Affilte: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet & A;Reference number: $52107; MUID:95127729; PMID:7827104
A;Accession: $52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies: Salmonella enterica subsp. enterica serovar Typhi divoce; this species has also been called Salmonella typhi cipace; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 Cipacesion: AB0858

Riparkhil, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

Ayauthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Airitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serox A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-511 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N'Alternate names: lactotransferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-33 <Q1A>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.6%; Score 48; DB 2; 54.5%; Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.0%; Score 44; DB 2; 58.3%; Pred. No. 5.7;
                                                                Score 51; DB
Pred. No. 0.46
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                            71.8%;
63.6%;
                          Query Match
Best Local Similarity 63.67
Ender 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lactoferrin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWERNMRKVR 12
                                                                                                                                                                                                           1 CFOWERNMRKV 11
                                                                                                                                                                                                                                                                           38 CYQWQRRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                           S52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A28438
                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                             A.Molecule type: mRNA
A.Residues: 436-487, 7A', 489-711 <RAD>
A.Residues: 436-487, 7A', 489-711 <RAD>
A.Residues: 436-487, 7A', 489-711 <RAD>
A.Croser-references: EMBLAM18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
B.Penella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A.Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth A.Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Resdues: 3-701, SWRPWY <PAN>
A;Experimental source: normal breast tissue
B;Experimental source: normal breast tissue
Bur. J. Blochem, 145, 659-666, 1984
A;Title: Human lactofransferrin: amino acid sequence and structural comparisons with oth
A;Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                              핕
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Map position: 3q21-3q23
(Superfamily: transferrin; transferrin repeat homology
(Superfamily: transferrin; transferrin; iron binding; milk
(S.Keywords: duplication; glyoprotein; iron binding; milk
(S.Keywords: auplication; glyoprotein; iron binding; milk
(S.10-711/Product: lactotransferrin #status experimental <MAT>
(S.20-711/Product: lactotransferrin repeat homology <TRH1>
(S.20-50,500main: transferrin repeat homology <TRH2>
(S.20-65,30-56,135-218.177-133,190-201,251-255,503-65,135-609/Disulfide bonds: #status e
(S.20-65,30-56,135-218.177-133,190-201,251-255,503-609/Disulfide bonds: #status e
(S.157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Capra aegagrus hircus (domestic goat)
C.Species: Capra aegagrus hircus (domestic goat)
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
R.Le Provost, F.; Nocatt, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A./Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A./Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A./Molecule type: mRNA
A./Molecule type: mRNA
A./Molecule type: mRNA
A./Molecule type: mRNA
C.Superfamily: transferrin; transferrin repeat homology
C.Keywords: duplication; glycoprotein
F.359-666/Domain: transferrin repeat homology <TRH2>
F.252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 purification by aminohexyl affir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMOLECULE type: protein
A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A;Note: this is the final paper in a series
R;Houen, G.; Hoegdall, B.V.; Barkholt, V.; Norskov, L.

Bur. J. Biochem. 241, 303-308, 1996
A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinalities: note number: S74119; MUID:97054624; PMID:8898921
R;Rado, T.A.; Wei, X.; Benz Jr., B.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Reference number: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 1; Length 711; Pred. No. 0.00046; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A;Residues: 'G', 23-24,'R', 26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:119368; OMIM:150210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 CPOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A61169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - goat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB:LIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

0

· 0

Gaps

ò

A; Accession: A28438

Accession: A41205

Query Match

Matches

; 0

```
A;Gene: ODA4
A;Gene: ODA4
A;Gene: ODA4
A;Gene: ODA4
A;Map position: IX
A;Inta; 14/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 1
3334/3; 3686/3; 3882/3; 4246/3
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nuclectide binding; P-loop
F;1919-1926/Region: nuclectide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: B85431
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of Chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Chlamydomonas reinhardtii
CiDate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
CiAccession: T0830
Rimitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
                                                                                                                                         A;Residues: 1-275 <WIL>
A;Cross-references: EMBL:281089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A;Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Residues: 1-1432 <STO>
A.Gross-references: GB:NC_001268; NID:97270600; PIDN:CAB80318.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: DNA
A;Residues: 1-4568 <MIT>
A;COSS-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                              A,Map position: X
A,Introns: 67/1; 153/1
C,Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 2; Length 1432;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.7%; Score 41; DB 2; Length 275; 63.6%; Pred. No. 10; 2; Indels ative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trichohyalin like protein [imported] - Arabidopsis thaliana
                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dynein beta heavy chain - Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: T08030
A,Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 YDWEQNARKLR 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 FOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                           A; Gene: CESP: F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                       A; Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: AT4q36520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                   R/Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A/Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: E90094
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-205 <DOU>
A;Cross-references: GB:AF165818; NID:913794510; PIDN:AAK39885.1; GSPDB:GN00150
                                                                                                                                                                                                                                                                                               A.Cross-references: EMBL:J03298
R.Liu, Y., Teng, C. 1.
M. Biol. Chem. 266, 21880-21885, 1991
A.Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A.Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C.Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1; Length 707;
Pred. No. 18;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26S proteasome SU B5 [imported] - Guillardia theta nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.7%; Score 41; DB 2; Length 205; 75.0%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F:1-19/Domain: signal sequence #status predicted <SIG>F:20-707/Product: lactotransferrin #status predicted <MAT>F:358-695/Domain: transferrin repeat homology <TRH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
/Realdues: 1-15 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 < 110 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F53H4.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R,Dobson, R. submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.2%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.07
The 6 Conservative
C; Accession: A28438; A41205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z19587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 CLRWQNEMRKV 47
                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 3-707 <PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: prsB5
A;Map position: 1
A;Genome: nucleomorph
C;Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: E90094
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CFFWERNL 70
```

A; Molecule type: DNA

C; Genetics:

1 CFQWERNM 8

à

0;

Matches

```
Sybecies: Nostoc sp.
A;Note: Nostoc sp.
A;Stranko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sp.
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ansa; Reference number: AB1807; MUD:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHC class I histocompatibility antigen alpha chain HLA-A34 precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: O2-Uul-1996 #sequence revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: 137477; S16771; S16767
R;Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour, J. Immunol: 149, 3411-3415, 1992
A;Title: Distinctive HLA-A, B antigens of black populations formed by interallelic conver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-298 KKDR>
A;Residues: 1-298 KKDR>
A;Cross-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4323
                                                    hypothetical protein F30B5.4 - Caenorhabditis elegans Cipacies: Caenorhabditis elegans Cipacies: Caenorhabditis elegans Cipace 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C;Accession: T25571 R:Miller, N.; Bradshaw, H. R:Miller, N.; Bradshaw, H. Submitted to the EMBL Data Library, December 1995 A;Description: The sequence of C. elegans cosmid F30B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X61704; NID:g32161; PIDN:CAA43873.1; PID:g32162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Gene: CESP:F30B5.4
A.Introns: 140/3; 179/2; 223/1
C.Superfamily: Caenorhabditis elegans hypothetical protein F30B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.3%; Score 40; DB 2; Length 361; 60.0%; Pred. No. 20; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-361 <MIL>
A;Residues: 1-361 <MIL>
A;Cross-references: EMBL:U42437; PIDN:AA83493.1; CESP:F30B5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 2; Length 298; Pred. No. 25; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: 137476; MUID:93056508; PMID:1431115
A; Accession: 137477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWERNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CIQWELNRRR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 FHWORNYRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FQWERNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Status: preliminary A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                            A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Characteristics of the sequence revision 02-Mar-2001 #text_change 09-Nov-2001 Characteristics of the sequence revision 02-Mar-2001 #text_change 09-Nov-2001 Characteristics of the sequence revision 02-Mar-2001 #text_change 03-Nov-2001 R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hudnes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000 A; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000 A; Multer, J.L.; V.; Liu, S.K.; Liu, Z.A.; Lucos, J.S.; Maykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Sakano, H. A; Multors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference and analysis of chromosome 1 of the plant Arabidopsis. A; Reference and analysis of chromosome 1 of the plant Arabidopsis. A; Reterence number: A86141; MulD:21016719; PMID:11130712 A; Reference and analysis of chromosome 1 of the plant Arabidopsis. A; Reterence by E. DNA A; Residues: 1-289 <STO> A; Cross-references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141 A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C)Accession: B60950
R;Law, A.; Scott, J.
J. 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A;Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Residues: 1-274 <LAW>
A, Residues: 1-274 <LAW>
A, Note: authors translated the codon ATA for residue 8 as Val
C, Superfamily: apolipoprotein B
C, Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Rattus norvegicus (Norway rat)
C.Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3K hypothetical protein F28L5.13 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                               Length 4568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.3%; Score 40; DB 2; Length 274; ilarity 66.7%; Pred. No. 15; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.3%; Score 40; DB 2; Length 289; larity 58.3%; Pred. No. 16; Conservative 0; Mismatches 5; Indels
                                                                                                        57.7%; Score 41; DB 2; Length 456
41.7%; Pred. No. 1.8e+02;
tive 4; Mismatches 3; Indels
F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apolipoprotein B-100 - rat (fragment)
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                       1852 CFÓWQSQLRYIQ 1863
                                                                                                                                                                                                                                        1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CFTWEEYARHVR 19
                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 WERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 WDRNLRKFR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
```

Query Match

Best Loca Matches

RESULT 12

```
A;Note: this allele is designated A*3401 (formerly HLA-Aw34.1)

R;Madrigal, J.A.; Bellich, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour,
submitted to the EMBL Data Library, August 1991
A;Description: Molecular definition of HLA-A,B antigens of black populations: Implicatio
A;Reference number: S16766
A;Residues: S16766
A;Molecule type: mRNA
A;Residues: 1-2, V', 4-89, N', 91-120, 'I',122-128,'S',130-137,'R',139-179,'L',181-248,'I',
A;Coss-references: EMBL:X61705
A;Note: this allele is designated A*3402
C;Genetics:
A;Gene: GDB:HLA-A
A;Coss-references: GDB:119310; OMIM:142800
C;Genetics:
A;Gene: GDB:HLA-A
A;Coss-references: GDB:119310; OMIM:142800
C;Genetics:
A;Coss-references: GDB:119310; OMIM:142800
C;Guperfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: heterodimer; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>F;220-285/Domain: immunoglobulin homology <NMM>F;220-285/Domain: immunoglobulin homology <NMM>F;1-24/Domain: immunoglobulin homology <
```

Gaps 0 54.9%; Score 39; DB 2; Length 365; larity 66.7%; Pred. No. 31; Conservative 2; Mismatches 1; Indels Query Match Best Local Similarity Matches 6; Conserv

·:

4 WERNMRKVR 12

84 WDRNTRKVK 92 g

RESULT 15

Outer capsid protein VP4 - human rotavirus B
C;Species: human rotavirus B
C;Species: human rotavirus B
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 19-Feb-1999
C;Accession: A45687
R;Mackow, E.R.; Werner-Eckert, R.; Fay, M.E.; Tao, H.; Chen, G.
J; Virol. 67, 2730-2738, 1993
A;Title: Identification and baculovirus expression of the VP4 protein of the human group A;Reference number: A45687; MUID:93233240; PMID:8386274

A, Accession: A45687

A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-749 <MAC>
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:130353, NCBIP:130355)
C;Superfamily: rotavirus core protein

.**.** Query Match

54.9%; Score 39; DB 2; Length 749;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 5; Indels

ö

Gaps

1 CFQWERNMRKVR 12 à

195 CFTWDMNCANVR 206

Search completed: February 21, 2003, 07:47:56 Job time : 10.65 secs

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:25:55 ; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-84 71 1 CFQWERNMRKVR 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0* Maximum Match 100* Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	PO2788 homo ganien	10 camel	_	edung	- 73	_				P41187 liberibacte	Q9xz18 drosophila			Q58878 methanococc	P06797 mus musculu	P07154 rattus norv	015398 homo sapien				O35186 rattus norv		P11652 propionibac		P09445 cricetulus	P13639 homo sapien	_	P58252 mus musculu	7	93528	5554	Ŋ	3639 homo sa
SUMMARIES	ID	iρχ	TRFL CAMDR	TRFL CAPHI	TRFL HORSE	TRFL MOUSE	DYKB CHLRE	YKYL CAEEL	1A34 HUMAN	VP4 ROTGA					YE83 METUA	CATL_MOUSE	CATL_RAT	YOOR HUMAN		ATX1 ARATH	DMD CANFA	CATK_RAT		4				EF2_MESAU	EF2 MOUSE	EF2_RAT	PHYC SORBI	Y4LN RHISN	VIF SIVS4	5H4_HUMAN
	A DB	1							5	σ		92 1		2																				
	Length	1	708	70	69	70	4568	45	36	74	14	29	20	62	15	33	33	76	78	117	368	32	33	63	85	82	82	82	85	85	113	16	21	38
-40	Query	95.							54.9																							49.3	σ.	٠
	Score	68	51	51	43	42	41	40	99	99	38	93	38	37	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	36	32	35	35
	Result No.		7	m	4	ហ	9	7	æ	ማ	10	77	12	13	14	15	16	17	18	61	20	27	22	23	7.4	25	5 2 6	7.7	28	29	30	31	32	33

Q13515 homo sapien Q9pjj9 chlamydia m Q9ulc6 homo sapien O67763 aquifex aeo Q9x6y2 aquifex pyr Q9vm75 drosophila P2334 bacillus st P01432 naja mossam Q92aj2 listeria mo Q92aj2 listeria mo Q99upq staphylococ Q59195 synechocyst P53661 mycoplasma	
BFS2 HUMAN SYH CHLMU PDDII HUMAN RPOC AQUAE RPOC AQUAE RL28 BR28 BR28 BR28 BR28 BR28 BR28 RL28 LISWO RL28 LISWO RL28 SYRAY Y125 MXCCA	
напанананан	
4115 428 6628 11576 2096 602 622 622 622 622 622	
44444444444 00000000000000000000000000	
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	
& & & & & & & & & & & & & & & & & & &	

# ALIGNMENTS

06:51:45 2003

a

Tue Dec

SEQUENCE OF 3-711 FROM N.A.

TISSUE=Mammary gland;

```
SEQUENCE OF 237-711 FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansaria B., Schutz R.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Sagripanti J.L.;
                                                                                                                                                                                                                                                                                                                                                           "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90064528; PubMed-2585506; Anderson B.F., Baker B.N.; Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker B.N.; Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
                                                                                                                                                                                                                                                                                                       MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rado T.A., Wei X., Benz B.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library an expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                               SEQUENCE OF 20-711.
MEDIAINE=85076667; PubMed=6510420;
MEDIAINE=85076667; PubMed=6510420;
MELZ-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural comparisons with other transferrins.";
                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE-82046817; PubMed-6794640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jolles P.; ""An 88 amino acid long C-terminal sequence of human
                                   MEDLINE=90326549; PubMed=2374734;
Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 670:243-254(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; Pubmed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                               Nucleic Acids Res. 18:4013-4013(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                   J. Biochem. 145:659-666(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88001031; PubMed=3477300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=82262043; PubMed=7049727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBS Lett. 142:107-110(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 436-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 -- >methionine mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blood 70:989-993 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 609-711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .actotransferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker E.N.;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Enropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manual Control of the control of the
                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N., "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
"Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change.";
Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Secreted.
DOWAIN: COMPOSED OF TWO HOMOLOGOUS DOWAINS.
SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    from human lactoferrin.";
Agric. Biol. Chem. 54:1803-1810(1990)
                                                                                 Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF332168; AAG48753 1; EMBL; BC018822; AAH15822.1; EMBL; M73700; AAA59479.1; EMBL; X52941; CAAA594795.1; EMBL; U95626; AAB57795.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X53961, CAA37914.1, -.
EMBL, U07643, AAB60324.1; -.
EMBL, M93150, AAA36159.1; -.
EMBL, M83202, AAA59511.1; -.
EMBL, M83205, AAA56665.1; -.
EMBL, M18642, AAA86665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS THR-30 AND ARG-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1LCF; 31-AUG-94.
1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
1LFH; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9873069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S11228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
```

12-MAR-97. 21-APR-97.

1LFI; 31-OCT-93. 1LGB; 31-AUG-94. -AUG-94 08-NOV-96 08-MAR-96.

1BKA; 1LGC;

```
642
708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
В
                                                           DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                          DISULFID
                                                                                                                                                                                                                    METAL
METAL
METAL
METAL
METAL
METAL
BINDING
                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                      METAL
                                                                                                                                                                                                       WETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRFL_CAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
         SOT THE FILL BETT THE FILL BET
                                                         ·
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                Camelus dromedarius (Dromedary) (Arabian camel).
Sukaryota: Metazoa; Chordata; Craniata; Vortebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSEP, 077811, 1BIX.
HSEP, 077811, 1BIX.
PEAM, PRO010156, Transferrin.
PEAM, PRO0402; TRANSFERRIN.
PROSTITE, PRO0205, TRANSFERRIN.
PROSITE, PRO0205, TRANSFERRIN.
PROSITE, PRO0206, TRANSFERRIN.
PROSITE, PRO0207; TRANSFERRIN.
TRANSFERRIN.
TRANSFERRIN.
TRANSFERRIN.
TRANSFERRIN.
Transport, Iron transport, Glycoprotein, Metal-binding, Repeat,
                    Length 711;
Score 68; DB 1; Length /LL. Pred. No. 0.00026;
                                                                                                                                                                                                   TREL CAMDR STANDARD; PRT; 708 AA. 09TUM), 09MXS; 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUM-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
 95.8%; Scor.
91.7%; Pred. No. u.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [nt. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ131674; CAB53387.1; -.
EMBL; AF165879; AAF82241.1; -.
                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
363
363
363
708
64
64
55
217
192
200
264
399
                                                                                1 CFQWERNMRKVR 12
                                                                                                                 39 CFÓWORNMRKVR 50
           Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Mammary gland;
MEDLINE=94380047; PubMed=8093048;
MEDLINE=94380047; PubMed=8093048;

le Provost F., Nocart M., Guerin G., Martin P.;
le Provost F., Nocart M., Guerin G., Martin P.;
le Provost F., Nocart M., Guerin G., Martin P.;
le Fubracterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 syntemy group.";
Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
le FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
le SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capra hirous (Goat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.8%; Score 51; DB 1; Length 708; 66.7%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         F -> S (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
LLS -> PLF (IN REF. 2).
L -> F (IN REF. 2).
A -> P (IN REF. 2).
A -> P (IN REF. 2).
A -> Q (IN REF. 2).
A -> Q (IN REF. 2).
W, OBOCLT5AOB69D430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 2 (BY SIMILARITY)
ANION (BY SIMILARITY)
ANION (BY SIMILARITY)
N-LINKED (GLCNAC. )
N-LINKED (GLCNAC. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRFL CAPHI SIMNUAL, (29477), 029479, 12-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-UDK-2002 (Rel. 41, Last amotation update) 15-UTM-2002 (Rel. 41, Last amotation update)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 CAQWORRMKKVR 49
```

695 AA

STANDARD;

```
TRFL HORSE
077811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
REPEAT
REPEAT
                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and proposit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                      HSSP, 077698; ICEZ.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
PROSITE; PS00205; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN.
PROSITE; PS00207; TRANSFERRIN.
PROSITE; PS00207; TRANSFERRIN.
PROSITE; PS00207; TRANSFERRIN.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.8%; Score 51; DB 1; Length 708; 63.6%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F2EDA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON I (BY SIMILARITY).
IRON I (BY SIMILARITY).
IRON I (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I -> V (IN REF. 2)

L -> R (IN REF. 2)

C -> K (IN REF. 2)

S -> R (IN REF. 2)

S -> R (IN REF. 2)

D -> G (IN REF. 2)
                                                                                                                                                                                                                                                                              BY SIMILARITY.

1.
2.
3.
4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANION (BY
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77358 MW;
                                                                                                                                 EMBL; U53857; AAA97958.1; -. EMBL; X78902; CAA55517.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 63.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  708 AA;
                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                    Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                         CHAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   resolution.",
J. Mol. Biol. 289:303-317(1999).

-!- FOUCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-!- FOUCTION: TRANSFERRINS ARE IRON IN ASSOCIATION WITH THE BINDING
OF AN AIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!- SUBINIT: MONOMER.
-!- SUBLINITE: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E WBL, AJ010930, CAA09407.1; -.

R PDB; 1BJX; 02-DEC-99.

R PDB; 1B7Z; 02-FEB-99.

R PDB; 1B7Z; 02-FEB-99.

R PDB; 1B7Z; 02-FEB-99.

R PDB; 1B7Z; 02-FEB-99.

R PRINTS: PRO0422; TRANSFERIN. 2.

R PRINTS: PRO0504; TRANSFERIN. 1; 2.

R PROSITE; PS00205; TRANSFERIN. 2; 2.

R PROSITE; PS00207; TRANSFERIN. 2; 2.

R PROSITE; PS00207; TRANSFERIN. 2; 2.

R PROSITE; PS00207; TRANSFERIN. 3; 1.

R TRANSFERIN. 3; 1.

R TRANSFERIN. 3; 1.

R TRANSFERIN. 3; 1.

R TRANSFERIN. 3; 1.
                                                                                                                                                                                                                                                                                           Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                 Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                        SEQUENCE FROM N.A.

Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/Genbank/DDBJ databases.
                          15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LACTOTRANSFERRIN
                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                              TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
                                                                                                 Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695
695
695
695
7179
1179
1187
1187
1187
690
690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; 3D-structure.
NON TER 1
SIGNAL <1
                                                                                                                                            NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
151
121
163
163
176
237
237
354
411
411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
```

0

Gaps

;

1; Indels

Mismatches

ω ;

CFQWERNMRKV 11 38 CYQWQRRMRKL 48

Н

à 셤

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-14 FROM N.A.

MEDLINE=92042099; PubMed=1939212;

Liu Y., Teng C.T.;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266:21880-21885(1991).

-I- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Uterus;
MEDLINE-87280033; PubMed-3611056;
Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                         60.6%; Score 43; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                   07BB84D50E1B165D CRC64;
                                                                                                                                                                                      IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                  SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                    (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRFL_MOUSE STANDARD; PRT; 707 AA. P08071; P70690; Q61799; Q922P2; P08071; P70690; Q61799; Q622P2; P1-4106-1988 (Rel. 08, Created) P1-41Nx-2002 (Rel. 41, Last sequence update) P5-41Nx-2002 (Rel. 41, Last annotation update) Pactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 5.4;
4; Mismatches
                                                                                                                            1 IRON 1
1 IRON 1
1 IRON 2
1 IRON 2
1 IRON 2
1 IRON 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                                     75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
    1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 CAKFORNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uterine secretions."
                                                                                                                                                                                                                                                                                                                                                                                                 695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
  444466

60444669

60444669

604446

604446

604446

604446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446

60446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moriishi K.;
                                      DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
SEQUENCE
DISULFID
DISULFID
                                                                                                                                         METAL
METAL
METAL
METAL
METAL
METAL
METAL
BINDING
                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRFL MOUSE
  STATE BELLE BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANION (POTENTIAL).

ANION (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MR -> IQG (IN REF. 1).

R -> Q (IN REF. 2).

M -> L (IN REF. 2).

A -> D (IN REF. 2).

A -> D (IN REF. 2).

E -> G (IN REF. 1).

E -> G (IN REF. 1).

MY, F26AB0340AAC19AB CRC64;
                                                                                                                                                                                                                                                       fransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.2%; Score 42; DB 1; Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (BY SIMILARITY).
1 (BY SIMILARITY).
1 (BY SIMILARITY).
2 (BY SIMILARITY).
2 (BY SIMILARITY).
2 (BY SIMILARITY).
3 (BY SIMILARITY).
5 (BY SIMILARITY).
                                                                                                                                                                                                                                                                               BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                            2.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 8.1;
2; Mismatches
                                                                                                                                                                           InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00421; TRANSFERRIN.
SMART; SMO0094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON 1
IRON 1
IRON 2
IRON 2
IRON 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON 1
                                                                                                                    EMBL; BC006904; AAH06904.1; -.
                                                                                                                               EMBL; M74778; AAA39427.1; -.
PIR; A28438; A28438.
HSSP; P02788; 1CB6.
MGD; MGI:96837; Ltf.
                                                                                               EMBL; J03298; AAA40525.1; -.
EMBL; D88510; BAA13633.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              702
665
550
693
693
533
605
648
78
110
210
271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451
613
613
481
118
494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
82
359
382
449
629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
82
359
382
449
629
707 AA;
                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                             SIGNAL
CHAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                  Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
METAL
```

g 4

Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein F30B5.4 in chromosome IV

Caenorhabditis elegans.

F30B5.4

STRAIN=Bristol N2; Miller N., Bradshaw H.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A. NCBI_TaxID=6239;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.

Waterston R.;

REVISIONS Submitted

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    J. Cell Sci. 107:635-644 (1994).

-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                 Mitchell D.R., Brown K.S., "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                              DYNEIN HAS ATPASE ACTIVITY.
SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                      Chlamydomonas reinhardtii.
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLLED COLL (POTENTIAL).
MICROTUBLIS-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U02963; AAA19956.1; -.
InterPro; IPR004273; Dynein heavy.
Pfam; PF03028; Dynein heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.
DOMAIN 277 293 COLLED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 4568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                    15, Last sequence update)
19, Last annotation update)
flagellar outer arm.
               PRT; 4568 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                    Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                    MEDLINE=94274778; PubMed=8006077;
                                      (Rel. 35, Created)
(Rel. 35, Last seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             519961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.7%;
              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293
11175
1400
1650
1825
2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2537
                                                                (Rel. 39,
                                                                                             ODA4 OR ODA-4 OR SUP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3106 316
3339 342
3648 372
1919 192
2202 220
2230 2530
2879 288
                                                                              Dynein beta chain,
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                 NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2831
                                                                                                                                                                                                                                            chain genes.";
J. Cell Sci. 1
                                      01-NOV-1997
01-NOV-1997
                                                                  30-MAY-2000
              DYHB CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNIB GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DYHB_CHLRE
```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

. 0

Gaps

. 0

56.3%; Score 40; DB 1; Length 455; 60.0%; Pred. No. 12; 1. Mismatches 3; Indels

6; Conservative

Best Local Similarity

Matches

Query Match

EMBL, U42437; AAA83493.2; -.
WormPep; F30B5.4; CE28552.
Hypothetical protein.
SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;

```
SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=92235211; PubMed=8475492;
Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit E.D., Parham P.;
"Structural diversity in the HLA-A10 family of alleles: correlations
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.";
                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                              P30455; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
                                                                                                                       365 AA
                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A. (A*3401/A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Antigens 41:72-80(1993)
                                                                                                                     STANDARD;
                                   102 CIQWELNRRR 111
1 CFQWERNMRK 10
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with serology.";
                                                                                                                                                                                                                                       HLA-A OR HLAA.
                                                                                                                     1A34 HUMAN
                                                                                   RESULT 8
1A34_HUMAN
à
```

ö

Gaps

0;

3; Indels

4; Mismatches

5; Conservative

Matches

1852 CFQWQSQLRYIQ 1863

1 CFQWERNMRKVR 12

455 AA.

PRT;

RESULT 7
YEYL CAREL

JOSEPH STANDARD;

AC 019910;

DT 16-OCT-2001 (Rel. 40, Created)

01-JUN-1994 (Rel. 29, Last sequence update) 01-JUN-1994 (Rel. 29, Last annotation update) Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).

Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
Viruses, dsRNA viruses; Reoviridae; Rotavirus.
NCBL_TaxID=12705;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its modified and this statement is a long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                               POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                         DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 1; Length 365;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             063BF63E6E6E01F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               AW-34 (A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I -> V (IN A*3402).

/FTId=VAR 004379.

K -> N (IN A*3402).

FTIG=VAR 004379.

R -> I (IN A*3402).

FTIG=VAR 004380.

/FTIG=VAR 004381.

/FTIG=VAR 004381.

/FTIG=VAR 004383.

V -> R (IN A*3402).

/FTIG=VAR 004383.

M -> L (IN A*3402).

/FTIG=VAR 004383.

/FTIG=VAR 004383.

/FTIG=VAR 004383.

/FTIG=VAR 004384.

L -> I (IN A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      004385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 AA; 41055 MW;
                                                                                                                                                                                               EMBL; X61704; CAA43873.1; -.
                                                                                                                                                                                                                                                                    InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                           Pfam, PF00047; ig; 1.
Pfam; PF00129; MFC I; 1.
ProDom; PD00050; MFC I; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              308
332
332
365
1110
1188
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138
               IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                        MHC I; Transmembrane;
                                                                                                                                                                                                                         PIR; S16767; S16767.
PIR; S16771; S16771.
HSSP; O19673; 1HSB.
MIM; 142800; -.
                                   MICROGLOBULIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129
                                                                         A*3401
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Ekropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Planet P., Jagoueix S., Bove J.M., Garnier M.;
"Detection and characterization of the African Citrus Greening
Liberobacter by amplification, cloning and sequencing of the rplKAJL-
rpoBC operon.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DBPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                       Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M., "Identification and baculovirus expression of the VP4 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB. 1995 (Rel. 31, Created)
1-FEB. 1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RA polymerase beta subunit) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liberibacter africanus (Liberobacter africanum).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae, Candidatus Liberibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                 human group B rotavirus ADRV.",
J. Virol. 67:2730-2738(1993).
-!- SUBCELLULAR LOCATION: Outer capsid.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%; Score 39; DB 1; Length 749; 50.0%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D1223527DEAE0F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93233240; PubMed=8386274;
                                                                                                                                                                                                                                                                                                                                                  EMBL; M91434; AAA47338.1; -.
InterPro; IPR000416; Cap VP4.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 CFTWDMNCANVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     698
749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=Nelspruit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527
568
620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPOB LIBAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
```

ô

Gaps

ő

2; Mismatches

6; Conservative

ð

Best Local Similarity

Matches

749 AA.

VP4 ROTGA STANDARD; F 004916; 01-JUN-1994 (Rel. 29, Created)

RESULT 9 VP4_ROTGA

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Gocage R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Moortman J.R., Palazej R.G., Champe M., Pefeiffer B.D.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Bason A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolbhakov S.,
Borkova D., Botchan M.R., Bouck J., Rokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
A Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera;
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                          -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                       CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCormick A.V., Goldberg M.L.; "Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.5%; Score 38; DB 1; Length 146; 60.0%; Pred. No. 8.1; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00562; RNA pol B; 1.
PROSITE; PS01166; RNA FOL BETA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
NON TER 146 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 39, Created)
(Rel. 39, Last Bequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001572; RNA_pol_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U09675; AAA19557.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWERNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 CVQWSRGARK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09XZL8; 09V391;
30-MAY-2000 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nebula protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLA DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Females
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
NLA DROME
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID DDT TO DDT TO
```

```
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liush E., Kodira C.D., Kraft C., Karvitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
Liak C., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D.,
RA Markulov G., Milahina N.V., Mobarry C., Morris J., Mosherfi A.,
Nelson D.R., Nelson K., Nixon K., Nixohy D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Raine B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
Shier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syiekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Hang Z.-Y., Wassarman D.A., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;
R. The genome sequence of Drosophila melanogaster.";
R. The genome sequence of Drosophila melanogaster.";
R. Science 287:2185-2195-21000.
C. -- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21016721; PubMed=11130714;
MEDLINE=21016721; PubMed=11130714;
Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
Tabata S., Kaneko T., Nakamura T., Hosouchi T., Kawashima K.,
Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
Matanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.5%; Score 38; DB 1; Length 292; 54.5%; Pred. No. 16; 24.5%; Pred. 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AA; 31423 MW; 64FIBBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
17-007-2001 (Rel. 40, Last annotation update)
CYP91A1 OR AT5G36220 OR T30G6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF147700; AAD33987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003712; AAF55285.1; -. FlyBase; FBgn0026629; nla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 FÓWLRSFRLR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 FOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C911 ARATH (
Q9FG65; O65789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C911_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

; 0

```
A Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M., A Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M., A Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P., R. Leonard S., Meyer R., Mullvaney E., Ozersky P., Riley A., Strowmatt C., Ra Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N., Rarnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J., RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M., RA Martienssen R., McCombie W.R., Milson R.K., Murphy G., Bancroft I., RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T., RA Langham S.-A., McCullagh B., Rober J., Gyrmonprez B., Zimmermann W., RA Engerger U., Wedler H., Balke K., Wedler E., Deters S., Hempel S., Van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., Reldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W., Schoof H., Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F., Thaliana ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its modified and profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
TRANSMEM 6 26 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizutani M., Ward E., Ohta D.,
"Cytochrome P450 superfamily in Arabidopsis thaliana: isolation of
cDNAs, differential expression, and RFLP mapping of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.5%; Score 38; DB 1; Length 502; 83.3%; Pred. No. 28; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochromes P450.";
Plant Mol. Biol. 37.39-52(1998).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING 440 440 HEME (BY SIMILARITY).
SEQUENCE 502 AA; 56723 MW; 1A348A8DD76A41BO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
25-Zibosomal protein L28.
RPMB OR TTE1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D78606; BAA28538.1; -.
HSSP; P14779; 1JPZ.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINE=98281573; PubMed=9620263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB026661; BAB09361.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 3-502 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:823-826(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 CFEWER 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CPQWER 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                υ
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RL28 THETN
Q8R9Ū1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
          A START TO DE START TO DESCRIPTION OF START TO DESCRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensesisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINEJELN. N.A.

STRAINEJEL / DSW 2661 / ATCC 43067;

STRAINEJEL / DSW 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Utterback R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Utterback T.K., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Length 62;
Pred. No. 5.1;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE013107; AAM24713.1; -. Ribosomal protein; Complete proteome. SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein MJ1483,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U67589; AAB99498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 QWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 RWKPNIRKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGR; MJ1483; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YE83 METJA
Q58878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
YE83 METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAGE SECOND SECO
```

POTENTIAL

us-09-743-107b-84.rsp

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As compared to cathepsin B, cathepsin I exhibits higher activity towards protein substrates, but has little activity on Z-Arg-NHMec, and no peptidyl-dipeptidase activity.
-!- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87033683; PubMed=3533924; Portroy D.A., Exidexson A.H., Rochan J., Ravetch J.V., Unkeless J.C.; Portroy D.A., Exidexation of a mouse cysteine proteinase."; J. Biol. Chem. 261:14697-14703(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUM-2002 (Rel. 41, Last annotation update)
Cathepsin L precursor (BC 3.4.22.15) (Major excreted protein) (MEP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Joseph L.J., Chang L.C., Stamenkovich D., Sukhatme V.P., "Complete nucleotide and deduced amino acid sequences of human and murine preprocathepsin L. An abundant transcript induced by transformation of fibroblasts."

J. Clin. Invest. 81:1621-1629(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stearns N.A., Dong J., Pan J.X., Brenner D.A., Sahagian G.G., "Comparison of cathepsin L synthesized by normal and transformed cells at the gene, message, protein, and oligosaccharide levels."; Arch. Biochem. Biophys. 283:447-457(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88076849; PubMed=3689328;
Troen B.R., Gal S., Gottesman M.M.,
"Sequence and expression of the cDNA for MEP (major excreted protein), a transformation-regulated secreted cathepsin.";
Biochem. J. 246:731-735 (1987).
                                                           52.1%; Score 37; DB 1; Length 152; 50.0%; Pred. No. 13;
                                                                                                                         3; Indels
152 AA; 17659 MW; 90227132448E8802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND CARBOHYDRATE-LINKAGE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: LYBOSOMAL.
                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91112761; PubMed=2275556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=88213715; PubMed=2835398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
SEQUENCE OF 89-300 FROM N.A.
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                    Local Similarity
nes 5; Conserv
                                                                                                                                                                           2 FOWERNMRKV 11
                                                                                                                                                                                                                                    68 FDWERNINNI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                CATL MOUSE
P06797;
SEQUENCE
                                                        Query Match
                                                                                                                                                                                                                                                                                                                  CATL MOUSE
TO CATL MOUSE
TO D CATL MOUSE
TO D 1-10AN
DT 01-10AN
DT
                                                                                                                Matches
                                                                                       Best
                                                                                                                                                                                                                                 d
                                                                                                                                                                           à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                    InterPro; IPR000668; Peptidase Cl.
InterPro; IPR000169; SHprot_acsite.
Ffam: PR00112, Peptidase Cl; 1.
ProDom; PR00705; Paptidase Cl; 1.
ProDom; PR00118; Peptidase Cl; 1.
PROSITE; PS00139; THIOL PROTEASE CYS; 1.
PROSITE; PS00639; THIOL PROTEASE HS; 1.
PROSITE; PS00640; THIOL PROTEASE ASN; 1.
Hydrolase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 1; Length 334;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                       CATHEPSIN L, HEAVY CHAIN.
CATHEPSIN L, LIGHT CHAIN.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FE6747043307AD98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .).
M -> I (IN REF. 2).
G -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATION PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 21, 2003, 07:27:59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37547 MW;
                                                                                                                  EMBL; X06086; CAA29470.1; --
EMBL; J02583; AAA37445.1; --
EMBL; M20495; AAA39984.1; --
EMBL; X04392; CAA27980.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.1%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                              PIR; S01177; KHMSL.
PIR; S13890; S13890.
                                                                                                                                                                                                                                        MGD; MGI:88564; Ctsl
                                                                                                                                                                                                           1CJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 WEKNIMRMIQ 60
                                                                                                                                                                                                                          MEROPS; C01.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Job time : 5.6 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
 ò
```

```
Q91zd5 mus musculu
Q91z75 mus musculu
Q31215 mus musculu
O19441 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q85487 zea mays (m
Q9hpa3 halobacteri
Q9sx8s arablidopsis
Q19153 caenorhabdi
Q819ul thermoanaer
                                                                                                                                                                                                                         Q9sw68 arabidopsis
O31090 rhizobium 1
Q96m21 homo sapien
Q8r2a4 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                     Q9szt6 arabidopsis
023154 arabidopsis
Q9lhal arabidopsis
Q8s487 zea mays (m
        Q9xhp1 sesamum ind
Q8yp77 anabaena sp
Q9daz8 mus musculu
                                                                                                                                                          Q9krf0 vibrio chol
O92283 molluscum c
Q77855 human immun
                                                                                                                                                                                                                                                                                                                                                                        P96223 mycobacteri
023155 arabidopsis
09szt6 arabidopsis
                                                                                                                                                                                                                                                                                                              Q9zkp4 helicobacte
O44473 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                        Q9c714 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09yqcl human immun
09yqc0 human immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarxhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-MAY-2000 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.7%; Score 63; DB 4; Length 711; 90.9%; Pred. No. 0.0035; 1. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TCD2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         711 AA.
                                                                                                                                                                                                  Q77855
Q9SW68
                                                                                                                                                          Q9KRF0
                                                                                                                                                                                                                                                                                                                                                    Q9C714
P96223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HPA3
Q9SX85
        Q9XHP1
                                                                                                                                                                                                                                                                                     Q8R2A4
                                                                                                                                                                                                                                                                                                         Q9ZKP4
                                                                                                                                                                                                                                                                                                                                                                                                                  91ZS60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9LHA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   088487
                                                                                                                                                                                                                                                               Q96M21
                                                                                                                                                                                                                                                                                                                                044473
      15
                                                                                                                                                                                                                                                                              8887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 CFQWQRNMRKV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactotransferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSUE=PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8TCD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
71108

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100

7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              023230 arrabidopsis
Q9n906 trypanosoma
Q77856 human immun
Q9G910 human immun
Q9G6n2 arrabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Odxse2 ralstonia s
O9xfd5 oryza sativ
O8tax2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8tcd2 homo sapien
Q9ucy5 homo sapien
Q9tr80 ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O81653 hemerocalli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8z462 salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ognus2 homo sapien
Ogsrz guillardia
Og3780 caenorhabdi
                                                                                                                             2003, 07:25:55 ; Search time 20.8 Seconds (without alignments) 118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                           , 671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UCY5
Q9TR80
Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XFD5
Q8TAX2
                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q93780
O81653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8XSE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8TCD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bp_rvirus:*
Bp_bacteriap:*
Sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                          1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                  US-09-743-107B-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
110
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
10
10
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bp plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPIREMBL 21:*
                                                                                                                               February 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500.6
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
500.0
                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
```

Database :

Searched:

Sequence:

Run on:

·:

Result

~

ö

Gaps

.. 0

```
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                       "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                               62.0%; Score 44; DB 16; Length 511; 58.3%; Pred. No. 7.5; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                   EMBL, ALC27276, CAD06049.1, -.
Hypothetical protein, Complete proteome.
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative ICC protein homolog.
ICC OR RSP0534 OR RS00414.
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||: | :
244 CFQWEKGTRTAK 255
                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia.
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8XSE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XFD5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9XFD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8XSE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XFD5
                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC CONTRACTOR SOLUTION OF SOLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                              Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                    ٥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                      Length 38;
                                                                                                                                                                                                                                                                                                                 Score 59; DB 4; Length 38;
Pred. No. 0.00085;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.6%; Score 48; DB 6; Length 33; 54.5%; Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                   InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Blophys. Acta 1243:25-32(1995).
HSSP; 077699; 1CE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                       seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; IBKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                  SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                 83.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                    2 FOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                               21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella.
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9TR80
                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09TR80
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Salanoubat M., Genin S., Arriguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                              Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.6%; Score 43; DB 16; Length 279; 50.0%; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31541 MW; ABB38818004B2EDA CRC64;
                  QBXSE2;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                             Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 415:497-502(2002).

EMBL; AL646079; CAD17685.1; -
InterPro; IPR004844; M-restrase.

InterPro; IPR004844; S/T phosphtse.
Pfam; PF00149; Metallophos; I.
Plasmid; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                         STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytochrome P450 (Fragment).
```

ო

```
TISSUE=PLACENTA,

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isolai T., Ota T., Hayashi K., Shiratori A., Sudo H.,

Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Wamamoto J., Wakamatau A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.,

Ninomiya K., Iwayanagi T.,

Ninomiya K., Iwayanagi T.,

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                 59.2%; Score 42; DB 4; Length 466; 66.7%; Pred. No. 16; cive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                 PROSITE; PS00499; C2 DOMAIN 1; UNKNOWN 1.
PROSITE; PS50004; C2 DOMAIN 2; 1.
PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
SEQUENCE 466 AA; 53192 MM; E4113A5062F58D6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000243; Proteasome B. InterPro; IPR001353; Protsme protease.
                                                                                                                                                                                                          EMBL, AKO02037; BAA92048.1; -... HSSP; P21707; 1BYN.
InterPro; IPR000008; C2.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP00168; C3; 1.
PRINTS; PR00360; C2DOMAIN.
SWART; SM00239; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guillardia theta (Cryptomonas phi).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF165818; AAK39885.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00227; proteasome; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00141; PROTEASOME.
                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||| :|
269 CFQWESTLR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 CFFWERNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWERNM 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWERNMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleomorph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteasome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q98RR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q98RR2
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     098RR2
              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                              Gaps
Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                     Liu J., Yang J.;

Liu J., Yang J.;

"Suppression subtractive hybridization (SSH) identified candidate genes that are differentially expressed at rice young panicle.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL, AR140486; AAD29659.1;

InterPro; IPRO01128; Cytochrome_P450.

Pfam; PF00067; p450;

PRO0385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TJ-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ1175 fis, clone PLACE1007375, weakly similar to phorbol
ester/diacylglycerol-binding protein UNC-13.
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                       59.2%; Score 42; DB 10; Length 105; 70.0%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.2%; Score 42; DB 4; Length 306; 66.7%; Pred. No. 10; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Submitted (MAR-2002) to the BMBL/GenBank/DDBJ databases.
BMBL; BCO25708; AAH25708.1; -..
Hypotherical protein.
SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
                                                                                                                                                                                                                                                                                                      SEQUENCE 105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TAX2;
01-UNN-2002 (TrEMBLrel. 21, Created)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annoration update)
Similar to hypothetical protein FLJ11175.
                                                                                                                                                                                                                                                 PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1. Heme; Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 AA.
                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                          SEQUENCE FROM N.A.
TISSUE=PANICLE;
                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWERNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                               61 CFOWERLGKK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 CFOWESTLR 277
                                                               NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWERNMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NUS2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8TAX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9NUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
Q9NUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8TAX2
   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC DIT DIT DIT DIT DIT DIT DIT DIE DIE OCC OCC OCC
```

ö

; 0

```
..
0
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21223349; PubMed=11323671;
MEDLINE=21223349; PubMed=11323671;
Publine=21223349; PubMed=11323671;
Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an enslaved algal nucleus.";
Nature 410:1091-1096(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.7%; Score 41; DB 8; Length 205; Best Local Similarity 75.0%; Pred. No. 10; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AA; 22691 MW; D30F5289CBC85049 CRC64;
                                                                                                                                                                                                                     Bukaryota; Cryptophyta; Cryptomonadaceae; Guillardia
NCBI_TaxID=55529;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
26S proteasome SU BS.
```

4

275 AA

PRELIMINARY;

```
STRAIN=TREU927;
                                                           01-JAN-1998
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHR1.67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .906N60
                                       023230
                                                                                                                                                                                                                                                                                                                                                                                                                                             906N6Ö
                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                             023230
                                                                                                                                                                                                                                                                                                                                                                                                                                    906N60
                                        ò
                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. STELLA D'ORO; TISSUE-SENESCING PETALS;
MEDLINE-99339248; PubMed=10412903;
Panavas T., Pikula A., Reid P.D., Rubinstein B., Walker E.L.;
Panavas T., Pikula A., Reid P.D., Rubinstein B., Walker E.L.;
Plant Mol. Biol. 40:237-248(1999).
-1-SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
BMBL; AR082028; AR034853.1; -.
InterPro; IPR001128; Cytochrome_P450.
PRINTS; PR00385; P450.
PROSITE; PR00386; CYTOCHROME P450; UNKNOWN_1.
Heme: Monocoxygenase; Cytochrome_P450.
NON_TER
                                                                                     Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hemerocallis hybrid cultivar.
Skaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales,
Hemerocallidaceae, Hemerocallis.
                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                          "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
EMBL; Z81089; CAR03137.1; -. SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                              57.7%; Score 41; DB 5; Length 275; 63.6%; Pred. No. 14; 2; Indels ative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 71.4%; Score 41; DB 10; Length 372; Similarity 71.4%; Pred. No. 19; 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                              Dobson R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 372 AA; 41909 MW; 55FB3EAF9699595E CRC64;
                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Senescence-associated protein 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                        372 AA
                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
       093786;
01-FEB-1997 (TrEMBLrel. 02, Cr
01-AUG-1998 (TrEMBLrel. 07, La
01-DEC-2001 (TrEMBLrel. 19, La
F53H4.4 protein.
                                                                                                                                                                                                                                                                                        Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                     |||::||| |
262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                         2 FOWERNMRKVR 12
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                            NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=80862;
                                                                                                                                             Dobson R
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  081653;
                                                                                                                                                                                                                                                                                                                                                                                                     081653
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
081653
à
```

```
.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                  01-MAY-1999 (TEMBELEI. 10, Last sequence update)
01-JUN-2010 (TEMBELEI. 17, Last annotation update)
Trichohyalin like protein.
C7A10.840 OR AT4G36520.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Schueller C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hall N., Bowman, S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S., Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D., Gerrard C., Rajandream M.A., Barrell B.G.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. Brbil., ALSSY82, CAB95377.1; -- EMBL/GenBank/DDBJ databases. InterPro: IPR002035; VWF.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.7%; Score 41; DB 10; Length 1432; 54.5%; Pred. No. 79; 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.7%; Score 41; DB 5; Length 2186; 71.4%; Pred. No. 1.2e+02; rative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 299708; CABL6841.1; -
EMBL; ALL61S89; CABR0318.1; -
SEQUENCE 1432 AA; 163973 MW; 96CE6FECB9BF0538 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2186 AA; 245737 MW; 78BB75505012005A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  PRT; 1432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 2186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conserved hypothetical protein CHR1.67
                                                       Created)
                                              (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50234; VWFA; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.5
Matches 6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 YDWEQNARKLR 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Irypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       588 CYEWERN 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWERN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

RESULT 14

ö

Gaps

ó

0; Indels

Matches

us-09-743-107b-84.rspt

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                          MEDLINE=95191002; PubMed=7884875; Mulder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J., Soherpbirer H.J., de Perre P., Boer K., Goudsmit J.; Scherpbirer H.J., de Perre P., Boer K., Goudsmit J.; Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is unrelated to time of HIV-1 RNA positivity in the child."; DMBL; 247869; CAA87882.1; -... InterPro; IPR000777; GP120.

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120; 1.

AIDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  56.3%; Score 40; DB 15; Length 91; 60.0%; Pred. No. 6.5; ative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  91 AA; 10519 MW; EB20C63A22DA1288 CRC64;
                                           01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 01-DEC-2001 (TremBlrel).
                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                    91 AA.
                    PRT;
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 QWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 QWDRTLOKVR 76
                                                                                                                                                                                                                                                                                                                                                                   NON TER
NON TER
SEQUENCE
            977856
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
977856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9Q9L0
               ð
```

ô

Gaps

0

56.3%; Score 40; DB 15; Length 115; 60.0%; Pred. No. 8.3; Live 3; Mismatches 1; Indels

Best Local Similarity 60.0 Matches 6; Conservative

|||::|:| 61 QWEKTLRQVR 70 3 OWERNMRKVR 12

à

115 AA; 12832 MW; 86E509D6F6978127 CRC64;

SEQUENCE Query Match

NON TER NON TER

Tanuri A., Machado E., Caride E., Costa L.J., Telles J.G.,
"Primary infections with HIV-1 of women and their offspring in Rio de
Janeiro, Brazil: Finding of recombinant of HIV-1 subtypes B and F.";
Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI53457; AAFI6896.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120;
AMDS; Coat protein; Glycoprotein.

Q9Q9L0; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Envelope glycoprotein (Fragment).

115 AA.

PRT;

PRELIMINARY;

0909L0

Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;

SEQUENCE FROM N.A.

STRAIN=VTRJ07;

ACCOORDING TO BE ACCOORDING THE ACCOORDING THE ACCOORDING THE ACCOORDING THE ACCOORDING THE ACCOORDING THE ACCOUNTY ACCO

Search completed: February 21, 2003, 07:44:38 Job time : 21.8 secs

Peptide for anti-u Human lactoferrin Human lactoferrin

Human lactoferrin

Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
Advanced glycosyla
Human lactoferrin
Advanced glycosyla
Human lactoferrin
Advanced glycosyla
Lactoferrin
Anti microbial pep
Lactoferrin-relate
Lactoferrin derive
Lactoferrin derive

Anti-parasitic lac Anti-parasitic lac Peptide for anti-u

Lactoferrin derive Lactoferrin derive Bovine lactoferrin Bovine lactoferrin Lactoferrin-derive Lactoferrin-derive Anti-parasitic pep Thrombus formation

Lactoferrin deriva

Lactoferrin-derive Lactoferrin derive

Lactoferrin-derive

us-09-743-107b-85.rag

OM protein

Run on:

Sequence:

```
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                   Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:85.
                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                         AAR98553
AAR91852
                                                                                                                                                                         AAW26150
AAW14036
                                                                              AAY78032
AAR21810
         AAY78035
AAY78062
AAY78063
AAY78031
                              AAY78064
AAY78065
                                        AAY78034
AAY78066
AAY78067
                                                                                                    AAR48531
AAR57461
                                                                                                                                                   AAW03045
                                                                                                                                                                    AAR87622
                                                                                                              AAR57462
                                                                                                                   AAR84698
                                                                                                                         AAR84699
                                                                                                                              AAR80263
                                                                                                                                                         AAR90607
                                                                                          AAR44841
                                                                    AAY78033
                                                                         AAY68867
                                                                                                                                                                                                                               AAY78085 standard; Peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                    221
221
113
114
115
116
117
117
117
118
118
118
                                                                                                                                                                                                                                                    25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
WPI; 2000-147388/13.
WO200001730-A1.
                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                           06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                      06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                13-JAN-2000
                                                                                                                                                                                                                                                                                                           Synthetic.
AAY78085;
                                                                                                                                                                                                                      RESULT 1
                                                                                                                                                                                                                           AAY78085
 Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                  lactoferrin
                                                                                                                                                                                                                                                                                                                                                                        lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                  Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                  Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                       lactoferrin
                                                                                                                                                                                                                                                                                                                                                             lactoferrin
                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                               (without alignments)
56,502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                       Description
                                     February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
                                                                                                                                                                                                                                                                                                                                                             Human
Human
                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                        Human
      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                  908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                             AAY78038
AAY78046
AAY78047
                                                                                                                                                                                                                                                                                                                                                                             AAY78037
AAY78048
AAY78049
AAY78036
AAY78036
                                                                                                                                                                                                                                                                                                                                                  AAY78085
AAY78081
                                                                                                                                                  Listing first 45 summaries
                            protein search, using sw model
                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                       Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                             A_Geneseq_101002:*
                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                   US-09-743-107B-85
71
                                                                       1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                   Query
                                                                                                                                                                                                                                                                                                                                                        100.0
                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                    711
65
66
66
66
66
66
66
                                                                   Perfect score:
                                                                                  Scoring table:
```

Database:

Result No.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food Claim 22; Page 36; 102pp; English. (ASCI-) A+ SCI INVEST AB. WPI; 2000-147388/13 Hanson LA, Query Match Matches Ношо AAY78081 RESULT à 엄

AAY78001 to AAY78100 represent peptides having sequences based on human

Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

```
;
                                                                                                                                                                                lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                            AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-incobial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 71; DB 21; Length 12; 100.0%; Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78081 standard; Peptide; 12 AA.
                                                                                                     Claim 22; Page 36; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     est Local Similarity 100 atches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWOENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the creditic lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                          Length 12;
                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                          94.4%; Score 67; DB 21;
91.7%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78038 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 70; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0004614,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                           Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWOKNMRKVR 12
                                                                                                                                                                                                                                                                             12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78038;
                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8×3999999999999
                                                                                                                                                                                                                                                                                                                                                                                      ò
```

Tue Dec

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78001 to AAY78100 represent peptides having sequences based on human
             Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                         Gaps
 fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                    Length 12;
                                                                                                                                                                Score 66; DB 21; Lengtu ....
Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                           AAY78046 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 35; 102pp; English.
                                                                                                                                                                                  93.0%;
Local Similarity 91.7%;
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                          1 CFOWDENMRKVR 12
                                                                                                                                                                                                                                                                                              1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13.
                                                                                                                                               12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78046;
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                          AAX78046
                                                                                                                                                                                                                                                                                                                                                                                                               88888888888
                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                           d
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin. The periodes are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections or fragment can be used for treating and/or prevention of infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food suffes such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                      Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                          Score 66; DB 21; Length 12;
Pred. No. 0.00016;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.0%; Score 66; DB 21; Length 12; 91.7%; Pred. No. 0.00016; Artive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dolphin GT;
                                                                                                                                                                                                                                                                                                                          Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baltzer L,
                                                                                                                                                                                                                           AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 73; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I,
                                             93.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                         bactericidal; preservative.
                                                                                                                                                                                                                                                                                          (first entry)
                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASCI-) A+ SCI INVEST AB.
                                                                                                            1 CFOWOENMRKVR 12
                                                                                                                                         1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 11; Conserv
                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AA;
               12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                          25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                          AAY78047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                               Query Match
                                                                            Matches
                                                                                                                                                                                                        AAY78047
ID AAY7
                                                                                                                                                                                           RESULT
XX SS
                                                                                                                                                                                                                                          ð
                                                                                                                                         셤
```

AAY78048 standard; Peptide; 13 AA.

(first entry)

25-APR-2000

AAY78048;

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an infant and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                           Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.0%; Score 66; DB 21; Length 13; 91.7%; Pred. No. 0.00018; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 70; 102pp; English.
                                                                                                                          AAY78037 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0004614.
                                                                                                                                                                                                                                                                                                                                        bactericidal; preservative.
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB.
1 CFQWQENMRKVR 12
                                 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-1998;
                                                                                                                                                                                                      25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                  AAY78037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                 Н
                                                                                                        ò
```

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or provention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 93.0%; Score 66; DB 21; Length 13; Local Similarity 91.7%; Pred. No. 0.00018; les 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:49.
                                                                                                Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78049 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
                                                                                                                                                                                                                                                                                                                                    99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWQENMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 AA;
                                                                                                                                                                                                                                                                 WO200001730-A1.
                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000
                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78049
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   田林なななは
```

. 0

Gaps ·,

Best Local Similarity 91.7 Matches 11; Conservative

g 8

RESULT 7

99WO-SE01230

06-JUL-1999;

13-JAN-2000

WO200001730-A1

Synthetic.

98SE-0002562 98SE-0004614

17-JUL-1998; 29-DEC-1998; (ASCI-) A+ SCI INVEST AB.

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human jactoferrin have been shown to have desired
                Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; uninary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                 Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 74; 102pp; English
                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                    98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                      98SE-0002441.
                                                                                                                                                                                                        99WO-SE01230.
                                                                                                                                                                                                                                                                                                  (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                                                                       WO200001730-A1
                                                                                              Homo sapiens,
                                                                                                                                                                                                       06-JUL-1999;
                                                                                                                                                                                                                                                   17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                    06-JUL-1998;
                                                                                                                                                                         13-JAN-2000
                                                                                                          Synthetic.
```

```
anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                            Score 66; DB 21; Length 13;
Pred. No. 0.00018;
0; Mismatches 1; Indels
                                                                                                                                                                                                      93.0%;
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                           13 AA;
                                                                                                                                                             Sequence
```

11; Conservative 1 CFQWQENMRKVR 12 2 CPÓWORNMRKVR 13 Query Match Matches ð

ö

Human lactoferrin derived peptide SEQ ID NO:36. AAY78036 standard; Peptide; 14 AA. (first entry) 25-APR-2000 AAY78036; AAY78036 

Homo sapiens

99WO-SE01230. bactericidal; preservative. WO200001730-A1. 06-JUL-1999; Homo sapiens 13-JAN-2000. Synthetic. Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such wann lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections,
                                                                                                                                                                                                                                                                                                              inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.0%; Score 66; DB 21; Length 14; 91.7%; Pred. No. 0.00019; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                  Dolphin GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:50.
                                                                                                                                                                                                                                Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78050 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFOWORNMRKVR 14
                                                                                                                                                                                                                                                              WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 AA;
                                                                                                                                                                                                                                Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
```

Dolphin GT;

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as webrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
                                                                                                                                                                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66; DB 21; Length 14;
Pred. No. 0.00019;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                         Baltzer L,
                                                                                                                                                                                                           Claim 15; Page 75; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                      Mattsby-Baltzer I,
              98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-APR-2000 (first entry)
                                                                          (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CFOWORNMRKVR 14
                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200001730-A1.
                 06-JUL-1998;
                                            29-DEC-1998;
                               17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000
                                                                                                       Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
ਨੋ
```

Gaps . 0

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also the infood stuffs such as infant formula food. The peptides are also though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower costs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The agent is low oln.. It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR98531-54 are peptides used in an anti-ulcer agent. The acin toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                                                                                                                                                                                                                                                                                                                                                        93.0%; Score 66; DB 21; Length 14; 91.7%; Pred. No. 0.00019; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-ulcer agent; low toxicity; stable; heat-resistant.
   Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - has low toxicity, is
Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                            Claim 18; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MORG ) MORINAGA MILK IND CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-ulcer agent contg. peptide -
heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 11; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CFOWORNMRKVR 14
                                 WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-318857/32.
                                                                                                                                                                                                                                                                                                                                                                                                             14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP08143468-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98554;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR98554
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

ö

AAY78062 standard; Peptide; 15 AA.

RESULT 14

ó

AAY78062

25-APR-2000 (first entry)

AAY78062;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane) infections, colitis, and Candida infection on a mucosal membrane) inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                 Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Even though native human lactoferrin have been shown to have desired
                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
Score 66; DB 17; Length 15;
Pred. No. 0.0002;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66, DB 21; Length 15;
Pred. No. 0.0002;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dolphin GT;
                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer L,
                                                                                                                                                                         AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.0%;
93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0002562.
                                                                                                                                                                                                                                       (first entry)
                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                             1 CFOWDENMRKVR 12
                                                                                           2 CFOWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-1998;
                                                                                                                                                                                                                                       25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-2000,
                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                       AAY78035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                            Matches
                                                                                                                                                          AAY78035
```

12

CFOWQENMRKVR

4 CPOWORNMRKVR 15

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                Human, lactoferrin, modification, infection, inflammation, tumour,
food, infant formula, anti-inflammatory, anti-microbial, anti-tumour,
urinary tract infection; colitis, Candida infection, fungicidal,
bactericidal, preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.0%; Score 66; DB 21; Length 15; 91.7%; Pred. No. 0.0002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baltzer L, Dolphin GT;
                                                                                                  Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78063 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                            98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                                                                                                                                                      WO200001730-A1.
                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1998;
                                                                                                                                                                                                                                                                                                        13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanson LA,
                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78063
ID AAY
XX
AC AAY
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

ω

us-09-743-107b-85.rag

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bacterial and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                         Human, lactoferrin, modification, infection, inflammation, tumour;
food, infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                        Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
                    25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
                                                                                                                                                                                                                                                    WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                         13-JAN-2000.
                                                                                                                                                                                                            Synthetic.
```

Gaps :0 93.0%; Score 66; DB 21; Length 15; 91.7%; Pred. No. 0.0002; Live 0; Mismatches 1; Indels 0; Mismatches 11; Conservative Best Local Similarity Query Match Matches

. 0

1 CFOWQENMRKVR 12

Search completed: February 21, 2003, 07:37:15 Job time : 28.35 secs

4 CFOWORNMRKVR 15 Ωp ò

Sequence

Sequence

Sequence

Appli Appli

Sequence

Sequence

Sequence

Sequence

Sequence Sequence Sequence Sequence

Scoring table:

Searched:

Database :

Result Š.

Perfect score:

Sequence:

Sequence

Sequence

```
Sequence 3, Application US/08204487

Sequence 3, Application US/08204487

Batent No. 5565425

GENERAL INFORMATION:
APPLICANT: NAKASHINA, HIDEKI
APPLICANT: NAKASHINA, HIDEKI
APPLICANT: TANAKA, SHIGHAI
APPLICANT: TANAKA, SHIGHAI
APPLICANT: TONAKA, TOSHILIR
APPLICANT: TONAKA, TOSHILIR
APPLICANT: TONAKA, TOSHILIR
APPLICANT: TANAKA, TOSHILIR
APPLICANT: WAWSAKI, YOSHILIR
APPLICANT: THEBRAIL
APPLICANT: THE OF INVENTION: INHIBITORS
ANDRESSEE: ADDRESS:
ADDRESSEE: THIBBAULT
ADDRESSEE: THIBBAULT
ADDRESSEE: THIBBAULT
ADDRESSEE: THIBBAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/NG-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILICATION NUMBER: US/08/204,487
FILING DATE: 0.2-MAR.1994
CLASSIFICATION: 514
US-08-464-182A-2
US-08-406-271-2
US-08-421-632-2
US-09-421-632-2
US-09-932-190-2
US-08-154-019-4
US-08-154-019-4
US-08-164-113-33-4
US-08-164-167-4
US-08-175-4
US-08-175-681-2
US-08-175-681-2
US-08-175-681-2
US-08-175-681-2
US-08-175-681-2
US-08-175-681-2
US-08-175-681-2
US-08-175-101-2
                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
    TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 53
CITY: BOST
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
    Sequence 8, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 24, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Appli
, Appli
, Appli
, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Appl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                 February 21, 2003, 07:25:59; Search time 8.65 Seconds (without alignments) 40.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Sequence 29, Sequence 6, As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3,
Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
               GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.*
                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-891-174-3
US-08-204-487-1
US-08-256-771-25
US-08-381-984-24
US-08-381-984-25
US-08-381-984-25
US-09-508-734-4
US-09-508-734-6
US-09-508-734-6
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-891-174-10
US-08-204-487-7
US-09-508-734-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-07-755-161A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-464-182A-5
US-08-406-271-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -08-464-182A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -08-693-274A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-07-891-174-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-204-487-3
                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
                                                                                                                                                            US-09-743-107B-85
71
1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                             Copyright
```

```
; ANTI-SENSE: NO
; FRAGMENT TYPE:
US-08-628-380-8
                                                                                                                                                                                                                                                                                                                        07601
                                                  US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                       ò
                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
                                                    Length 18;
                                                  Query Match 93.0%; Score 66; DB 1; Length 18; Best Local Similarity 91.7%; Pred. No. 5.4e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.0%; Score 66; DB 2; I 91.7%; Pred. No. 5.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 436
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PUBLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON EBG., DAVIA A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SIGNATION:
TELECOMMUNICATION SIGNATION:
TELEFAN: 201 343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Packensack Avenue
Hackensack
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                  Klauber & Jackson
OTHER INFORMATION: (20-37)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE: internal US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWDENMRKVR 12
                                                                                                                           1 CFOWQENMRKVR 12
                                                                                                                                                           1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                               RESULT 2
US-08-485-948-8
     ;
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                             ð
```

1 CFOWORNMRKVR 12

```
UNS-01-628-300-8
| Partent No. 5893-181
| Partent No. 5893-181
| Partent No. 5893-181
| CARREAL INCOMPTION MINISTER NO. 5893-181
| CARREAL INCOMPTION AND MINISTER NO. 5893-181
| CARRESTONDING AND MINISTER NO. 5993-181
| COURTER NO. 5993-181
| COURTEN NO. 5993-181
| COURTER N
```

```
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAPLOTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.0%; Score 66; DB 2; Length 18; Best Local Similarity 91.7%; Pred. No. 5.4e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                       ZIP: 07601

ZIP: 07601

MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Jackson E89., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 489-5800
TELEFERAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995,
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3. Application US/07755161A Patent No. 5304633 GENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFÓWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.C.
U.S.A.
                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20005
                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
```

```
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" AUTHORS. AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
SUFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOCUMENT NUMBER:
FILING DATE:
PRILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: modified site
LOCATION: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
ANTI-SENSE:
```

93.0%; Score 66; DB 1; Length 20;

```
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: (Note= "thiol group of
OTHER INFORMATION: (Operation 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08204487

Sequence 1, Application US/08204487

Septembrain Sefsas

General Information;
Applicant: Yamamoro, Naoki
Applicant: Nakashira, Hideki
Applicant: Tanaka, Shigeaki
Applicant: Danaka, Shigeaki
Applicant: Danaka, Shigeaki
Applicant: Canari Costiaki
Title Of Invention: Viral Infection and Proliferation
Title Of Invention: Unibilities

NUMBER OF SEQUENCES: 8

NUMBER OF SEQUENCES: 8

SARREPONDENCE ADDRESS:
Annear Annear Annear Infection
Annear Annear Annear Annear Infection
Annear Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66, DB 1; Length 20;
Pred. No. 6e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
RESPERNCE DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWDENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 53
CITY: BOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME:
                                                ö
                                                Gaps
                                                ö
                                                1; Indels
                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ATTILE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
                   91.7%; Pred. No. 6e-05;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: 10
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-371-8856
                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
CHROMOSOME/SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                 1 CFQWQENMRKVR 12
                                                                                                                                                                            2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C. COUNTRY: U.S.A.
                      Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE
                                                                                                                                                                                                                                                                           RESULT 6
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNITS
```

NAME/KEY: modified site

ö

; 0

```
93.0%; Score 66; DB 1; Length 20; 91.7%; Pred. No. 6e-05;
                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                    1 CFQWQENMRKVR 12
                                                                                                                                                      2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWDENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CFOWORNMRKVR 13
                                         Query Match
Best Local Similarity
                                                                                                                                                                                                               RESULT 9
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
     US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                        93.0%; Score 66; DB 1; Length 20; 91.7%; Pred. No. 6e-05;
                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                           ) LUCATION: 1..20

) OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE

) OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"

US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/256,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/
                                                             20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 amino acids
                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                       NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                 1 CFOWOENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                   2 CPÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                   à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Sequence 25, Application US/08256771
Patent No. 565591
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "Cys residues are protected to OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
93.0%; Score 66; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IRW Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                         STREET: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 STAY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: Ully 22, 1994
CLASSIFICATION: 514
```

```
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
FILE REPERENCE: PA/SYG/OND.
FILE REPERENCE: PA/SYG/OND.
CURRENT APPLICATION NUMBER: PCI/KR99/00373
FRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
INDRIFFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.0%; Score 66; DB 1; Length 20; 91.7%; Pred. No. 6e-05; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IDM Compatible
COMPUTER: IDM COMPATIBLE
OFFICE SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-508-734-4; Sequence 4, Application US/09508734; Patent No. 6423509
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                               XY: U.S.A.
20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 1; Length 20;
Pred. No. 6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: APril 11, 1995
  Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-381-984-25

Sequence 25, Application US/08381984

Patent No. 5804555

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

IITLE OF INVENTION: ANTIOXIDANT

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 252
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CFÓWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQENMRKVR 12
                                                                                                                                                                                        STREET: 805 Fifte CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

ö

```
LOCATION: 21

IDENTIFICATION METHOD:
CHER INFORMATION: (ye residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 93.0%; Score 66; DB 1; Length 25; Il Similarity 91.7%; Pred. No. 7.5e-05; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN N. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: AMINO ACID STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified site
                                                                                                                                      TELEPHONE: 202-371-885
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 4
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME/SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWOENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CFÓWÓRNMRKVR 15
                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                               TOPOLOGY: li
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-755-161A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: usesful microorganism thereof
TITLE OF INVENTION: usesful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT PAPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 6
LENGTH: 24
                                                                                                                                                             ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.0%; Score 66; DB 4; Length 24; Best Local Similarity 91.7%; Pred. No. 7.2e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                             Query Match

93.0%; Score 66; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Was-07-75-161A-10

Sequence 10, Application US/07755161A

Sequence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Diskland:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09508734 Patent No. 6423509
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; CAGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Wenderc
STREET: 805 Fiftee
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                 1 CFOWDENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWQENMRKVR 12
                                                                                                                                                                                                                                          2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-508-734-6
                                                                    US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                 ð
```

; 0

```
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21
                                                          GENERAL INFORMATION:
APPLICANT: Mamoru TONITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fitteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 05-5EP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek JT.
REGISTRATION NUMBER: 33,367
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITS:
```

```
DEBUTIFICATION METHOD:

COTHER INFORMATION:

COTHER
```

```
February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PUB.WB _Dub.pep:*

3: \cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: \cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

5: \cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: \cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

7: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

7: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

8: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

9: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

10: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

11: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

12: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156504 segs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                             US-09-743-107B-85
71
                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 30, Appl Sequence 37353, A Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 28, Appl Sequence 31, Appl Sequence 2, Appli Sequence 6, Appli Sequence 3, Appli Sequence 23, Appli , Appli , Appli Sequence 7, Appli Sequence 4, Appli Sequence 22, Appl Sequence 2, Appli Sequence 8, Appli Sequence 29, Appl Sequence 20, Description US-10-066-500-58 US-10-066-500-58 US-10-002-796-58 US-10-066-273-58 US-10-066-494-58 US-09-976-165-28 US-09-976-165-31 US-10-023-096-2 US-09-798-869-6 US-09-798-869-3 US-09-798-869-23 US-09-798-869-7 US-09-798-869-7 US-09-798-869-20 US-09-798-869-20 US-09-798-869-22 US-09-798-869-8 US-09-798-869-29 US-09-798-869-30 SUMMARIES Query Match Length DB Score Result 

Sequence 12, Appl Sequence 10, Appl Sequence 5, Appli Sequence 244, App Sequence 11, Appl Sequence 11, Appl Sequence 1229, A Sequence 1329, A Sequence 43, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 26, Appli Sequence 10, Appl Sequence 10, Appl Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 26, Appli Sequence 27, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli	Sequence 16, Appl Sequence 46393, A
10 US-09-995-542-12 10 US-09-995-542-10 10 US-09-995-542-10 10 US-09-986-5-5-14 10 US-09-205-658-24 11 US-09-986-301-11 11 US-09-995-301-11 11 US-09-995-301-11 10 US-09-995-301-11 10 US-09-915-24-12129 10 US-09-915-242-12129 10 US-09-915-242-13026 10 US-09-773-6-5-59 10 US-09-773-6-5-59 10 US-09-798-869-26 10 US-09-798-869-10 10 US-09-798-869-20 10 US-09-798-869-20	10 US-09-917-340-16 10 US-09-864-761-46393
22233333333333333333333333333333333333	40
CO	
м м попичина попичина попичин	3 3 3
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	4 4 5 5

## ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.0%; Score 66; DB 9; Length 15; 91.7%; Pred. No. 6.5e-05; ive 0; Mismatches 1; Indels
       SQUENCE 2, Application US/09798869

Publication No. US20030022821A1

GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVETNBAL
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A3404-PCT-USA-A
FILE REFERENCE: A3404-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: C10/2027
PRIOR APPLICATION NUMBER: C7/GB99/02851
PRIOR APPLICATION NUMBER: C17/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JOHN SIGNED SVENDSEN APPLICANT: (YSTEIN REKDAL APPLICANT: BALDUR SVEINBJ (RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 11, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-798-869-20
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

ö

```
Query Match 93.0
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: CAPRINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-6
                                                                                                                                                                                                          JS-09-198-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
CORRESPONDENCE: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   93.0%; Score 66; DB 9; Length 25; 91.7%; Pred. No. 0.00011; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A.
APPLICANT: LARS VORLAND
FILE REPERENCE: A34049-PCT-USA-A
FILE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
FRIOR APPLICATION NUMBER: CTT/GB99/02851
FRIOR APPLICATION NUMBER: GB9818938.4
FRIOR FILING DATE: 1999-08-28
FRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
CRANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10505/P58185C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-WAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/023,096 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10023096; Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REPERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CFOWORNWRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
·.
                                                  0
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
Score 66; DB 9; Length 694;
Pred. No. 0.0028;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.0%; Score 49; DB 9; Length 15; 63.6%; Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.7%; Score 63; DB 9; Length 15; ilarity 91.7%; Pred. No. 0.0002; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-7/98-809-3

US-09-7/98-809-3

Publication No. US20030022821A1

GERREAL INFORMATION:
APPLICANT: UOHN SIGUED SVENDSEN
APPLICANT: HALDUR SVEINBLEN
APPLICANT: BALDUR SVEINBLEN
APPLICANT: BALDUR SVEINBLEN
APPLICANT: BALDUR SVEINBLEN
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
RIOR APPLICATION NUMBER: CGT/GB99/02851
PRIOR FILING DATE: 1990-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 3

SEQ ID NO 3
                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                             APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: HALDUR SYBINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCES: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                           Sequence 6, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
  93.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWDENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CFOWOWNMRKVR 14
                                                                                                       1 CFOWDENMRKVR 12
                                                                                                                                                    22 CFÓWORNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
```

```
Query Match 63.4
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWDENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CLRWONEMRKV 13
1 CFOWDENMRKV 11
                       3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: MURINE
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: MURINE
US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-22
                                                                                                        RESULT 8
US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                  q
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: synthetic peptide (modified form of homo sapiens; OTHER INFORMATION: sequence)
US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 64.8%; Score 46; DB 9; Length 15; Best Local Similarity 63.6%; Pred. No. 0.11; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.0%; Score 49; DB 9; Length 25; 63.6%; Pred. No. 0.062; 2; Indels tive 2; Mismatches 2; Indels
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09798869;
Publication No. US20030022821A1;
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GE9918938.4
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-3
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELED for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                             WESULY 6

US-09-798-869-23

Sequence 23, Application US/0979869

Publication No. US20030022821A1

GENERAL INFORMATION:

APPLICANT: JOHN SIGUED SVENDSEN

APPLICANT: HALDUR SVEINBI (RNSON

APPLICANT: HARS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: PCT/GB99/02851

PRIOR APPLICATION NUMBER: CTG/GB99/02851

PRIOR APPLICATION NUMBER: GB9818938.4

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 25
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 63.6
Matches 7; Conservative
7; Conservative
                                         1 CFOWDENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CYÓWÓRRMRKL 13
                                                                                   3 CYÓWÓRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Matches
```

0;

Gaps

o O

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.4%; Score 45; DB 9; Length 15; 63.6%; Pred. No. 0.17; 1ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.4%; Score 45; DB 9;
63.6%; Pred. No. 0.27;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOS-09-79-80-80-22, Application US/09798869

Publication No. US20030022821A1

GENERAL INFORMATION:
APPLICANT: OCHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REWDAL
APPLICANT: HALDUR SVEINBJ (RNSON)
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPREBACE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FARENCE Mindows Version 4.0
                                                                         APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: HALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCE: A34049-PCT-USA-A
CURRENT PELICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1009-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRABESEQ FOR WINGOWS VERSION 4.0
Sequence 4, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.2%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.51; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 9; Length 15;
Pred. No. 0.51;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOS-09-798-869-29

JOS-09-798-869-29

JUDIcation No. US20030022821A1

GENERAL INFORMATION:

APPLICANT: JOHN SIGURD SVENDSEN

APPLICANT: (YSTEIN REKDAL

APPLICANT: HALDUR SVEINBJ (RNSSON

APPLICANT: BALDUR SVEINBJ (RNSSON

APPLICANT: BALDUR SVEINBJ

TITLE OF INVENTION: BIOACTIVE PEPTIDES

TILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: PCT/GB99/02851

PRIOR APPLICATION NUMBER: GB9818938.4

PRIOR FILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 29
JOSTON PRESENT OF SERVICE OF STATE OF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.5%,
G; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWDENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CLRWQWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: BOVINE
US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

RESULT 12 US-09-798-869-30

```
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Wensheng
Title Delicant: Rank, David R.
APPLICANT: Chen, Wensheng
Title OF INVENTION INFORMATION:
TITLE OF INVENTION: HURAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: MURBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/20,466
PRIOR APPLICATION NUMBER: US 60/20,466
PRIOR APPLICATION NUMBER: US 60/22,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-0-92
PRIOR PILING DATE: 2000-0-92
PRIOR PILING DATE: 2001-01-30
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·:
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.2%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.51; 2; Indels tive 3; Mismatches 2; Indels
                                                                                           APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYETEN REKDAL
APPLICANT: BALDUR SVETNBJ (RNSSON
TITLE OF INVERTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798, 869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CT/GB99/02851
PRIOR APPLICATION NUMBER: G99818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 37353, Application US/09864761
; Patent No. US20020048763A1
Sequence 30, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: BOVINE
US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-37353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3130R1C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

OTHER INFORMATION: MAP TO APO00114.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN BOTH LIVER, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN PELL LIVER, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN FIRE SIGNAL = 0.84

OTHER INFORMATION: SWISSPROT HIT: P36677, EVALUE 1.00e-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.3%; Score 40; DB 10; Length 239; Best Local Similarity 63.6%; Pred. No. 16; Matches 7; Conservative 3; Mismatches 1; Indels
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 31353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1.
US-10-06-500-58
; Sequence 58, Application US/10066500
; Patent No. US20020177165A1
; GENERAL INFORMION:
; APPLICANT: Avi J. Achkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: Kevin P. Baker
. APPLICANT: David A. Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholas F. Paoni
Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Audrey Goddard
Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colin K. Watanabe
P.Mickey Williams
William I. Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luc Desnoyers
Dan L. Eaton
Napoleone Ferrara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mary E. Gerritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sherman Fong
Wei-Qiang Gao
Hanspeter Gerber
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   James Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
```

```
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT RAPLICATION NUMBER: 10/002,796
PRIOR APPLICATION NUMBER: 06/05914
PRIOR APPLICATION NUMBER: 60/05915
PRIOR APPLICATION NUMBER: 60/05915
PRIOR PAPLICATION NUMBER: 60/05915
PRIOR PAPLICATION NUMBER: 60/05915
PRIOR PAPLICATION NUMBER: 60/05915
PRIOR PLILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/066364
PRIOR PLILING DATE: 1997-10-27
PRIOR PLILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/066364
PRIOR PLILING DATE: 1997-10-27
PRIOR PLILING DATE: 1997-10-27
PRIOR PLILING DATE: 1997-10-29
PRIOR PLILING DATE: 1998-10-29
PRIOR PLILING DATE: 1998-10-29
PRIOR PLILING DATE: 1998-10-29
PRIOR PLILING DATE: 1998-09-10
PRIOR PLILING DATE: 1999-09-10
PRIOR PLI
```

Page

PRIOR FILING DATE: 1997-10-29

PRIOR FILING DATE: 1998-07-14

PRIOR FILING DATE: 1998-06-19

PRIOR PILING DATE: 1998-06-19

PRIOR PILING DATE: 1998-06-19

PRIOR PAPILCATION NUMBER: 09/18629

PRIOR PILING DATE: 1998-06-19

PRIOR PELING DATE: 1998-06-19

PRIOR PELING DATE: 1998-06-19

PRIOR PELING DATE: 1998-06-19

PRIOR PILING DATE: 1998-06-19

PRIOR PELING DATE: 1998-06-19

PRIOR PELING DATE: 1998-06-10

PRIOR PELING DATE: 1998-06-10

PRIOR PELING DATE: 1999-06-19

PRIOR PELING DATE: 1999-06-14

PRIOR PELING DATE: 1999-10-18

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 2001-03-09

PRIOR PELING DATE: 1998-07-14

PRIOR PELING DATE: 1998-07-14

PRIOR PELING DATE: 1998-07

ö Gaps . Length 747; Query Match 52.1%; Score 37; DB 9; Length 747
Best Local Similarity 45.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 3; Indels PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR PLING DATE: 1998-09-16
PRIOR PLING DATE: 1998-09-16
PRIOR PLING DATE: 1998-09-17
PRIOR PLING DATE: 1998-09-17
PRIOR PLING DATE: 1998-10-10
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR APPLICATION NUMBER: PCT/US98/25109
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR PLING DATE: 1998-11-20
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-0-0-0
PRIOR PLING DATE: 1999-0-0-0
PRIOR PLING DATE: 1999-0-0-0
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-0-0-0
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21547 Sequence 58, Application US/10002796; Publication No. US20030032057A1; GENERAL INFORMATION: Luc Desnoyers
Dan L. Eaton
Napoleone Ferrara
Sherman Fong
Wei-Qiang Gao
Hanspeter Gerber
Mary E. Gerriteen
Audrey Goddard
Austin L. Gurney
Ivar J. Kljavin APPLICANT: Avi J. Ashkenazi APPLICANT: Kevin P. Baker APPLICANT: David A. Botstein 311 CVRWQINSRRI 321 1 CFQWQENMRKV 11 RESULT 15 US-10-002-796-58 APPLICANT: APPLICANT: APPLICANT: ò

APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130R1C1

Nicholas F. Paoni Margaret Ann Roy Timothy A. Stewart Daniel Tumas

Colin K. Watanabe P.Mickey Williams William I. Wood

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Ivar J. Kljavin Jennie P. Mather Mary A. Napier

James Pan

CURRENT APPLICATION NUMBER: US/10/002,796
UNRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1998-09-21 L8341 PRIOR FILING DATE: 1998-09-10 PRIOR FILING DATE: 1998-09-10 PRIOR FILING DATE: 1998-09-10 PRIOR FILING DATE: 1998-09-10 PRIOR FILING DATE: 1998-03-09 PRIOR FILING DATE: 1999-03-09 PRIOR FILING DATE: 1999-04-15 PRIOR FILING DATE: 1999-04-15 PRIOR FILING DATE: 1999-06-14 PRIOR FILING DATE: 1999-06-15 PRIOR FILING DATE: 1999-06-15 PRIOR FILING DATE: 1999-06-15 PRIOR FILING DATE: 1999-06-15 PRIOR FILING DATE: 1999-06-16 PRIOR FILING DATE: 2000-03-16 PRIOR FILING DATE: 2001-03-16 PRIOR FILING DATE: 2001-03-09 PRIOR FILING DATE: 2001-03-09

Search completed: February 21, 2003, 08:08:09 Job time: 11.55 secs

δ

```
pyridoxamine 5'-ph
pyridoxamine 5'-ph
probable pyridoxam
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                   lactotransferrin p
                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical prote
hypothetical prote
probable tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical prote
RNA la protein - b
pyruvate carboxyla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pýruvate carboxýla
hypothetical prote
trichohyalin like
                                                                                                                                                                                                                                                                                                                                                                                               lactoferrin - shee
lactoferrin - goat
                                                                                                                                                                                                                                                                                                                                                                                                                lactoferrin precur
dynein beta heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable triacylgl
anthranilate synth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malate dehydrogena
malate dehydrogena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical prote
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                33.3K hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine proteinase
                                                 February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec
                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical
                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                     283224
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                   283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                G86403
T22597
AB0858
C71467
S50977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E98169
AB3118
T19429
P1BVBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H97451
AB2670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F90580
T01607
                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T00362
B85431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG3441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DERTMX
                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                  US-09-743-107B-85
71
                                                                                                        1 CFOWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                   %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1174
1174
1208
1432
206
                                                                                                                                                                                                                                                  PIR 73:*
1: Dir1:*
2: pir2:*
3: pir3:*
                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                        Sequence:
                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                  Database
                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                     No.
```

333		53.5			EFRT2	translation elonga translation elonga
ა	, w w w w w w	00000000000000000000000000000000000000	858 892 893 893 893 893 893 893 893 893 893 893	7001000	A455440 A45213 D6438 B65435 B65485 F90936 F27145	ranslation elonga DNA excision-repai hypothetical prote hypothetical prote hypothetical prote hypothetical prote
ህ 41 41 41 41 41 ህ O H U W 41 N		2222222		000000	A99515 AD2346 C81729 T45825 T45824 D44588	lipoprotein limpor hypothetical prote Mtr/Thab/Tyro perm hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote
}	<u>,                                     </u>			i	ALIGNMENTS	
RESULT 1 IFHUL lactotransferrin precursor [val N;Alternate names: lactoferrin C;Species: Home sapiens (man) C;Date: 31-Mar-1992 #sequence r C;Accession: G01394; S11228; Ā4	nsferrin prate names: 18: Homo sag 31-Mar-1992	n prec es: 1¿ sapié 1992 ‡	precursor [va : lactoferrin apiens (man) 92 #sequence 94; S11228; Ā	rali In Ir A45	[validated] - human rin no ce revision 21-Nov-1997 #text 7	ext_change_08-Dec-2000 \$20041; S07160; A61169; A31000;
R;Cho, Y submitte A;Refere A:Access	id to the ince numblion: GO	e EMBI ber: (	L Data Li G06820	lbra	Library, March 1994	
A;Status A;Molecu	le type	minary : mRN?	y; translated A HO.	late	ed from GB/EMBL/DDBJ	
A;Cross- R;Rey, M	referenting Wo	ces: I	EMBL: U076 k, S.L.;	deBoe	EMBL:U07643; NID:9467236; PIDN:AAB60324.1; ik, S.L.; deBoer, H.A.; Pieper, F.R.	50324.1; PID:g467237
A; Reference	Compleince numbion:	te nuc ber: 2	cleotide S11228; N	Beg	quence of human mammary 0:90384839; PMID:2402455	gland lactoferrin.
A; Molecu A; Molecu A; Residu A; Cross-	le type les: 1-1, referen C.T.; L	: mRN; 48, 'T' ces: E	A ',150-422 EMBL:X539 '; Yanq'	2, 'C 361; N.;	A, Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-148, T'. 150-422, C'. 424-711 <rey> A; Cross-references: EMEL:X3961; NID:g34415; PIDN:CAA37914. R; Tenq. C.T.; Liu, Y.; Yanq, N.; Walmer, D.: Panella, T.</rey>	7914.1; PID:934416 f.
Mol. End. A;Title: A;Refere)	locrinol Differ	ential	1969-1981 1 molecul 845401; N	ar TUID	1992 mechanism of the estrogen 0:93125571; PMID:1480183	gen action that regulates lactofer
A; Access A; Molecu A; Residu	le type es: 1-1!	5401 : DNA 5 <ten< td=""><td>^ ! ~</td><td>;</td><td></td><td></td></ten<>	^ ! ~	;		
A;Cross. A;Experil A;Note:	reteren mental : sequence	ces: ( source extr	GB:S52659 e: placer racted fr	om on	<pre>NID:g263311; PIDN:AAB24877.1 NCBI backbone (NCBIP:122202</pre>	377.1; PID:g263312 22202)
R;Powell Nucleic A A;Title:	Acids Re Nucleot	Ogder es. 18 tide e	n, J.E. 8, 4013, sequence	199 of	90 human lactoferrin cDNA.	
A; Molecu	ion: S10	0324 : mRNA		1		
A; Residu A; Cross- R; Stowel	referencia, K.M.;	LI <pc< td=""><td>EMBL:X529</td><td>41; Fun</td><td>NID: 934411; PIDN: CAA3711 bk, W.D.; Tweedie, J.W.</td><td>116.1; PID:934412</td></pc<>	EMBL:X529	41; Fun	NID: 934411; PIDN: CAA3711 bk, W.D.; Tweedie, J.W.	116.1; PID:934412
Biochem. A;Title: A;Refere:	Expressince numb	, 349- sion c per: S	-355, 199 of cloned 815853; M	dib	ıman lactoferrin in baby ):91264786; PMID:2049066	-hamster kidney cells.
A;Access A;Status A;Molecu A;Residu	lon: SI: nucle: le type: es: 20-3	icaci mRNA 1 <st< td=""><td>id sequen A [1&gt;</td><td>e U</td><td>not shown; not compared</td><td>With conceptual translation</td></st<>	id sequen A [1>	e U	not shown; not compared	With conceptual translation
A; Access A; Molecu	ion: S2( le type: es: 20=3	3841 : prot	tein , 20-31	Ē		

0

Gaps

```
Cypecies: Mus musculus (house mouse)
Cypecies: Mus musculus (house mouse)
Cybate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CyAccession: A28438; A41205
CyAccession: A28438; C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secr.
A;Reference number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assignment of the relevant locu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplication; glycoprotein
F;355-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riliu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
Affitle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; WUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2323
R;Le Provost, F:; Nocart, M.; Guerin, G:; Martin, P.
Biochem. Biochem. Biochem. 1324-1337, 1994
A;Fille: Characterization of the goat lactoferrin cDRA: assignment of the reA;Fille: Characterization of the goat lactoferrin cDRA: assignment of the reA;Fille: Characterization of the goat lactoferrin cDRA: assignment of the reaction of
                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fil-19/Domain: signal sequence #status predicted <SIG>
F;20-707/Product: lactotransferrin #status predicted <MAT>
F:388-695/Domain: transferrin repeat homology <TRH2>
F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 2; Length 708;
Pred. No. 1.4;
2; Mismatches 2; Indel's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.4%; Score 45; DB 1; Length 707; 63.6%; Pred. No. 7; ive 1; Mismatches 3; Indels
         Length 33;
                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: transferrin; transferrin repeat homology C;Keywords: duplication; glycoprotein
DB 2;
                                                                                      3; Mismatches
    Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactoferrin precursor - mouse
N;Alternate names: lactotransferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%;
    70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 3-707 <PEN>
A;Cross-references: EMBL:J03298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.07
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.5.
Fr. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-15 <LIU>
A;Cross-references: GB:M74778
                                                                                          7; Conservative
                                                                                                                                                                            1 CFOWDENMRKV 11
                                                                                                                                                                                                                                                         19 CYÓWÓKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWOENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 CYOWORRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 CLRWQNEMRKV 47
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-708 < LEP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A28438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: JC2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A41205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactoferrin - goat
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A28438
                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                A; Molecule type: mRNA

A; Mesidues: 436-487, A', 489-711 <RAD>

A; Residues: 436-487, A', 489-711 <RAD>

A; Cross-references: EMBL:M.8642; NID:9186815; PIDN:AAA86665.1; PID:9386855

B; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.

Cancer Res. 51, 3037-3943, 1991

A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt

A; Reference number: A61169; MUID:91235214; PMID:1674448
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Pitle: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR
A;Riference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 3-701, SMKPVN < PAN>
A;Eserimental source: normal breast tissue
B;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A;Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purification by aminohexyl affin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: duplication; glycoprotein; iron binding; milk
7-1-19/Domain: signal sequence #status predicted <SIG>
7-1-19/Domain: signal sequence #status predicted <SIG>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRHL>
F;360-699/Domain: transferrin repeat homology <TRHL>
F;360-699/Domain: transferrin repeat homology <TRHZ>
F;39-65,39-56,135-218,17-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Rhinding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Molecule type: protein
A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A; Note: this is the final paper in a series
R; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Bur. G. Blochem. 241, 303-308, 1996
Bur. G. Blochem. 241, 303-308, 1996
A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an inhibitor of platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Accession: S52107
R; Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biochys. Acta 1243, 25-32, 1995
A; Title: Isolation and characterization of sheep lactoferrin, A; Reference number: S52107; MUID: 95127729; PMID: 7827104
A; Accession: S52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 1; Length 711
Pred. No. 0.0016;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Superfamily: transferrin; transferrin repeat homology C.Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Cross-references: GDB:119368; OMIM:150210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 3q21-3q23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 CFOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-33 <QIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A61169
                                                                                                                                                                            A; Accession: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S74119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB:LTF
```

RESULT 2

g à

0

Gaps

; 0

Gaps

RESULT 5

```
hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Pate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyaccession: AB0858
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova; Reference number: AB0802; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ristephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac. A;Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable tyrosine transport - Chlamydia trachomatis (serotype D, strain UW3/Cx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
C;Genetics:
A;Gene: STY3070
                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: Z81089; PIDN: CAB03137.1; GSPDB: GN00028; CESP: F53H4.4
                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: C71467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: X
A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.7%; Score 41; DB 2; Length 275; 63.6%; Pred. No. 13; 2; Indels Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
hypothetical protein F53H4.4 - Caenorhabditis elegans
                                                                                                                                                                                   A,Reference number: 219587
A,Accession: T22597
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.7%; Score 41; DB 2; 58.3%; Pred. No. 25;
                                                                                                                     R,Dobson, R. submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FOWDENMRKVR 12
                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-275 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA A; Residues: 1-511 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                            C,Accession: T08030
R,Mitchell, D.R.; Brown, K.S.
J. Cell Saci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: 216302; MUD:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; areaen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. G.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86403
A;Accession: G86403
A;Accession: Communication of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross_references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141 C;Genetics: A;Map position: 1
                                                                       dynein beta heavy chain - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: T08030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4568 <MIT>
A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
```

..

63.4%; Score 45; DB 2; Length 4568; 50.0%; Pred. No. 48; 3; Indels tive 3; Mismatches 3; Indels

Conservative

Query Match Best Local Similarity Matches 6; Conserv

à

C;Reywords: nucleotide binding; P-loop F;1912-1926/Region: nucleotide-binding mctif A (P-loop) P;2202-2209/Region: nucleotide-binding mctif A (P-loop) F;2530-2537/Region: nucleotide-binding mctif A (P-loop)

A; Experimental source: strain 21gr

A; Gene: ODA4

33.3K hypothetical protein F28L5.13 - Arabidopsis thaliana

C; Accession: G86403

59.2%; Score 42; DB 2; Length 289; 58.3%; Pred. No. 9.2;

4; Indels

1; Mismatches

ilarity 58.3%; Conservative

Local Similarity les 7; Conserv

Best Loc Matches

Query Match

A; Molecule type: DNA A; Residues: 1-289 <STO>

RESULT 7

```
A;Accession: C71467
A;Status: preliminary
A;Molecule type: DNA
```

ô

```
Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: AGK L 612
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: Atu4566
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.5.
                                                                                                                                                                                                                                                                                                                                      158 CFGKKENMROMR 169
                                                                                                                                                                                                                                                                                   1 CFQWQENMRKVR 12
       A;Residues: 1-267 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 WQENWRYV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 WQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                               A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: E98169
                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
AB3118
                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                      ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-431 <URR>
A;Cross-references: EMBL:Z74053; NID:g1430962; PIDN:CAA98561.1; PID:e252970; PID:g143096
A;Experimental source: strain S288C
                     A; Cross-references: GB: AE001354; GB: AE001273; NID: g3329280; PIDN: AAC68414.1; PID: g332928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: S77802

C, Accession: S77802

C, Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.; Mol. Microbiol. 16, 955-967, 1995

A, Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiold A; Reference number: S77739; MUID: 96059641; PMID: 7476192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-431 <MUR>
A; Residues: 1-431 <MUR>
A; Residues: 1-431 <MUR>
A; Cross-references: BmB1: Z48008; NID: g642799; PIDN: CAA88056.1; PID: g642801
B; Andre, B.; Vissers, S.; Urrestarazu, L.
submitted to the BmB1 Data Library, February 1995
A; Description: The sequence of a 42 kb segment located on the left arm of chromosome A; Reference number: S52492
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
850977
hypothetical protein YDL005c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein D2930; hypothetical protein YD8119.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisian 12-May-1995 #text_change 19-Apr-2002
C;Accession: S50977; S52514; $67537
R;Murphy, L.; Richards, C.; Gentles, S.; Harris, D.
submitted to the EMBL Data Library, January 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C'Species: Mycoplasma capricolum
C'Date: 09-Oct_1997 #sequence_revision 31-Oct-1997 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Cross-references: EMBL:Z48432; NID:g683669; PIDN:CAA88354.1; PID:g683692 R;Urrestarazu, L.A.; Andre, B.; Vissers, S. submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Status: nucleic acid sequence not shown; translation not shown A:Molecule type: DNA
                                                                                                                                                                                 Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.3%; Score 40; DB 2; Length 431; 100.0%; Pred. No. 31; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             877802
hypothetical protein MC003 - Mycoplasma capricolum (fragment)
                                                                                                                                                                            Score 40; DB 2;
Pred. No. 30;
0; Mismatches
                                                                                               A,Gene: tyrP_1 C,Superfamily: tyrosine-specific transport protein
                                               A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
                                                                                                                                                                         Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: SGD:MBD2
A;Cross-references: SGD:S0002163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S50976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S67535
                                                                                                                                                                                                                                                                                                                              317 FOWDEKKRKV 326
                                                                                                                                                                                                                                                                              2 FOWDENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-431 < AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
A;Residues: 1-415 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 QENMRKVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S77802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S50977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S52514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S67537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 4L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
```

```
C; Accession: E98169
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2011
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Agrobacterium tunefaciens
C;Species: Agrobacterium tunefaciens
C;Date: 11.-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession. AB3118
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2.317-2322, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serine proteinase Atu4566 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine proteinase XF0267 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #text_change 11-Jan-2002
A;Cross-references: EMBL:Z33006
A;Experimental source: ATCC 27343
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ster, E.W.

Yittle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AB3118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-660 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88879.1; PID:g15158646; GSPDB:GN00170
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Residues: 1-660 <KUR>
A,Cross-references: GB:AE008689; PIDN:AAL45360.1; PID:g17743054; GSPDB:GN00187
A,Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                 Score 39; DB 2; Length 267; Pred. No. 28; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.9%; Score 39; DB 2; Best Local Similarity 87.5%; Pred. No. 72; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%; Score 39; DB 87.5%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
```

. 0

0;

4 WQENMRKV 11

à

```
A;Geme: CBSP:C24H11.8
A;Map position: 3
A;Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIBURE
RNA la protein - broad bean mottle virus (strain Bawden)
RNA la protein - broad bean mottle virus (strain Bawden)

Sycontains: ATP-dependent helicase (EC 3.6.1.-); mRNA (guanine-N7-)-methyltransferase (E 5.9ecies: broad bean mottle virus

C;Species: broad bean mottle virus

C;Species: broad bean mottle virus

C;Batc: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 19-Jan-2001

C;Accession: A41699

N;Dlangy 185, 553-562, 1991

A;Title: The nucleotide sequence and genome organization of the RNA-1 segment in two broad A;Reference number: A41699; MUD:92074218; PMID:1962437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession, maion RNA
A;Residues: 1-966 <DZI>
A;Residues: 1-966 <DZI>
A;Residues: 1-966 <DZI>
A;Cross-references: GB:M65138; NID:g210662; PIDN:AA42740.1; PID:g210663
A;Cross-references: GB:M65138; NID:g210662; PIDN:AA42740.1; PID:g210663
C;Superfamily: cucumber mosaic virus RNA 1 protein
C;Keywords: hydrolase; methyltransferase; mRNA capping; nucleotide binding; P-loop; S-ad
F;80-168/Domain: methyltransferase #status predicted <MTF>
F;680-697/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z19123
A;Accession: T19429
A;Scalus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-681 «WIL»
A;Cross-references: EMBL:Z81475; PIDN:CAB03914.1; GSPDB:GN00021; CESP:C24H11.8
A;Experimental source: clone C24H11
                                                                                                                                                           Appothetical protein C24H11.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T19429
R;Lloyd, C.
Submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.9%; Score 39; DB 2; Length 681; 60.0%; Pred. No. 74; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.9%; Score 39; DB 1; Length 966; Best Local Similarity 53.3%; Pred. No. 1.1e+02; Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 21, 2003, 07:47:57 Job time : 10.65 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 CFKENKDWIENMRSV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQ----WQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | | | | 192 RWQKNRRRVR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QWQENMRKVR 12
   126 WOENMRYV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                       RESULT 14
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

ö

Gaps

ï

Gaps

```
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-85 71 1 CFQWQENMRKVR 12 Title: Perfect score: Sequence: Scoring table:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt 40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	P02788 homo sapien	came]	Q29477 capra hircu		Q39565 chlamydomon		_	_	Q9zwi9 oryza sativ	Q8r9ul thermoanaer	Q9r014 mus musculu	P48163 homo sapien	P13697 rattus norv			P13639 homo sapien		P58252 mus musculu	P05197 rattus norv		Q58118 methanococc	P76909 escherichia	buchi	homod	homo	3 schi	P26448 saccharomyc	P49307 rhizobium m	P48991 anabaena sp	7 enterococ	034374 bacillus su	10 caeno	Q15696 homo sapien
ID	TRFL HUMAN	TRFL CAMDR	TRFL_CAPHI	TRFL MOUSE	DYHB CHLRE	TRFL HORSE	Y125 MYCCA	V1A BBMV	PHYC ORYSA	RL28 THETN	CATJ MOUSE	MAOX HUMAN	MAOX RAT		EF2 CRIGR	EF2 HUMAN	EF2 MESAU	EF2 MOUSE	EF2 RAT	RA16 SCHPO	Y708 METUA	YNJD ECOLI	RPSD_BUCAI	ABCR HUMAN			BUB2 YEAST	MOCA RHIME	F16P ANASP	DDL ENTHR	YJIB_BACSU	YKYL CAEEL	U2R2_HUMAN
DB	-1	Н	Н	Н	Н	Н	Н	щ	Н	<u>,-</u> 1	Н	М	Н	-	Н	Н	Т	Н	Н	Н	Н	Н	Н	Н	Н	Н	-	7	Н	Н	Н	~	-
Query Match Length	711	708	708	707	4568	695	267	996	1137	62	333	572	572	857	857	857	857	857	857	892	172	217	612	2273	2483	238	306	317	349	358	396	455	482
Query Match	93.0	69.0	0.69	n	e.	57.7	4.	4.	54.9	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	52.1	52.1	52.1	52.1	52.1	50.7	50.7	50.7	50.7	50.7	0	50.7	50.7
Score	99	49	49	45	45	41	39	39	39	38.	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37	36	36	36	36	36	36	36	36
	   <del>   </del>   <del> </del>	7	m	4	Ŋ	و	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q04916 rotavirus ( P29691 caenorhabdi	P03588 brome mosai Q10201 schizosacch	O67648 aquifex aeo O28816 archaeoglob	Q9qze3 rattus norv Q9jsz7 neisseria m	09k0y2 neisseria m 09z7pl chlamydia p	P44693 haemophilus Q15695 homo sapien
VP4 ROTGA EF2 CAEEL	V1A_BMV YBX7_SCHPO	LPXC_AQUAE YES6_ARCFU	CATQ_RAT MURG_NEIMA	MURG_NEIMB SYH CHLPN	yeba habin uzri_human
749	961 962	282	343 355	355 430	475
50.7	50.7	50.0 49.3	49.3	49.3 49.3	49.3 49.3
36	36 36	35.5	35	3 3	35
6 6 4 70	36 37	38 39	40	4243	44 5

## ALIGNMENTS

7

3-711 FROM N.A.

OF

```
McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
"Mol. Biol. 209:711-734 (1989).
                                                                                                                                                                                                                                                                                                                                                             "The present state of the human lactotransferrin sequence. Study and
                                                                                                                                                                                                                                                                                                                                                                               alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
                                                                                                                                                                                                                                                                                                     MEDLINE=82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-253-->methionine mutant."; Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                            MEDLINE=85076667; PubMed=6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'An 88 amino acid long C-terminal sequence of human
                                                    Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353
                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 670:243-254(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acta Crystallogr. D 51:629-646(1995).
                                                                                          Nucleic Acids Res. 18:4013-4013 (1990)
                                                                                                                                                                                                                                              J. Biochem. 145:659-666(1984)
              IISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=82262043; PubMed=7049727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 142:107-110(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 237-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blood 70:989-993(1987).
                                                                                                              [9]
SEQUENCE OF 20-711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 609-711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lactotransferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resolution,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker E.N.
                                                                                                                                                                                                                                                                                                                                             Jolles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jolles
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no new modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE FOR KARPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                 MEDLINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
                                                                                                                                                                                                                                                                                                                                                         PubMed=9873069;
Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Quasiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
Bl Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
"Familial subepithelial corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene.";
Mol. Vision 4:31-32(1998).
                                                                                                     MEDLINE-99192677; PubMed-10089508; Manage D. H., Baker E.N.; Jameson G. B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.; "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                            Acta Crystallogr. D 54:1319-1335(1998).
                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                        Agric. Biol. Chem. 54:1803-1810(1990).
                                                    Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF332168; AAG48753.1; -. EMBL; BC015822; AAH15822.1; -. EMBL; BC015823; AAH15823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U07643; AAB60324.1; -.
EMBL; M93150; AAA36159.1; -.
EMBL; M83202; AAA59511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M83205; AAA58656.1; -. EMBL; M18642; AAA86665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M73700; AAAS9479.1; -. EMBL; X52941; CAA37116.1; -. EMBL; U95626; AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X53961; CAA37914.1; -.
                                                                                                                                                                                                                                                                                                                                            VARIANTS THR-30 AND ARG-48.
                                                                                                                                                                                                                                                                                         from human lactoferrin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1LCF; 31-AUG-94.
1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-96.
12-MAR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S11228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1LGB;
1LGC;
1BKA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1DSN;
1HSE;
1VFD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1LFH;
1LFI;
                                     awamori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
```

us-09-743-107b-85.rsp

```
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                           DISULFID
                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                         CONFLICT
                                                      DISULFID
                                                                  DISULFID
                                                                                                                                                                                    BINDING
                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                               CONFLICT
                                                                                                          METAL
METAL
METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!-SUBBLIT: MONOMER (BY SIMILARITY).
-!-SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!-SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                 Gaps
                                                                                                                                                                                                    Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AJ131674; CAB53387.1; -.
EMBL, AF165879; AAF82241.1; -.
EMBL, AF65879; AAF82241.1; -.
EMBL, AF65879; IRAX.
ELINES.
ELINES.
ERINES, PRO0405; transferrin, 2.
PRINES, PRO0405; TRANSFERRIN.
ERINES, PRO0405; TRANSFERRIN.
ERINES, PRO0206; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 2; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.
                                 ..
0
       Query Match 93.0%; Score 66; DB 1; Length 711; Best Local Similarity 91.7%; Pred. No. 0.00037; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                           TRFL_CAMDR
STANDARD; PRT; 708 AA.
Q9TUMO; Q9MCSS;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
LACTOTRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
708
708
708
708
64
217
1192
200
264
399
                                                                                                                                                                                                                                                                                                                                       TISSUE=Mammary gland;
                                                   1 CFQWQENMRKVR 12
                                                                       39 CFOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                          SEOUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3620
3600
3600
364
364
1136
367
367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
CHAIN
REPEAT
REPEAT
                                                                                                       RESULT
TRFL_CA
                                                                     임
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Mammary gland;
MEDLINE=94380047; PubMed=8093048;
le Provost F., Nocart M., Guerin G., Martin P.;
le Provost F., Nocart M., Guerin G., Martin P.;
'Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 synteny group.",
Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
-! FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANYON, USUALLY BICARBONATE.
-! SUBUNIT: MONOMER (BY SIMILARITY).
-! SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Mammalia; Butharia; Cramiata; Vertebrata; Buteleostomi; Mammalia; Butharia; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%; Score 49; DB 1; Length 708; 66.7%; Pred. No. 0.39; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTT N-S (IN REF. 2).

S -> A (IN REF. 2).

LLS -> PLF (IN REF. 2).

LLS -> PLF (IN REF. 2).

L-> F (IN REF. 2).

A -> P (IN REF. 2).

R -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1996 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-2092 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 CACWORRMKKVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 (
708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRFL CAPHI
ID TRFL CAPHI
AC 029477; 029479;
DT 15-DEC-1998 (Rel.
                                                                                                                                                                                                     NCBI_TaxID=9925;
```

Tue Dec

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                            Iransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.0%; Score 49; DB 1; Length 708; 63.6%; Pred. No. 0.39; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 I -> V (IN REF. 2).
88 L -> R (IN REF. 2).
124 Q -> K (IN REF. 2).
154 F -> P (IN REF. 2).
304 S -> P (IN REF. 2).
414 D -> G (IN REF. 2).
77358 MW; FZEDA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . . ) (
N-LINKED (GLCNAC. . . )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
-!- DOMAIN; COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
LACTOTRANSFERRIN,
                                                                                                                                                                                                                                                                                                                                          2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (
N-LINKED (
I -> V (IN
L -> R (IN
Q -> K (IN
                                                                                                                                                                               InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR PER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
                                                                                                                                           EMBL; U53857; AAA97958.1; -.
                                                                                                                                                         EMBL; X78902; CAA55517.1; -. HSSP; 077698; 1CE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                708 AA;
                                                                                                                                                                                                                                                                                                                                         REPEAT
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                  CHAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDULACY. TENG C.T.;
Liu Y., Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991)
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                  Eukaryota; Metaria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
LACTOTRANSFERRIN.
1.
TRFL MOUSE STANDARD; PRT; 707 AA. P08071; P70590; Q61799; Q922P2; 01-AUG-1988 (Rel. 08, Created) 15-UN-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J03298; AAA40525.1; -.
EMBL; D80810; BAA13633.1; -.
EMBL; BC006904; AAH06904.1; -.
EMBL; M74778; AAA39427.1; -.
PIR; A28418; A28438.
HSSP; P02788; LCB6.
MGD; MGI:96837; Ltf.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00205; TRANSFERRIN 1; 1. PROSITE; PS00206; TRANSFERRIN 2; 2. PROSITE; PS00207; TRANSFERRIN 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-14 FROM N.A.
MEDLINE=92042099; PubMed=1939212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00405; transferrin, 2.
PRINTS; PR00422; TRANSFERIN.
SMART; SM00094; TR FER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
707
357
                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
REPEAT
                                    PACTOR OF THE TARKEN TO THE TARKEN THE TARKEN TO THE TARKEN TO THE TARKEN TO THE TARKEN THE TARK
```

ô

Gaps

;

7; Conservative

Best Local Similarity

Matches

ò d us-09-743-107b-85.rsp

Ŋ

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain genes.";
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERALING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYNEIN HAS ATPASE ACTIVITY.
SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 1; Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                              IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 2 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                         F26AE0340A4C19AB CRC64;
                                                                                                                                                                                                                                                                                                     ANTON (FOTENTIAL)

N-LINKED (GLONAC. . . ) (E
N-LINKED (GLONAC. . . )

MR -> IQG (IN REF. 1).

R -> Q (IN REF. 2).

M -> I (IN REF. 2).

S -> T (IN REF. 2).

S -> T (IN REF. 2).

S -> G (IN REF. 2).

L -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 4568 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                              ANION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                          77865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               63.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ODA4 OR ODA-4 OR SUP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 CLRWONEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                       707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYHB CHLRE
Q39565;
                                                                                                                                                  DISULFID
DISULFID
DISULFID
DISULFID
          DISULFID
                                              DISULFID
                                                                                          DISULFID
                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                    DISULFID
                                                                                DISULFID
                                                                                                                 DISULFID
                                  DISULFID
                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                               METAL
BINDING
BINDING
                                                                                                                                                                                                                                                                                                                               CARBOHYD
 REPEAT
                                                                                                                                                                                                                       METAL
METAL
METAL
                                                                                                                                                                                                                                                         METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYHB CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER.
-!- SUBCLIGILAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                    COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·
0
                                                                                                                                    EMBL, U02963; AAA19956.1; -
InterPro; IPR004273; Dynein heavy.
Pfan, PF03028; Dynein heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 1; Length 4568;
Pred. No. 15;
3; Mismatches 3; Indels
-1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 519961 MW; 9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;

"CDNA sequence of mare lactoferrin.";

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                        COILED COIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99296631; PubMed=10366507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                        293
11175
11400
1650
1885
2045
3162
3162
3425
3425
2209
2209
                                                                                                                                                                                                                                                                                                                                                                                                                   2886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||| :|
1852 CFQWQSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                             2831
3106
3339
3648
1919
2202
2530
                                                                                                                                                                                                                                                                                                                                                                                                                                 4568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRFL HORSE
077811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Milk;
                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
NP_BIND
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRFL HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
V1A_BBMV
                                                                                                                                                                                                                                                                                                                                                                     RESULT
 Š
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL).
                                                                 EMBL, AJ010930; CAA08407.1; -.

PDB; 1B1X; 02-DEC-98

PDB; 1B1V; 02-EFB-99

PDB; 1B72; 02-FFB-99

InterPro; IPR001156; Transferrin.

Pfan; PF00405; transferrin; 2

PRINTS; PR00422; TRANSFERRIN.

SMART; SM00094; TR FRR; 2.

PROSITE; PS00206; TRANSFERRIN 1; 2.

PROSITE; PS00206; TRANSFERRIN 3; 1.

PROSITE; PS00207; TRANSFERRIN 3; 1.

Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         07BB84D50E1B165D CRC64;
                                                                                                                                                                                                                                                                                                                                                   IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. . .)
                                                                                                                                                                                        LACTOTRANSFERRIN.
1.
2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                     511
521
531
636
66
66
98
198
198
259
                                                                                                                                                               Signal; 3D-structure.
NON TER 1
SIGNAL <1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::| ||:|||
| CAKFQRNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                        695 AA;
                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                   METAL
METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                             WETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

267 AA.

PRT;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EBLE outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
                                                                                                                                                                                                                                                                                                                       Dzianott A.W., Bujareki J.J.;
"The nucleotide sequence and genome organization of the RNA-1 segment in two bromoviruses: broad bean mottle virus and cowpea chlorotic mottle virus.";
Virology 185:55-562(1991).
-!- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
-:- FUNCTION: AND A METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                       STRAIN=ATCC 27343 / KID;
MEDLINE=96605041; PubMed=7476192;
Bork P., Ouzounis C., Casari G., Schneider R., Sander C.,
Dolan M., Gilbert W., Gillevet P.M.;
"Exploring the Mycoplasma capricolum genome: a minimal cell reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.9%; Score 39; DB 1; Length 267; 58.3%; Pred. No. 8.4; 2; Indels live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 AA; 30425 MW; D5912DD5B39A8451 CRC64;
                                                                                 Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
1A protein [Includes: Helicase, Methyltransferase].
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  966 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z33006; CAA83689.1; -.
InterPro; IPR001454; Hlgnase/hydrlase.
InterPro; iPR001459; Hypothet_cof.
Pfan; PF00702; Hydrolase; 1.
PROSITE; PS01228; COF_1; 1.
PROSITE; PS01229; COF_2; 1.
PROSITE; PS01229; COF_2; 2.
NON TER.
SEQUENCE 267 AA; 30425 MW; D5912DD5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92074218; PubMed=1962437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broad bean mottle virus.
                                                                     Mycoplasma capricolum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 CFGKKENMRQMR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQENMRKVR 12
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=12301;
                                                                                                                                           NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bawden;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAPPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bromovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V1A BBMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:
```

0,

```
Tanglosperms.";

Mol. Biol. Evol. 13:1141-1150(1996).

Mol. Biol. Evol. 13:1141-1150(1996).

- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARSORBS.

ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ASSORBS.

MAXIMALLY IN THE FAR-RED REGION OF THE SPECTRUM AND THE PER FORM THAT ASSORBS.

ARSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS.

CERCONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE RECONVERSION OF PR IN THE SAFENCES IN THE SAFENCE OF A NUCLEAR GENES. PER CONTROLS.

CERDES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHUROPPHALL A/B BINDING PROTEIN.

CC PROTOCHLAROPPHYLLIDE REDUCTAGE, RNA, ETC. IT ALSO CONTROLS.

THE EXPRESSION OF ITS OWN GENES, IN A NEGATIVE FEEDBACK FASHION.

CC --- SUBUNIT: HOWODINGR (BY SIMILARITY).

CC --- STMILLARITY: CONTAINS 1 PAS-ASSOCIATED CHERMINAL (PAC) DOMAIN.

CC --- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Nipponbare;
Tahlr M., Kanegae H., Takano M.;
"Phytochrome C (PHYC) gene in rice: isolation and characterization of a complete coding sequence.";
(In) Plant Gene Register PGR98-210.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 275-378 FROM N.A.
MEDILINE-97019052; PubMed-8865668;
Mathews S., Sharrock R.A.;
"The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot
                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                54.9%; Score 39; DB 1; Length 966; 53.3%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                  966 AA; 109621 MW; DF592681D7231C8D CRC64;
                                                                                                                                                                                     PIR; A41699; PIBVBB. ...
INTECTPO; IPRO02588; Wmethyltransf.
IntectPro; IPR000606; Viral helicasel.
Pfam; PF01443; Viral helicasel; I.
Pfam; PF01660; Vmethyltransf; I.
Pfam; PF0160; Vmethyltransf; I.
Pfam; PF01609; Vmethyltransfirates.
NP_BIND 699 AIP (POTENILAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYC_ORYSA STANDARD; PRT; 1137 AA. Q9ZWT9; P93429; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 53.3%; Pred. No.
                                                                                                                                                                    EMBL; M65138; AAA42740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 CFKENKDWTENMRSV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQ----WQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phytochrome C.
                                                                                                                                                                                                                                                                                                                NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHYC_ORYSA
    à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MB4 / JCM 11007, MEDIJNB-21.992816; PubMed=11997336; MEDIJNB=21.992816; PubMed=11997336; MEDIJNB-21.992816; PubMed=11997336; Chen Y., Tan Y., Xue Y., Tan M., Hanng L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.9%; Score 39; DB 1; Length 1137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          904 1124 HISTIDINE KINASE.
322 322 CHROMOPHORE (BY SIMILARITY).
292 279 F -> S (IN REF. 2).
292 292 C -> S (IN REF. 2).
1137 AA; 125982 MW; F2A520181CFE7B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
25-JUN-2002 (Rel. 41, Last annotation update)
RPMB OR TTE1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 39;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004359; HIS.KIN sig.
InterPro; IPR003661; His.KinA.
InterPro; IPR001610; PAC.
InterPro; IPR001014; PAS. domain.
InterPro; IPR00101294; Phytochrome.
Pfam; PF00312; signal; 1.
Pfam; PF00312; signal; 1.
Pfam; PF00312; signal; 1.
Pfam; PF010319; PAS; 2.
Pfam; PF01590; GAF; 1.
Pfam; PF01590; GAF; 1.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPARE.
SMART; SM00387; HATPARE.
SMART; SM00388; HisKA; 1.
SMART; SM00086; PAC; 1.
SMART; SM000091; PAS; 2.
IGREMARY; SM00091; PAS; 2.
PROFESTER PROFESTER
PROFESTER PROFESTER
PROFESTER PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
PROFESTER
P
                                                                                                                                                                                                                                                                EMBL, U61207, AAB41996.1; -.
InterPro, IPR003594; ATPbind_ATPase.
InterPro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS5012; PAS; 2.
PROSITE; PS00245; PHYTOCHROME 1; 1.
PROSITE; PS50046; PHYTOCHROME 2; 1.
                                                                                                                                                                                                                                          EMBL; AB018442; BAA74448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            777 CLEWNÉAMOKI 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RL28 THETN
Q8R9U1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RL28_THETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
à
```

Φ

```
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                 CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fracey A
                                                                                                                                                               CARBOHYD
                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                      CARBOHYD
                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                      T 12
HUMAN
                                                                                CHAIN
                                                                                                                                                                                                                                                                      Matches
  ò
                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee&isb-sib.ch).
                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                               ö
                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tisljar K., Deussing J., Peters C.; "cathepain J, a novel murine cysteine protease of the papain family with a placenta-restricted expression."; FBBS Lett. 455:299-304(1599).
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
            Genome Res. 12:689-700(2002).
-!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                  CATU_MOUSE STANDARD; PRT; 333 AA.

Q9R014; Q9WV51;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2002 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Cathepsin J precursor (BC 3.4.22.-) (Cathepsin P) (Catlrp-p)
                                                                                                                                                                                     53.5%; Score 38; DB 1; Length 62; 60.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                               CAADB605C81D495D CRC64;
complete sequence of T. tengcongensis genome.";
                                                                                                                                                                                                            3; Mismatches
                                                                                                                                       EMBL, AE013107, AAM24713.1; -.
Ribosomal protein, Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1349426; Ctsj.
InterPro; IPR000668; Peptidase Cl.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase Cl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/61; TISSUE=Embryo;
MEDLINE=99456833; PubMed=10526153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF136272; AAF13142.1; -.
EMBL; AF158182; AAD41898.1; -.
HSSP; P07711; 1CJL.
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00705; PAPAIN.
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C01.038; -.
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                    QWQENMRKVR 12
                                                                                                                                                                                                                                                 :|:|:|||
27 RWKPNIRKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                        CTSJ OR CISP.
             Genome Res.
                                                                                                                                                                                                              9
                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                          CAIJ MOUSE
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                              RESULT 11
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAOX HUMAN STANDARD; PRT; 572 AA.
P48163; Q16855; Q9BWX8; Q9UIY4; Q9H1W3;
01-FEB-1396 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Malic enzyme 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chou W.Y., Huang S.M., Chang G.G.;
"Nonidentity of the cDNA sequence of human breast cancer cell malic
"Indidentity of the normal human cell.";
J. Protein Chem. 15:273-279(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94244767; PubMed=8187880;
Loeber G., Dworkin M.B., Infante A., Ahorn H.;
"Characterization of cytosolic malic enzyme in human tumor cells.";
FEBS Lett. 344:181-186(1994).
Prodom, PD000158; Peptidase_C1; 1.
PROSITE; PS00139; THIOL PROTEASE_CYS; 1.
PROSITE; PS00649; THIOL_PROTEASE_HIS; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
Hydrolase; Thiol protease; Glycoprotein; Lybosome; Zymogen; Signal.
                                                                                                                                                                                          CATHEREIN TO TELLIDE.

BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.5%; Score 38; DB 1; Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37147 MW; F9A8FF1D5A13B721 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P -> PK (IN REF. 2)
                                                                                                                                              POTENTIAL.
ACTIVATION PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96397682; PubMed=8804575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=White adipose tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 27-572 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 8-572 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 WOENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|||| ::
51 WEENMRMIK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                         18
11137
1137
2275
2299
1134
1168
268
268
268
268
268
268
```

us-09-743-107b-85.rsp

σ

Page

```
EF2 CHICK
Q90705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN'1990 (Rel. 13, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Malic enzyme 1).
MEI OR MODI OR MOD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morioka H., Magnuson M.A., Mitsuhashi T., Song M.K.H., Rall J.E., Nikodem V.M.,
Nikodem V.M.,
"Structural characterization of the rat malic enzyme gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:4912-4916(1989).
-!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morioka H., Tennyson G.E., Nikodem V.M., "Structural and functional analysis of the rat malic enzyme gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nikodem V.M., Magnuson M.A., Dozin B., Morioka H.,
"Coding nucleotide sequence of rat malic enzyme mRNA and tissue specific regulation by thyroid hormone.";
Endocr. Res. 15:547-564 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley,
MEDLINE=86111765; PubMed=3753699;
Magnuson M.A., Morioka H., Tecce M.F., Nikodem V.M.;
"Coding nuclectide sequence of rat liver malic enzyme mRNA.";
J. Biol. Chem. 261:1183-1186(1986).
                                                                                                                                                                                                                                                                                                                                                                              53.5%; Score 38; DB 1; Length 572; 33.3%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                     572 AA; 64149 MW; EA4C8CB36F6C619C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
                                                                                                                                                                                                                                                                                                NADP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               572 AA.
                                                                                                                                                                                                                                                                                                                      P -> S (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 28;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
or send an email to license@isb-sib.ch)
                                                                                                                                                                                InterPro; IPR001891; Malic_oxred.
Pfan; PR00390; malic; 1.
PRINTS; PR00072; MALOXEDTASE.
PROSITE; PS00331; MALIC_ENZYMES; 1.
Oxidoreductase; NADP.
NP BIND
NP BIND
CONFLICT 438 438 P -> S (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Biol. 8:3542-3545(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90235791; PubMed=2699453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89096948; PubMed=3211151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE.
MEDLINE=89296914; PubMed=2740332;
                                  EMBL; X77244; CAA54460.1; -.
EMBL; U43944; AAC50613.1; -.
EMBL; AL391416; CAC35330.1; -.
EMBL; AL136970; CAC19505.1; -.
EMBL; AL049699; CAB52344.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       318
438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-35 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                       Genew; HGNC: 6983; ME1.
MIM; 154250; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         556 CYSWPEEVOKIO 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter."
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAOX RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P13697
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
STT WE DE REAL OF THE SECOND TO THE SECOND TO THE SECOND THE SECON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-21, AND PHOSPHORYLATION.

MEDLINE=91207327; PubMed=1708237;

Kim Y.W., Kim C.W., Kang K.R., Byun S.M., Kang Y.S.,;

Kim T.W., Kim C.W., Rang K.R., Byun S.M., Kang Y.S.,;

"Blongation factor-2 in chick embryo is phosphorylated on tyrosine as well as serine and threonine."; 4100-406 (1991).

Biochem Biophys. Res. Commun. 175:400-406 (1991).

- I- FUNCTION: THIS PROTEIN PROMEST THE GPP-DEPENNENT TRANSLOCATION OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim C.W., Jung E.J., Ahn H.J., Kim J.C., Kang K.R., Bom M.-O., Kim Y.W., Kang Y.-S.; Wholecular cloning of chicken elongation factor 2 (EF-2): sequence comparison with mammalian EF-2 and its expression in the early developmental stages of the embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 1; Length 572; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7D6EB48F3BA7D95B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
15-GNGation factor 2 (BF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 857 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00390; malic; 1.
PRINTS; PR00072; MALOXRDTASE.
PROSITE; PS00331; MALIC_ENZYMES; 1.
                                                                                                                                                                                                                                                            EMBL, M26594, AAA41563.1, ALT SEQ.
EMBL, M26581, AAA41563.1, JOINED.
EMBL, M26582, AAA41563.1, JOINED.
EMBL, M26583, AAA41563.1, JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M26591; AAA41563.1; JOINED.
EMBL; M26592; AAA41563.1; JOINED.
EMBL; M26593; AAA41563.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL, M26584, AAA41563.1, JOINED.
EMBL, M26585, AAA41563.1, JOINED.
EMBL, M26586, AAA41563.1, JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA41563.1; JOINED.
AAA41563.1; JOINED.
AAA41563.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A37228; DERIMX.
InterPro; IPR001891; Malic_oxred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA41563.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572 AA; 64002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Cells 3:27-33(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: | | ::|::
556 CYSWPEEVQKIQ 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M26587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M26588;
EMBL; M26589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M26590;
```

```
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elongation factor; GTP-binding, Protein biosynthesis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88198187; PubMed=2834376;
Nakanishi T., Kohno K., Ishiura M., Ohashi H., Uchida T.;
"Complete nucleotide sequence and characterization of the 5'-flanking region of mammalian elongation factor 2 gene.";
J. Biol. Chem. 263:6384-6391(1988)
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                         -!- PTM: HIS-714 IS MODIFIED IN DIPHTAMIDE (2-[3-CARBOXYAMIDO-3-(TRIMETHYL-AMMONIO) PROPYL] HISTIDINE). DIPHTAMIDE CAN BE ADPRIBOSYLATED BY DIPHTERIA TOXIN AND BY PSEUDOMONAS EXOTOXIN A (BY
                                                                                                                                                                                SIMILARITY) BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                  -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- PTM: PHOSPHORYLATION BY EF-2 KINASE COMPLETELY INACTIVATES EF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
DIPHTRAMIDE (BY SIMILARITY).
3680187581F518E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 857;
Pred. No. 44;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTP (BY SIMILARITY)
GTP (BY SIMILARITY)
GTP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO0040; BFG C.
InterPro; IPR004161; EFTU D2.
InterPro; IPR000705; EF GTPbind.
InterPro; IPR005255; Small GTP.
Pfam; PP00009; GTP BFTU; 1.
Pfam; PF00679; EFG C; 1.
IGRFAMS; ILGROGA1; small GTP; 1.
TIGRFAMS; ILGROGA1; small GTP; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  682 FOWATKEGVLCEENMRGVR 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U46663; AAA87587.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FOW-----QENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elongation factor 2 (EF-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                         (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P13551; 1FNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EF2 CRIGR
P09445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOUTH THE THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT THE TENT TO THE TENT THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is no new modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; Prove.,
Pram; Pro144; GTP_BFTU_LL,
PRINTS; PRO315; ELONGATNFCT.
TIGREAMS; TIGRO0231; small GTP; 1.
TIGREAMS; TIGRO0231; small GTP; 1.
ELONGATION: GTP-binding; Protein biosynthesis; Phosphorylation.
INIT_MET 0 BY SIMILARITY.
NP BIND 25 32 GTP (BY SIMILARITY).
-- TINN 103 107 GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
-- TINN 103 TO GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
PTM: PHOSPHORYLATION BY ZEP-2 KINASE COMPLETBLY INACTIVATES EF-2. PTM: HIS-714 IS MODIFIED IN DIPHTAMIDE (2-[3-GARBOXYAMIDO-3-FTKIMETHYL-AMMONIO) PROPYL] HISTORINE). DIPHTAMIDE CAN BE ADPRIBOSYLATED BY DIPHTEMIA TOXIN AND EVERDIOMONAS EXOTOXIN A. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.5%; Score 38; DB 1; Length 857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95264 MW; DCE0A55CFBCB8886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: February 21, 2003, 07:28:00 Job time : 5.6 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P1351; IFNM.
INTERPRO; IRROOG640; EFG C.
INTERPRO; IPROO04161; EFTÜ D2.
INTERPRO; IPRO00795; EF GTPbind.
INTERPRO; IPRO5225; Small GTP.
Pfam; PPO0009; GTP_EFTU; 1.
Pfam; PPO0679; EFG C; 1.
Pfam; PPO03144; GTP_EFTU D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J03200; AAA50386.1; -. PIR; A28660; A28660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 682 FOWATKEGALCEENMRGVR 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 FOW------QENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                           EF-G/EF-2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      857 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
```

Sequence:

Run on:

Searched:

Maximum

Database

Q9vil8 drosophila Q9xz30 drosophila Q8sct3 pseudomonas

Q97ti8 Clostridium Q96m21 homo sapien Q9swe2 ralstonia s Q9swb4 streptomyce P7972 brachydanio Q9vbk9 drosophila Q9nzw0 homo sapien Q9nzw3 homo sapien Q91sy homo sapien Q91sy homo sapien Q94991 oryza sativ Q94991 homo sapien

Q8u788 agrobacteri

Q9xvdl caenorhabdi Q9bnx0 unidentifie O9bnw0 peripatus s O9bnw7 scolopendra

2945t7 hordeum vul Q9bme7 aedes aegyp Q95p39 aedes aegyp Q8t4s0 aedes aegyp Q8f4r9 aedes aegyp Q9m7s9 oryza sativ Q8mvm1 triticum ae

```
Q8TCD2;
01-UTN-2002 (TTEMBLrel. 21, Created)
01-UTN-2002 (TTEMBLrel. 21, Last sequence update)
01-UTN-2002 (TTEMBLrel. 21, Last annotation update)
11-Cotoransferrin.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY_2000 (TrEMBLrel. 13, Created)
01-MAY_2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61, DB 4; Length 711; Pred. No. 0.0091; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022447, AAH22347.1; SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 AA.
                                                                                                                                                                                                                                                                                           711 AA
                                                                                                                                                                                                                                                   ALIGNMENTS
                QBSCT3
O97TI8
                                      QBXSE2
Q9EWB1
Q9EWB4
                                                              P79722
Q9VBK9
Q960C1
                                                                                                                    Q949E1
094937
Q8U788
Q9XVD1
Q9BNX0
Q9BNW0
                                                                                                                                                                           Q945T7
Q9BME7
Q95P39
                                                                                                                                                                                                                  Q9M7A9
Q8VWN1
                                                                                    Q9NZW0
Q9NZW3
Q38115
                                                                                                                                                                                                  Q8T4S0
Q8T4R9
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                             Q96RS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                               Q96M21
                       16
                                                                                                                    10
                                                                                                                             Match 85.9%;
Local Similarity 90.9%;
Les 10; Conservative (
                                                                                                     σ
                                                                                                                                                                                   വവ
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
1 CFQWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFOWORNMRKV 49
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
54.9
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PROSTATE;
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UCYS
                                                                                                                                                                                                                                                                                          Q8TCD2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
                                                                                                                                                                                                                                                                          RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
Q9UCY5
                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0906612 arabidopsis
090863 human immun
090863 human immun
0937780 caenorhabdi
0901265 mus musculu
091275 mus musculu
091275 sus musculu
082462 salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oaplen
vynx36 homo sapien
084824 chlamydia t
012124 sarrham
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8tcd2 homo sapien
Q9ucy5 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29nus2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ucy5 homo sapier
Q9tr80 ovis aries
                                                             (without alignments)
118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                    February 21, 2003, 07:25:55; Search time 20.8 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08tax2
09nx36
                                                                                                                                                           671580
      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                        Potal number of hits satisfying chosen parameters:
                                                                                                                                         671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q93780
Q9DAZ8
Q91ZD5
Q91Z75
Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9C6N2
090863
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8TCD2
Q9UCY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9V346
Q8TAX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   084824
                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q12124
Q9NUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29NX36
                                                                                                                                                                                                                                                                                                                                               unclassified:*
                                                                                                                                                                                                                                                       sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                      sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                      Bp_rvirus:*
Bp_bacteriap:*
                                                                                                                                                                                                                                                                                               organelle:*
                                                                                                                                                                        seq length: 0
seq length: 200000000
                                                                                US-09-743-107B-85
                                                                                                                                                                                                                                      sp_archea:*
sp_bacteria:*
                                                                                                   1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                       sp archeap:*
                                                                                                                                                                                                                                                                                sp_mammal:*
sp_mhc:*
sp_organelle:
                                                                                                                                                                                                                                                                                                                       sp_rodent:*
                                                                                                                                                                                                                                                                                                                sp plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                sp virus:*
                                                                                                                                                                                                                                 21:*
                                                                                                                                                                                                                                                                                                      sp_phage: *
                                                                                                                                                                                                                                 SPIREMBL
                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11444110
                                                                                  Title:
Perfect score:
                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein
                                                                                                                                                                        Minimum DB
Maximum DB
```

ö

Gaps

0;

42969976474

Result No.

```
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein gp120 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                   Nature 408:816-820(2000).
EMBL; AC079280; AAG50577.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel, 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 58.3
es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CFTWEEYARHVR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 EWKENLRKV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NJS182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TER TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ghana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 093780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q93780
ID Q9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                   Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 33;
                                                                                                                                                                                                                                                                                   Score 57; DB 4; Length 38;
Pred. No. 0.0021;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                InterPro, IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M., Biochim. Biophys. Acta 1243:25-32(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.4%; Score 50; DB 6; 63.6%; Pred. No. 0.035; ative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                       seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; IBKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE-21016719; Pubmed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=95127729; PubMed=7827104;
                                                         SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, 077698; 1CE2.
InterPro; 1PR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Lat
01-JUN-2001 (TrEMBLrel. 17, Lat
Hypothetical 33.3 kba protein.
                                                                                                                                                                                                                                                                                   80.3%;
90.9%;
                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                               2 FQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                       21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9TR80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29C6N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9C6N2
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TREATED STATES OF THE STATES O
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chaefi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chae B., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Con L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

And J. L., Jenkins J., Hass B., Hansen N.F., Hughes B., Fulii C.Y.,

And Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Knaykin E.,

And Gill J.E., Achkins J., Johnson-Hopson C., Khan S., Knaykin E.,

And C.J., Xco H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

And Langin-Hooper S., Lee J.M., Leus G.A., Li J.H., Li Y.-P.,

And J. Liu S.X., Liu Z.A., Lucse J.S., Maiti R., Marziali A.,

Milischer J., Miranda M., Nguyen M., Rooney T., Rowley D.,

Pat G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Utterback T., Van Aken S., Vaysberkaia V.S., Walker M.,

" "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brandful J.A.M., Ampofo W.K., Janssens W., Adu-Sarkodie Y., Apeagyei F., Anyomi F., Aidoo S., Barnor J.S., Yamamoto N., Ishikawa K., Sata T., Kurata T.; "Genetic and phylogenetic analysis of HIV-1 strains from Southern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.2%; Score 42; DB 10; Length 289; 58.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 15; Length 81; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; 4.228659; CAA.12841.1; -. InterPro; IRN00777; GP120. Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 289 Aa; 33338 MW; 753AA27BED0F840C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 AA; 9138 MW; 2D43DCD554295572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
```

us-09-743-107b-85.rspt

m

Page

.; 0

Gaps

.; 0

F53H4.4

```
STRAIN=CS7BL/67; TISSUE=PLACENTA; Deussing J., Kouadio M., Rehman S., Werber I., Schwinde A., Peters C.; "Identification and Characterization of a Dense Cluster of Placenta-specific Cysteine Peptidases and Related Genes on Mouse Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                               57.7%; Score 41; DB 11; Length 332; 55.6%; Pred. No. 19; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.7%; Score 41; DB 11; Length 332; ilarity 55.6%; Pred. No. 19; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
MGD; MGI:1916256; 1600000123Rik.
InterPro; IPR000668; Peptidase Cl.
InterPro; IPR000169; SHProt_acsite.
Pfam; PR00112; Peptidase Cl. 1.
PRINTS; PR00705; PAPAIN.
ProDom; PD000158; Peptidase Cl; 1.
PROSITE; PS00639; THIOL, PROTEASE HIS; UNKNOWN 1.
SEQUENCE 332 AA; 37298 MW; 0804FIBASH6538E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 332 CATHEPSIN-3.
332 AA; 37326 MW; 4184B90725B41C0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMEL AYO3474, AAK58450.1;

MGD; MGI:2151929; Cts3.

InterPro; IPR000668; Peptidase_C1.

InterPro; IPR00169; SHProt_acsite.

Pfan; PF00112; Peptidase_C1; 1.

ProDom; PD000158; Peptidase_C1; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cathepsin-3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     4 WOENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                     52 WEENMKKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|||:|::
52 WEENMKKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 WOENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cathepsin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91ZD5
Q91ZD5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91Z75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91275
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291275
          88888888888
                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OC OC OE DIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE TISSUE=PLACENTA;

MAISTINE=21085660, DubMed=11217851;

A Azawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kuehl P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

B Brownstein M.J., Bult C., Fletcher C., Fullita M., Marcholi M.,

B Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

K. Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sako K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Dan Marcholiani V., Weitz C., Whittaker C., Wilming L.,

Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Dan Marcholiani V., Weitz C., Whittaker C., Wilming L.,

Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Dan Marcholiani V., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Dan Marcholiani V., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                     Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
EMBL; Z81089; CAB03131.1; -. SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.7%; Score 41; DB 5; Length 275; 63.6%; Pred. No. 15; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
               01-FEB-1997 (TrEMBLrel. 02, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-UNN-2001 (TrEMBLrel. 17, Created) 01-UUN-2001 (TrEMBLrel. 17, Last seqn 01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK005389; BAB23995.1; -.
HSSP; P07711; 1CJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001)
                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1600000123Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||::||| |
262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FOWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C01.053; -
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=10090;
                                                                                              F53H4.4 protein.
                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1600000123RIK.
                                                                                                                                                                                                                                                                                                   Dobson R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

Q9DAZ8; Q9DAZ8

RESULT 7 Q9DAZ8

Matches

ð

ö

Gaps

·,

```
563 CFSWGENROOAR 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE_1534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella
enterica servorar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Profeobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 16; Length 511; Pred. No. 30;
                                                                                                                                                    57.7%; Score 41; DB 11; Length 333; 55.6%; Pred. No. 19; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                  PEQUENCE FROM N.T. SUB-SPLEEN,
Rehman S., Peters C., Deussing J.;
Rehman S., Peters C., Deussing J.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, ANG57446; AAL15416.1;
InterPro; IPR000668; Peptidase Cl.
InterPro; IPR000668; Peptidase Cl.
Prom, PR00112; Peptidase Cl; 1.
Propon; PD000158; Peptidase Cl; 1.
PROSITE; PS00639; THICL PROTEASE HIS; UNKNOWN 1.
SEQUENCE 333 AA, 37388 MM; 6DD0BEB91C033110 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AL627276; CAD06049.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last senotation update)
Hypothetical protein STX3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.7%; SCorr No. 30, 58.3%; Pred. No. 30, ... o; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2348 AA.
                                                                                                                                                                                                                                                                                    511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG8723 protein.
CG11198 OR CG8723.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWDENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:848-852
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
            SEQUENCE FROM N.A.
                                                                                                                                                                                                     4 WOENMRKVR 12
                                                                                                                                                                                                                          52 WEENMKKIK 60
                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9V346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9V346
                                                                                                                                                                                                                                                                                     Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
099346
1D 09934
AC 09934
DT 01-MA
DT 01-MA
DT 01-MA
DF CG111
OS DFOSIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ДQ
  ò
                                                                                                                                                                                                                                                                                       ð
```

```
RATAIN=EBRREAL STATE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2348 AA; 263722 MW; ED7E6FB9976E1CD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.7%; Score 41; DB 5; I
50.0%; Pred. No. 1.5e+02;
tive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro, IPR001882; Biotin attach.
Interpro; IPR000089; Biotin lipoyl.
Interpro; IPR000020; Carboxyl_trans.
Interpro; IPR000901; CPSase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00364; biotin lipoyl; 1.
Pfam; PF01039; Carboxyl trans; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF02786; CPSame L D2; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00866; CPSASE 1; 1.
PROSITE; PS00867; CPSASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 50.0
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQENMRKVR 12
                                                                                                                                                                                                 SECUENCE FROM N.A
                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biotin.
SEQUENCE
```

RESULT 12 Q8TAX2

```
STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 70.0%; Pred. No. 35; 7; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ALPHA S288C;
Andre B., Vissers S., Urrestarazu L.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z74053; CAA98561.1; -.
EMBL; Z48008; CAA88056.1; -.
EMBL; Z48008; CAA88056.1; -.
EMBL; ZA60312; CAA88056.1; -.
SEMBL; Z46432; CAA88056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urrestarazu L.A., Andre B., Vissers S.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murphy L., Richards C., Gentles S., Harris D.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrell B., Rajandream M.A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 AA; 44266 MW; 45B208AE61714A5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UVN-2002 (TrEMBLrel. 21, Last annotation update)
Chromosome IV reading frame ORF YDL005C.
MED2 OR D2930 OR YDL005C.
TYRP 1 OR CT817.
Chlamydia trachomatis.
Bacteria, Chlamydiales; Chlamydia.
WCBL_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis.";
Science 282:794-758(1998).
EMBL, AE00134; AAC68414.2;
InterPro; IPR002422; AA/rel prmease2.
InterPro; IPR00201; ArAA permease.
Fram; PF03222; Trp Tyr perm; 1.
PRINTS; PR00166; AROAAPRWEASE.
TIGREAMS; TIGR00837; araaP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 FOWDEKKRKV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FOWDENMRKV 11
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=AB972;
                                                                                                                                                                                                                                                                                                                                                                                                    Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID 012124

DT 01-NOV-1

DT 01-NOV-1

DT 01-NOV-1

DT 01-NOV-1

DE Chromoso

GN MED2 OR

OC EURARYOL

RA BERGUENCE

RA BURDS;

RA SEQUENCE

RA MURDAY J

RA SEQUENCE

RA SEQUENCE

RA SECUENCE

RA SECUENCE

RA BURDAY J

RA SECUENCE

RA BURDAY J

RA BURDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           012124
   DE RELEASE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natenabe K., Kumagai A., Itakura S., Yamazaki M., Taehiro H., Ota T., Suzubabe K., Kumagai A., Itakura S., Yamazaki M., Taehiro H., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO00468; BAA91185.1; -
InterPro; IPR001623; DnaJ.N.
FFam; PR00225; DnaJ.1.
SWRRT; SM00271; DnaJ. 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS50076; DNAJ 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.3%; Score 40; DB 4; Length 306; 55.6%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.3%; Score 40; DB 4; Length 326; 63.6%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025708; AAH25708.1; -..
Hypothetical protein.
SECUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                          01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ11175.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                  306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA FLJ20461 fis, clone KAT06105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.0
---- 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 CEQFQENIRKL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 CPOWESTLR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWDENMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       084824
084824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NX36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NX36
                                                                                          Q8TAX2
```

RESULT 13 9 EXN60

δ d RESULT 14

g

084824

0

.. 0

```
ö
                                                                                                                                 0; Gaps
                                                                       Query Match 56.3%; Score 40; DB 3; Length 431; Best Local Similarity 100.0%; Pred. No. 38; Matches 8; Conservative 0; Mismatches 0; Indels
KW Hypothetical protein.
SQ SEQUENCE 431 AA; 47717 MW; D3B0992B1F1A4892 CRC64;
```

Oy 5 QENWRKVR 12 |||||||| Db 122 QENWRKVR 129

Search completed: February 21, 2003, 07:44:39 Job time : 21.8 secs

```
lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lactoferrin
lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin
                                                                                                February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SIDS2/gcgdata/geneseq/genesegp-emb/AA1990.DAT:*
| SIDS2/gcgdata/geneseq/genesegp-emb/AA1991.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1991.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1993.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1993.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1995.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1995.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1995.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1997.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1999.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1999.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | SIDS2/gcgdata/geneseqy_embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1988.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1988.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1988.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1988.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1989.DAT:*
| SIDS2/gcgdata/geneseqy_embl/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT:*
|SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*
|SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                 908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78046
AAY78047
AAY78037
AAY78048
AAY78049
AAY78036
AAY78050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78038
                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_101002:*
.:_/SIDS2/gcgdata/
                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                      US-09-743-107B-86
70
                                                                                                                                                                                                       1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221122112212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
65
65
65
65
65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                       Sequence:
                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109876490
```

Peptide for anti-u Human lactoferrin Human lactoferrin Human lactoferrin Human lactoferrin Human lactoferrin	44444	10 H -H 10	Lactoferrin derive Lactoferrin derive Bovine lactoferrin Anti-parasitic lac Anti-parasitic lac Peptide for anti-u Lactoferrin-derive Lactoferrin-derive	1 1 11 11
AAR98554 AAY78035 AAY78062 AAY78031 AAY78064 AAY78064	моном	AAY6867 AAR21810 AAR4841 AAR48530 AAR48531	AARS7461 AARS7462 AAR84698 AAR80699 AAR80263 AAR80264 AAR98553 AAR91852	AAR90607 AAR87621 AAN26150 AAN14036 AAN14036 AAN70310
21 21 21 21 21 21 21 21	21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 22 21 21	21 13 15 15 15	112 116 117 117	113 113 113 113
112 112 116 116	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	000000000000000000000000000000000000000	000000000000000000000000000000000000000	0000000
99999999	0000000	9,9,9,9,9,9	a a a a a a a a a a a a a a a a a a a a	0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0	, 60 50 50 50 50 50 50 50 50 50 50 50 50 50	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 6 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
11 11 11 11 11 11 11 11 11 11 11 11 11	18 19 22 23	4.0.0000 4.0.0000	и и и и и и и и и и и и и и и и и и и	W 女 母 母 母 母 女 Ø O H Cl Cl d tD

#### ALIGNMENTS

```
Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                        Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                 Human lactoferrin derived peptide SEQ ID NO:86.
                   AAY78086 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                        98SE-0002441,
98SE-0002562,
98SE-0004614.
                                                                                                                                                                                                                                     99WO-SE01230.
                                                             (first entry)
                                                                                                                                                                                                                                                                                                   (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                                                                                                                          WO200001730-A1
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                                                                                                   17-JUL-1998;
29-DEC-1998;
                                                             25-APR-2000
                                                                                                                                                                                                               13-JAN-2000.
                                                                                                                                                                     Synthetic.
                                         AAY78086;
        RESULT 1
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
AAY78038
AC AAY7
XX AAY7
XX BE Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX BOCO
OS HOMO
OS Synt
XX BOCO
OS Synt
XX BOCO
DY BR OCO
D
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ö AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative. Gaps Even though native human lactoferrin have been shown to have desired 0; New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food 100.0%; Score 70; DB 21; Length 12; 100.0%; Pred. No. 2.6e-05; ive 0; Mismatches 0; Indels Dolphin GT; Human lactoferrin derived peptide SEQ ID NO:38. Mattsby-Baltzer I, Baltzer L, AAY78038 standard; Peptide; 12 AA. Claim 22; Page 36; 102pp; English 98SE-0002441. 98SE-0002562. 98SE-0004614. 99WO-SE01230. 25-APR-2000 (first entry) (ASCI-) A+ SCI INVEST AB. Query Match 100. Best Local Similarity 100. Matches 12; Conservative 1 CFOWOREMRKVR 12 1 CFÓWÓREMRKVR 12 WPI; 2000-147388/13. 12 AA; WO200001730-A1. sapiens. 06-JUL-1999; 06-JUL-1998; 17-JUL-1998; 29-DEC-1998; 13-JAN-2000 Hanson LA, Synthetic

```
..
0
binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                           92.9%; Score 65; DB 21; Length 12
91.7%; Pred. No. 0.00018;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78046 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                 Local Similarity 91.7
ses 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                               12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78046;
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
             8
```

ô

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and Candida infections (such as uninary tract infections and/or trumours. The peptides can also be used membrane), inflammations and/or tumours. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as an an an inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would contain the them to be used for the same purposes as lactoferrin at lower
fungicidal and bactericidal and may also be used as preservatives. 
Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                               ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                          Length 12;
                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baltzer L, Dolphin GT;
                                                                                                                                                                                        Score 65; DB 21;
Pred. No. 0.00018;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                              AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 73; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                        92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000 (first entry)
                                                                                                                                                                                      Query Match 92.9
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                              1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                    1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-147388/13.
                                                                                                                                                   12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L7-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78047;
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                          88888888
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the direculation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                 Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                               Score 65; DB 21; Length 12; Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.9%; Score 65; DB 21; Length 13; Best Local Similarity 91.7%; Pred. No. 0.0002; Matches 11; Conservative 0; Mismatches 1; Indels
                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dolphin GT;
                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:37.
                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                   AAY78037 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 70; 102pp; English.
                               92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                        bactericidal; preservative.
                                                                                                                                                                                                                                                                                    (first entry)
                                             Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB.
                                                                                                1 CFOWOREMRKVR 12
                                                                                                                                1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36-JUL-1999;
                                                                                                                                                                                                                                                                                      25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Sequence
                                                                                                                                                                                                                                                    AAY78037;
                                 Query Match
                                                                                                                                                                                 RESULT 5
                                                                                                  à
```

à q (first entry)

```
AAY78049 standard; Peptide; 13 AA.
                                              25-APR-2000
                       AAY78049;
 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or prevention of infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also be used in though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                        food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 21; Length 13;
Pred. No. 0.0002;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 74; 102pp; English.
                                                                               AAY78048 standard; Peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%;
                                                                                                                                                                                                                                                                                                                                                          98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                               98SE-0002441.
                                                                                                                                                                                                                                                                                                                        99WO-SE01230.
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB.
 12
                     2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-147388/13.
 CFOWOREMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AA;
                                                                                                                                                                                                                                                                          WO200001730-A1.
                                                                                                                              25-APR-2000
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                      29-DEC-1998;
                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                            17-JUL-1998;
                                                                                                                                                                                                                                                                                                 13-JAN-2000
                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                        AAY78048;
```

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                 Human, lactoferrin, modification, infection, inflammation; tumour, food, infant formula, anti-inflammatory; anti-microbial, anti-tumour, urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.9%; Score 65; DB 21; Length 13; 91.7%; Pred. No. 0.0002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lactoferrin derived peptide SEQ ID NO:36.
Human lactoferrin derived peptide SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78036 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AA;
                                                                                                                                                                                                                                                                                                    WO200001730-A1.
                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2000.
                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXHXXX
```

ó

Gaps

; 0

CFOWOREMRKVR 12 CFOWORNMRKVR 13

н 0

ð

RESULT 7

98SE-0002441. 98SE-0004614. 98SE-0002562.

(ASCI-) A+ SCI INVEST AB

99WO-SE01230.

36-JUL-1999; 06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

13-JAN-2000

WO200001730-A1

Synthetic.

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired
            Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                              Baltzer L, Dolphin GT
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                            Mattsby-Baltzer I,
                                                                                                                                                                                                                                                98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                 98SE-0002441.
                                                                                                                                                                                                    99WO-SE01230.
                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-147388/13.
                                                                                                                                      WO200001730-A1.
                                                                                                                                                                                                                                 06-JUL-1998;
                                                                                                                                                                                                                                                17-JUL-1998;
29-DEC-1998;
                                                                                          Homo sapiens
                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                     13-JAN-2000
                                                                                                                                                                                                                                                                                                                            Hanson LA,
                                                                                                       Synthetic.
```

anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower Gaps ; 0 92.9%; Score 65; DB 21; Length 14; 91.7%; Pred. No. 0.00021; live 0; Mismatches 1; Indels Query Match Best Local Similarity 14 AA; Seguence

11; Conservative 1 CFOWOREMRKVR 12 3 CFOWORNMRKVR 14 Matches g à

ö

AAY78050 standard; Peptide; 14 AA. 25-APR-2000 (first entry) AAY78050; RESULT 9 **AAY78050** 

Human, lactoferrin, modification, infection, inflammation, tumour; food, infant formula, anti-inflammatory; anti-microbial, anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

06-JUL-1999; 99WO-SE01230.

WO200001730-A1.

13-JAN-2000.

bactericidal; preservative

Homo sapiens

Synthetic

Human lactoferrin derived peptide SEQ ID NO:50. Homo sapiens 

```
;0
                                                                                                                                                                                                                                                                                                                                                                           AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.9%; Score 65; DB 21; Length 14; 91.7%; Pred. No. 0.00021; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                                                                                                                                                Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CFOWORNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78051
à
```

```
15 AA;
                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                               AAY78035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                       Sequence
                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                               AAY78035
                                                                                                                                                                                                          q
X2222X8
                                                                                                                           ò
                                                                                                                                                                              AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 21; Length 14; Pred. No. 0.00021; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                             Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - has low toxicity, is
                                                                             Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                           Claim 18; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MORG ) MORINAGA MILK IND CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-ulcer agent contg. peptide -
heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 11; 11pp; Japanese
                                                                             Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                         92.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide for anti-ulcer agent,
                    98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94JP-0283869.
          98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                       (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CFOWORNMRKVR 14
                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-318857/32
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     14 AA;
                     17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP08143468-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-1994;
         06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-1996.
                                                                             Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR98554;
                                                                                                                                                                                                                                                                                                                                                cost.
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
AAR98554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
   The agent is low oln.. It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
AAR98531-54 are peptides used in an anti-ulcer agent. The a in toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                                                                                                                                           Length 15;
                                                                                                                                                                                                                    Score 65; DB 17; Length 15
Pred. No. 0.00023;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                    ch 92.9%;
1 Similarity 91.7%;
11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-SE01230,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CFOWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13.
                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                      15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200001730-A1.
```

Human lactoferrin derived peptide SEQ ID NO:63.

(first entry)

25-APR-2000

AAY78063;

AAY78063 standard; Peptide; 15 AA.

RESULT 14 AAY78063

```
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                          Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula; anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                   Gaps
                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 21; Length 15;
Pred. No. 0.00023;
0; Mismatches 1; Indels
   DB 21; Length 15;
Score 65; DB 21; Length 15
Pred. No. 0.00023;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dolphin GT,
                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 81; 102pp; English.
                                                                                                                                                                    AAY78062 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mattsby-Baltzer I,
 92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-SE01230
                                                                                                                                                                                                                                                                                                                                          bactericidal; preservative.
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
                                Conservative
                                                           1 CPOWOREMRKVR 12
                                                                                        4 CPOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-147388/13.
              Local Similarity
ses 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                   25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                    AAY78062;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                           Matches
                                                                                                                                     RESULT 13
                                                                                                                                                       AAY78062
```

```
٥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                             Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.9%; Score 65; DB 21; Length 15; 91.7%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78031 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                              99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                              98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                             98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                98SE-0002562
                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CPÓWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                                                                                                                           WO200001730-A1.
                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                              06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                             29-DEC-1998;
                                                                                                                                                                                                                                                                              L3 - JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanson LA,
                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
AAY78031
ID AAY78
XX
AC AAY78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cost.
```

0;

Gaps

.; 0

0; Mismatches

11; Conservative

Best Local Similarity

Matches

CFQWQREMRKVR 12 4 CFOWORNMRKVR 15

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food study native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                 Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                  Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 68; 102pp; English.
                 25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-147388/13.
                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                      06-JUL-1998;
                                                                                                                                                                                                                                                                            13-JAN-2000.
                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
```

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

Dolphin GT;

ö 0; Gaps Match 92.9%; Score 65; DB 21; Length 16; Local Similarity 91.7%; Pred. No. 0.00024; nes 11; Conservative 0; Mismatches 1; Indels 16 AA; Query Match Best Loca Matches ð

g

Search completed: February 21, 2003, 07:37:15 Job time : 28.35 secs

~~~~~~~~~~~~~~~

```
FEATURE:
NAME KEY: Peptide
LOCALION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 24, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                       February 21, 2003, 07:25:59; Search time 8.65 Seconds (without alignments) 40.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3
Sequence 5
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Bequence Bequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-204-487-3

US-08-465-948-8

US-08-465-968-8

US-08-66-8-8

US-08-755-161A-3

US-08-256-771-24

US-08-256-771-24

US-08-281-984-24

US-08-381-984-25

US-08-381-984-25

US-08-381-1984-24

US-08-381-184-24

US-08-381-184-10

US-09-508-734-4

US-07-755-161A-10

US-07-755-161A-8

US-09-508-734-8

US-09-808-734-8

US-09-808-734-8

US-08-81-174-8

US-08-81-174-8

US-08-81-174-8

US-08-81-182A-6
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-464-182A-5
US-08-406-271-5
                                                                                                                                                                                                                 262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
                                                                                                                         US-09-743-107B-86
70
1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                  Searched:
                                                                           Run on:
```

```
Sequence 8, Application US/08628380 Patent No. 5891341 GENERAL INFORMATION:
                                                                                                                                                                                                                                          ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide DESCRIPTION: LF-C1, 8-25 HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                 New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO FRAGMENT TYPE: US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                    07601
                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                           US-08-628-380-8
                                                                                                                                                                                                                                                                              CITY: I
                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                              Gaps
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: YOUR MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
ITILE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%; Score 65; DB 2; Length 18; 91.7%; Pred. No. 9.9e-05; Azive 0; Mismatches 1; Indels
                                                         Length 18;
                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                     Score 65; DB 1; I
Pred. No. 9.9e-05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: UNNE 7, 1995
FILING DATE: APRLI 7, 1995
CLASSIFICATION NUMBER: 08/418,642
FILING DATE: APRLI 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentry Doles
                                                                                                                                                                                                                                                         Sequence 8, Application US/08485948
Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 Hackensack Avenue
OTHER INFORMATION: (20-37)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                     Query Match 92.9%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQREMRKVR 12
                                                                                                                              1 CFQWQREMRKVR 12
                                                                                                                                                                 1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-485-948-8
                                                                                                                                                                                                                     RESULT 2
US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
       ;
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                           g
```

1 CFOWORNMRKVR 12

```
.;
0
APPLICANT: LI, YONG MING
APPLICANT: MASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NOMBER OF SEQUENCES:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-08475-055-8
Squence 8, Application US/08475055
Patent No. 5962245
SPELICAT: VOR MING LI
APPLICANT: WOR MING LI
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: BADPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/628,380
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U$ 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: JGCKGON EGG, David A.
REGISTRATION NUMBER: 26,742
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1875-580
```

```
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: modified site
LOCATION: 2
LOCATION: 2
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.9%; Score 65; DB 1; Length 20;
SUFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION UNUMBER: 33,367
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 38 SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: AMINO ACID STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified site LOCATION: 19 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                          TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoch, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                              APLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY FAGNI INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ENGINE SEG. ID NO: 8:
SUBJUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-755-161A-3; Sequence 3, Application US/07755161A; Patent No. 5304633
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JARAN--
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE: internal US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                  07601
                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
```

```
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: O'S residue at location 19 connected by disulfide bond with
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
                     IDENTIFICATION METHOD:
OTHER INFORMATION: / hote= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: YAMAMOTO, NAOKI
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATRAU
APPLICANT: TANAKA, SHICERAL
APPLICANT: TANAKA, SHICERAL
APPLICANT: TANAKA, YOSHIMINO
APPLICANT: UNTHIDA, TOSHIMINO
APPLICANT: UNTHIDA, TOSHIMINO
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.9%; Score 65; DB 1; Length 20; 91.7%; Pred. No. 0.00011; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
                                                                                                                                     NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION: AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02109
                                                                                                                                                                                                                                                                                                                            TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                    VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                          .;
0
Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                   Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDRESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                  1 CFOWOREMRKVR 12
                                                                                                             2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 805 Fifte
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                             RESULT 6
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN:
                                                                  ð
```

; 0

US-08-256-771-24

```
ò
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/08256771

Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                     ch 92.9%; Score 65; DB 1; Length 20; 1 Similarity 91.7%; Pred. No. 0.00011; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                     LOCATION: 1.20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 805 Fifteenth Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: Us/22, 1994
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
TYPE: amino acid
                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                         MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                  NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                       2 CFOWORNMRKVR 13
                                                                                                                        linear
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                               US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                US-08-256-771-25

Sequence 25, Application US/08256771

Patent No. 556591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENITON: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENITON: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fiteenth Street, N.W., #700
CITY: Mashington
                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
// OTHER INFORMATION: /note= "Cys residues are protected to OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25
92.9%; Score 65; DB 1; Length 20; ilarity 91.7%; Pred. No. 0.00011; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.9%; Score 65; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IDEN COMPATIBLE
OWNEYTER: THE COMPATIBLE
OFFRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: JULY 22, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILIND DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                     1 CFOWOREMRKVR 12
                                                                                                                                 2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CFOWORNMRKVR 13
Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: W
STATE:
                                                                                                                                                                                             RESULT 9
                                                                                                                             Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

RESULT 10 US-08-381-984-24

```
Sequence 4, Application US/09508734

Sequence 4, Application US/09508734

Patent No. 6425509

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL PROPERTION:
TITLE OF INVENTION:
MASS production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION:
USeful microorganism thereof
CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT PILING DATE: 2000-06-01

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /note= "cysteine residues at positions 2 OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.9%; Score 65; DB 1; Length 20; 91.7%; Pred. No. 0.00011; tive 0; Mismatches 1; Indels
                                                                                                                        MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/381,984 FILING DATE: April 11, 1995 CLASSIFICATION: 25.2 PRIOR APPLICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER:
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET UNMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide FEATURE:
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserva
                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                         20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-508-734-4
                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 1; Length 20; Pred. No. 0.00011; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WACADEFICAT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984 FILING DATE: April 11, 1995 CLASSIFCATION: 252 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                              ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CARRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-381-984-25; Sequence 25, Application US/08381984; Patent No. 5804555
       Sequence 24, Application US/08381984
                         Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: MAMOO'L TOMITA et al.
TILE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relecommunication information: Telephone: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                           STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
```

ö

```
INCRATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thicl group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thicl group of Cys residue at location 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "thiol group of Cys residue at location 4 connected by disulfide bond with thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.9%; Score 65; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 0.00014; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
FILING DATE:
PRELICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                     ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek Jr.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified site
LOCATION; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 4
LOCATION: 4
LDENTIFICATION METHOD:
OTHER INFORMATION: Cya
OTHER INFORMATION: Lhio
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION: AUTHORS:
                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
AVPOTHETICAL:
ANTI-SENS:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-755-161A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                          RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: WASS production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: UNBER: US/09/508,734
; CURRENT FILING DATE: 1999-07-14
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NUMBER: KR1998-29351
; SOFTWARE: KOPATENTION: 171
; SEQ ID NO 6
; LENGTH: 24
                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                           0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                 Score 65; DB 4; Length 22;
Pred. No. 0.00012;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-07-755-161A-10
is Sequence 10, Application US/07755161A
Fatent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITILE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPEDUBNCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: Washington
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65; DB 4; I
Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CODNIKA:

COMPOTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb

**MEDIUM TYPE: IBM Compatible

**MEDIUM TYPE: IBM Compatible

**MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/07/755,161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%;
                                                                                            Query Match 92.9%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: DisplayWrite CURRENT APPLICATION DAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1991090 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
              TYPE: PRT
CORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                             1 CFQWQREMRKVR 12
                                                                                                                                                                                                                   2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-508-734-6
LENGTH: 22
                                                                                                                                                                                                                     a
                                                                                                                                                                               δ
```

ô

```
1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                     DOCUMENT NUMBER:
                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                           JOURNAL:
VOLUME:
                                                                                                         TITLE:
                                                                                                                                                                                            PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
US-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: I BM Compatible COMPUTER: I BM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: DisplayWrite CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/891,174 FILING DATE: 29-MAY-1992 CLASSIFICATION: 50-MAY-1992 PROR APPLICATION DATA: APPLICATION NUMBER: US 07/755,161 FILING DATE: 05-SEP-1991 ATTORNEY/AGENT INFORMATION: NAME: WARTEN M. Cheek UT. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                          ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: modified site
LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified site LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITS:
FEATURE:
```

```
DEBUTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of Cys residue at location 1"

OTHER INFORMATION: Cys residue at location 4"

OTHER INFORMATION: thiol group of Cys residue at location 4"

PUBLICATION INFORMATION: thiol group of Cys residue at location 4"

PUBLICATION INFORMATION: thiol group of Cys residue at location 4"

AUTHORS:

AUTHORS:

JOURNAL:

OUGHNET:

PAGES:

PAGES:

PAGES:

PAGES:

PAGES:

PAGES:

POCUMBER:

FILING DATE:

RELEVANT RESIDUES IN SEQ ID NO:

Query Match

Best Local Similarity 91.7%; Pred: No. 0.00014;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A CFOMORBMEKVR 12

Db 4 CFOMORBMEKVR 15

Db 4 CFOMORBMEKVR 15

Search completed: February 21, 2003, 07:50:37

Job time: 8.7 secs
```

```
February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               156504 seqs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                             US-09-743-107B-86
                                                                                                                                                                     1 CFQWQREMRKVR 12
                                                                                                                                                                                                     BLOSUM62
                                                                                                                                                            Perfect score:
                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                          Database:
                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                               Searched:
                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 5715, Appli Sequence 47, Appli Sequence 48879, A Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1340, Ap sequence 20, Applisequence 2, Applisequence 3, Applisequence 3, Applisequence 4, Applisequence 22, Applisequence 22, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 29, Applisequence 29, Applisequence 30, Applis Sequence 2, Appli Description US-09-798-869-20 US-10-023-096-2 US-09-798-869-2 US-09-798-869-23 US-09-798-869-4 US-09-798-869-4 US-09-798-869-8 US-09-798-869-8 US-09-798-869-7 US-09-798-869-2 US-09-798-869-2 US-09-798-869-2 US-09-798-869-2 US-09-798-869-2 US-09-798-869-30 US-09-798-869-30 US-09-798-869-30 US-09-864-761-47985 US-09-864-761-48879 US-09-867-550-1340 US-09-798-869-2 US-09-798-869-20 US-10-051-409-4 US-09-798-869-5 SUMMARIES Query Match Length 992.9 992.9 982.9 982.9 982.9 982.9 982.9 982.9 982.9 982.9 982.9 982.9 Score Result No.

Sequence 20, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON

RESULT 2 US-09-798-869-20

| | gth 15; .
Indels 0; Gaps 0; |
|--|---|
| S-09-904-536-9 S-09-904-536-9 S-09-904-536-13 S-09-904-536-13 S-09-904-536-13 S-09-904-536-14 S-09-904-536-14 S-09-904-536-14 S-09-904-536-16 S-09-904-536-16 S-09-904-536-17 | Score 65; DB 9; Length
Pred. No. 6.6e-05;
0; Mismatches 1; Ind |
| 209 10
209 10
200 10
20 | 92.9%;
91.7%;
ive |
| 35 50.0 209 10 US 36 50.0 209 10 US 37 48.6 269 9 US 34 48.6 269 9 US 35 50.0 360 9 US 36 50.0 205 US 37 48.6 264 10 US 38 10 US 38 10 US 38 10 US 39 48.6 269 9 US 31 48.6 269 9 US 32 48.6 269 9 US 34 48.6 269 9 US 35 50.0 360 9 US 36 50.0 205 US 37 48.6 264 10 US 38 10 US 3 | tch al Similarity 91. 11; Conservative CFOWOREMRKVR 12 CFOWQRAWRKVR 12 |
| 20
21
22
22
23
24
25
26
26
27
28
30
31
31
33
33
34
44
41
42
41
42
43
44
44
45
41
42
42
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
43
44
45
46
47
47
47
47
47
47
47
47
47
47
47
47
47 | Query Match Best Local Matches 1 1 CFQ 3 CFQ |
| S D C C C C C C C C C C C C C C C C C C | रे व |

```
RESULT 5
US-09-798-869-3
                                                                                                                                                                                                         9-698-861-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9-698-862-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Krizel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 9; Length 25; Pred. No. 0.00011; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Jacobson, Price, Holman & Stern
400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
        FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1050-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTERE for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
ITELEPHONE: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
PILING DATE: 30-SEPT-1996
APPLICATION UNMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-023-086-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   92.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
LARS VORLAND
                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
```

```
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens OTHER INFORMATION: sequence)
                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
Score 65; DB 9; Length 694;
Pred. No. 0.0025;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.4%; Score 57; DB 9; Length 15; 83.3%; Pred. No. 0.0014; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 9; Length 15; Pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                           | FULLICATION NO. USZUGJAUZZBZIAI |
| GENERAL INFORMATION: |
| APPLICANT: JOHN SIGGED SVENDSEN |
| APPLICANT: GYSTEIN REKDAL |
| APPLICANT: GYSTEIN REKDAL |
| APPLICANT: BALDUR SVEINBURSON |
| APPLICANT: LARS VORLAND |
| TITLE OF INVENTION: BIOACTIVE PEPTIDES |
| FILE REFERENCE: AJ404-PCT-USA-A |
| CURRENT APPLICATION NUMBER: US/09/798,869 |
| CURRENT PILING DATE: 2001-02-27 |
| PRIOR APPLICATION NUMBER: GB991838.4 |
| PRIOR FILING DATE: 1999-08-28 |
| NUMBER OF SEQ ID NOS: 30 |
| SOFTWARE: FREESEQ for Windows Version 4.0 |
| SEQ ID NO 6 |
| LIBNGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09798869
Fublication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: (VSTEIN RENDAL
APPLICANT: (STEIN RENDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                            ; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.18;
72.78;
  92.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                   1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWOREMRKVR 12
                                                                                                                                                    22 CFÓWORNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFOWOWNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 10, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: CAPRINE
```

Matches

```
Query Match 71.4%; Score 50; DB 9; Length 25; Best Local Similarity 72.7%; Pred. No. 0.032; Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: (YSTEIN REKDAL
APPLICANT: HALDUR SVEINBU (RNSSON
APPLICANT: LARS VORLAND
APPLICANT: LARS VORLAND
TITLE OF INVERTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSESQ FOR Windows Version 4.0
                                                                                                                                   APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE RFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-36
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAESEQ FOR WINGOMS VERSION 4.0
                                                                           Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-798-869-8
Sequence 8, Application US/09798669
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CLRWONEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWOREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CLRWQWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: MURINE
                                     RESULT 8
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨੇ
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 9; Length 25;
Pred. No. 0.007;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.4%; Score 50; DB 9; Length 15; 72.7%; Pred. No. 0.02; ive 1; Mismatches 2; Indels
1; Indels
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gegreence 4, Application US/09798869
Fublication No. US20030022821A1
GENERAL INFORMATION
JAPPLICANT: USTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEOTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SCOTTWARE: 23
LENGTH: 25
                                                                                                                                                                               Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: RYSTEIN REKOAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOWOREMRKV 11
                                     1 CFQWQREMRKV 11
                                                              3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CYÓWORRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWOREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: CAPRINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: MURINE
                                                                                                                                           RESULT 6
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                     ò
                                                                             d
```

ö

```
ô
                                                                                                                                                                                   Gape
                                                                                                                                                                                   ..
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine corner in other information: sequence)
US-09-798-869-8
                                                                                                                  Query Match 67.1%; Score 47; DB 9; Length 15; Best Local Similarity 72.7%; Pred. No. 0.062; Matches 8; Conservative 1; Mismatches 2; Indels
```

```
60.0%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.41; 2; Indels ive 3; Mismatches 2; Indels
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REXDAL
TITLE OF INVENTION: BALDIN SYEINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 30
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5715, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWOREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CFRWQWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-738-626-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-738-626-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens ; OTHER INFORMATION: sequence) US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.7%; Score 46; DB 9; Length 15; 63.6%; Pred. No. 0.091; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.0%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.41; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                             APPLICANT: GAILLY REALAL

APPLICANT: BALDUR SVEINAU

APPLICANT: LARS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 2001-02-27

PRIOR PILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1998-08-38

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FASLSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US/09/798,869
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 30 SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/09798869 Publication No. US20030022821A1
                                                   Sequence 7, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: BOVINE
US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-798-869-29
    RESULT 10
US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 29
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

; 0

Gaps

. 0

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.3%; Score 38; DB 9; Length 86; 45.5%; Pred. No. 9.8; tive 6; Mismatches 0; Indels
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TYCOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: ISEDA, MASATO
APPLICANT: ISEDA, MASATO
APPLICANT: OZAKI, AKIO
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/738;626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
SEQ ID NO 5715
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:::|::|
73 FEYRRQLRKIR 83
```

RESULT 12 US-09-798-869-30

```
SEQ ID NO 47985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/0988320
Fublication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: DeBarber, Andrea E.
APPLICANT: Dekker, Linda-Gail
APPLICANT: Bekker, Linda-Gail
APPLICANT: Bekker, Linda-Gail
APPLICANT: APPLICANT: As represented by The Secretary of the APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Dispartment of Health and Human Services
ITILE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
CURRENT FILING DATE: 2001-06-22
FRIOR FILING DATE: 2000-06-26
FRIOR ENTING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; OGGALISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-8888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.3%; Score 38; DB 9; Length 489; Best Local Similarity 54.5%; Pred. No. 51; Matches 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47985, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 489
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 ĆQKWPRRMRKM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-864-761-47985
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
## PRIOR APPLICATION NUMBER: PCT/USO1/00662
## PRIOR APPLICATION NUMBER: PCT/USO1/00662
## PRIOR PLILING DATE: 2001-01-30
## PRIOR PLILING DATE: 2000-09-21
## PRIOR PPLICATION NUMBER: US 60/234,687
## PRIOR PPLICATION NUMBER: US 60/234,687
## PRIOR PPLILING DATE: 2000-06-30
## PRIOR PPLILING DATE: 2000-06-30
## PRIOR PPLILING DATE: 2001-01-29
## PRIOR PPLING DATE: 2001-01-29
## PRIOR PPLING DATE: 2001-01-30
## PRIOR PPLING DATE: 2001-01-30
## PRIOR PPLING DATE: 2001-01-30
## PRIOR APPLICATION NUMBER: US 09/774,203
## PRIOR PRIOR APPLICATION: PREPRIED PRIOR P
```

0

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

- protein search, using sw model OM protein

Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-86 70 1 CFQWQREMRKVR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | lactotransferrin p | lactoferrin - goat | lactoferrin - shee | lactoferrin precur | dynein beta heavy | Н | \vdash | Н | hypothetical prote | _ | conjugation protei | probable traA prot | hypothetical prote | interleukin-2 rece | transcription regu | cell cycle arrest | protein sam2B - sp | probable monooxyge | probable cytochrom | hypothetical prote | cytochrome P450 ho | malate dehydrogena | malate dehydrogena | methylmalonyl-CoA | probable ATP-depen | protein T21E12.4 [| pyridoxamine 5'-ph | pyridoxamine 5'-ph | probable pyridoxam |
|--------|-------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|----------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| | QI | TFHUL | JC2323 | S52107 | A28438 | T08030 | T22597 | C84325 | T28820 | D81949 | S67085 | AC3154 | G98133 | AH3147 | S07442 | D86713 | A39654 | T09217 | C70655 | T00510 | T24218 | T00513 | DERTMX | S44415 | S04640 | T08316 | D87755 | H97451 | AB2670 | AG3441 |
| | BB : | Н | N | 7 | Н | N | 7 | ~ | 7 | 7 | N | 7 | N | ~ | Н | 7 | М | N | 7 | 7 | ~ | 7 | Н | 7 | 7 | ~ | ~ | 7 | ď | ~ |
| | Length | 711 | 708 | 33 | 707 | 4568 | 275 | 584 | 932 | 57 | 376 | 1266 | 1277 | 121 | 275 | 291 | 306 | 339 | 489 | 515 | 536 | 543 | 572 | 572 | 638 | 979 | 4464 | 206 | 206 | 208 |
| Query | Match | 92.9 | 77.1 | 74.3 | Н | 65.7 | 57.1 | 57.1 | 7 | 55.7 | 55.7 | 55.7 | 55.7 | 54.3 | 54.3 | 4. | 54.3 | 54.3 | 54.3 | 54.3 | 54.3 | 54.3 | 54.3 | 54.3 | ٠. | 54.3 | 54.3 | 52.9 | 52.9 | 52.9 |
| | Score | 65 | 54 | | 50 | | 40 | 40 | 40 | 39 | 39 | 39 | 39 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 37 | 37 | 37 |
| Result | No. | 1 | 61 | n | 4 | Ŋ | φ | 7 | α | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | | | 27 | 28 | 29 |

| 30 37 52.9 213 2 H83682
31 37 52.9 275 1 7C1113
33 37 52.9 289 2 646403
34 37 52.9 289 2 686403
35 36 51.4 142 2 R6353
37 36 51.4 142 2 R6353
37 36 51.4 192 2 AH2221
38 36 51.4 296 2 R7221
40 36 51.4 296 2 R7334
41 36 51.4 298 2 R7334
41 36 51.4 298 2 R7334
42 36 51.4 386 2 R7334
43 51.4 415 2 C71467
44 36 51.4 433 2 T32605
45 51.4 460 2 AB0130 | hypothetical prote | interleukin-2 rece | MHC class I histoc | 33.3K hypothetical | phytochrome C - so | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote | probable dimethyla | hypothetical prote | hypothetical prote | serine/threonine k | probable tyrosine | hypothetical prote | conserved hypothet |
|--|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| 37 52.9 213
37 52.9 284
37 52.9 284
37 52.9 284
37 52.9 1135
36 51.4 142
36 51.4 192
36 51.4 285
36 51.4 285 | H83682 | JC1113 | A45840 | G86403 | T14803 | AG3273 | C83633 | AH2221 | T47734 | G71337 | AD2346 | S76885 | B82921 | C71467 | T32605 | AE0130 |
| 37 52.9
37 52.9
37 52.9
38 511.4
36 511.4
36 511.4
36 511.4
36 511.4
36 511.4
36 511.4
36 511.4
37 511.4 | ~ | ,-1 | 7 | ~ | (1 | 7 | 7 | ~ | N | ~ | ~ | ~ | ~ | 7 | 7 | N |
| | 213 | 275 | 284 | 289 | 1135 | 142 | 144 | 192 | 276 | 285 | 298 | 372 | 386 | 415 | 433 | 460 |
| | 52.9 | 52.9 | 52.9 | 52.9 | 52.9 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 |
| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ | 37 | 37 | 37 | 37 | 37 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 |
| | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 3.7 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

RESULT 1

|
C; Species: Homo sapiens (man) |
|--|
|
C;Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000
C.accesion. Col394. c11228. 245401. c10324. S15851. S20841. S07160. A61169: A31000: S74 |
| |
|
submitted to the EMBL Data Library, March 1994 |
| A) Reference number: G06820 |
| A/Status: preliminary; translated from GB/EMBL/DDBJ |
| A, Molecule type: MRNA |
|
A.Feblatue: 1-/11 C-CHO>
A.Cross-references: EMBL:U07643: NID:0467236: PIDN:AAB60324.1: PID:0467237 |
|
R.Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Fieper, F.R. |
|
Nucleic Acids kes. 18, 5288, 1599
A.Title: Complete nuclectide secuence of human mammary cland lactoferrin. |
|
A; Reference number: S11228; MUID: 90384839; PMID:2402455 |
|
A,Accession: S11228 |
| A Molecule type: mRNA |
|
A;KeBIQUEB: 1-148/.1,120-4-22.7(*),424-/11.5KE1>
A:Grose-references: RMBL:X53961: NID:G34415: PIDD:GA37914.1: PID:G34416 |
|
R.Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T. |
| Mol. Endocrinol. 6, 1969-1981, 1992 |
|
A; Title: Differential molecular mechanism of the estrogen action that regulates lactofer |
|
A.Reference number: A45401; MUID:93125571; PMID:1480183 |
|
A;ACCEBIOL: A43401 |
| A:Residues: 1-15 <ten></ten> |
|
A; Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312 |
|
A;Experimental source: placenta |
|
A, Note: sequence extracted from NCBI backbone (NCBIP:122202) |
| R. Powell, M.J.; Ogden, J. B. |
| NUCCELC ACLUB KEB. 18, 40.15, 1994
A.mitia. Miniachtide economic of binar lastoferrin CDNA |
| A):Reference number: S10224; MUID:90326549; PMID:2344734 |
|
A;Accession: S10324 |
|
A Moderatile type: mRNA
* now: date type: mrna. |
|
A;KESTAUGES: 3-/11 < |
|
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W. |
| Biochem. J. 276, 349-355, 1991 |
| A; Title: Expression of cloned human lactoferrin in baby hamster kidney ceils. |
|
A, Reference number: S15853; MUID:91264786; PMID:2049066
h.acassion: c16863 |
| A:Status mucleic acid sequence not shown: not compared with conceptual translation |
| A; Molecule type: mRNA |
| A,Residues: 20-31 <st1></st1> |
| A; Accession: S20841 |
| A.Molecule Type: protein
A.Residius: 20-28 'X'.30-31 <st2></st2> |
| |

us-09-743-107b-86.rpr

```
74.3%;
                                       77.18;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:J03298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63....
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactoferrin - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 CLRWONEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWOREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFOWOREMRKV 11
                                                                                                                                                                                                          1 CFQWQREMRKV 11
                                                                                                                                                                                                                                                                                             38 CYOWORRMIKEL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 3-707 <PEN>
                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-15 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S52107
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A28438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A41205
                                       Query Match
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
S52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                  à
                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 436-487, 'A', 489-711 <RAD>
A; Cross-references: RMBLAM18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
B; Panella, T.J.; Liu, YI; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin A;Reference number: S74119; MUID:97054624; PMID:8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assignment of the relevant locus
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-933, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR
A;Reference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 3-701,'SWXPVN' <PAN-
A; Experimental source: normal breast tissue
R; Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Bur, J. Blochen. 145, 659-666, 1984
A; Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A; Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A,Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A,Note: this is the final paper in a series
A,Note: this is the final paper in a series
Eur. J. Biochem. 241, 303-308, 1996
A,Title: Lactoferrin: similarity to diamine exidase and purification by aminohexyl affi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Ke^words: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: UC2323
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the re A;Reference number: UC2323; MUID:94380047; PMID:8093048
A;Residues: U-2323
A;Molecule type: mRNA
A;Residues: 1-708 < LEP>
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin repeat homology < TRHES
C;Superfamily: transferrin repeat homology </td>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.9%; Score 65; DB 1; Length 711; 91.7%; Pred. No. 0.002; 1; Indels rative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: duplication; glycoprotein; iron binding; milk F;1-15/Domain: signal sequence #starus predicted <510> F;20-711/Product: lactotransferrin #starus experimental <MAT> F;21-356/Domain: transferrin repeat homology <TRH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 3q21-3q23
C;Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:119368; OMIM:150210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 CFOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S74119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: A31000
                                                                                                                                                                      A; Accession: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin - goat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB:LTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Ual-1955 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: 852107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
A;Tile: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: 852107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 262, 10134-10139, 1987
A,Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretises tages of A,Reference number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riliu, Y.; Teng, C.T.
J. Biol. Chem. 265, 21880-21885, 1991
A.fitle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41205
R;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fill9/Domain: signal sequence #status predicted <SIG>F:20-707/Porduct: lactotransferrin #status predicted <MAT>F:38-695/Domain: tantotransferrin repeat homology <TRH2>F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 1; Length 707;
Pred. No. 0.82;
1; Mismatches 2; Indels
Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 2; Length 33;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M74778
C;Superfamily: transferrin, transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;I-19/Domain: signal common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-33 <OIA>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
   DB 2;
Score 54; DB 2;
Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactoferrin precursor - mouse
N,Alternate names: lactotransferrin
```

```
Fing, W.V.; Kennedy, S.D.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, & J. Leitbauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H., Alam, M.; Freitas, T. Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Jature 404, 502-506, 2006, 2006, 2006, 2006, 2006, 2006, 2009 Astricted to Machine M.A.; Rajandream, A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491. A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84283.1; PID:g737971
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein NMA1014 [imported] - Neisseria meningitidis (strain Z2491 serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                          A,Molecule_type: DNA_
A,Residues: 1-584 <STO>
A,Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-932 <FAV>
A;Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A;Experimental source: strain Bristol N2; clone F07C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F07C3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct.1999 #sequence_revision 29-Oct.1999 #text_change 29-Oct-1999
C;Accession: T28820
R;Favello, A; Gattung, &
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F07C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Species: Neisseria meningitidis
C,Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C,Accession: D81949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%; Score 40; DB 2; Length 584; 41.7%; Pred. No. 37; ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.1%; Score 40; DB 2; Best Local Similarity 63.6%; Pred. No. 59; Matches 7; Conservative 1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 CFIWRKDMERKR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z20528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                         579 FOWORSARLVK 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <PAR>
                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: CESP:F07C3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T28820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: D81949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 5
                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: VNG1732C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                   C;Species: Chlamydomonas reinhardtii.
C;Species: Chlamydomonas reinhardtii.
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
R;Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Titles Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: Z16302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: IX
A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Residues: 1-275 <WIL>
A, Cross-references: EMBL: Z81089; PIDN: CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F53H4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Adre: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
R;Dobson, R.
Submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng173c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4568 <MIT>
A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 2; Length 4568;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: nuclectide binding; P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                         - Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: T22597
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain 21gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Experimental source: clone F53H4 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||| ::| ::
1852 CFQWQSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z19587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 FOWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FOWOREMRKVR 12
                                                                                      dynein beta heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: X
A;Introns: 67/1; 153/1
C;Superfamily: Caenorha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: ODA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
```

RESULT 7

Conservative

. ,

Matches

Query Match Best Local Similarity

A; Gene: NMA1014

qq

```
R; Weinberg, A.D.; Shaw, J.; Paetkau, V.; Bleackley, R.C.; Magnuson, N.S.; Reeves, R.; M. Immunology 63, 603-610, 1988
A; Title: Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).
A; Reference number: S07442; MUID:88212503; PMID:2835311
probable trad protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: G98133
R;Goodner, B., Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Atu4804 (imported) - Agrobacterium tumefaciens (strain C58, Dupont C,Species: Agrobacterium tumefaciens C,Species: Agrobacterium tumefaciens C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cjaccession: AH3147
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ster, E.W.

A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A,Reference number: AB2577; PMID:11743193

A,RACession: AH3147

A,Status: preliminary

A,Molecule type: DNA

A,Rocale type: DNA

A,Rocale type: CMS

A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE007870; PIDN: AAK88593.1; PID: g15158306; GSPDB: GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-2 receptor alpha chain precursor - bovine
N;Alternate names: CD25
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 22-Jun-1999
C;Accession: S07442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.3%; Score 38; DB 2; Length 121; 54.5%; Pred. No. 18; tive 1; Mismatches 4; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.7%; Score 39; DB 2; Length 12777.8%; Pred. No. 1.2e+02; Lindels tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: Atu4804
A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 CLAWORRNRV 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-1277 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1153 OWOREORDV 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: G98133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: AGR L 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2117-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: EMBL:275101; NID:g1431575; PID:e252673; PID:g1431578; GSPDB:GN00015;
A,Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
A,Accession: AC3154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conjugation protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Remidues: 1-1266 «KUR»
A;Cross-references: GB:AE008689; PIDN:AAL45649.1; PID:g17743373; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein YOR193w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein 04797
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67085
R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Reference number: S66885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.7%; Score 39; DB 2; Length 1266; ilarity 77.8%; Pred. No. 1.2e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 2; Length 376;
Pred. No. 36;
3; Mismatches 1; Indels
                                  55.7%; Score 39; DB 2; Length 57; 66.7%; Pred. No. 5.7; ative 1; Mismatches 3; Indels
```

55.7%;

Query Match Best Local Similarity 60.v. -hog 6; Conservative

à

RESULT 11

C, Accession: AC3154

A,Gene: MIPS:YOR193w A,Cross-references: SGD:S0005719 A,Map position: 15R

C;Genetics:

A; Molecule type: DNA A; Residues: 1-376 < HUG>

A, Map position: linear chromosome

Query Match Beet Local Similarity 7; Conserve

1142 ÓWÓŘÉQŘDV 1150

д

3 QWQREMRKV 11

A; Accession: S07442

```
A;Cross-references: EMBL:M20818; NID:g163208; PIDN:AAA51414.1; PID:g163209
C;Complex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains
C;Function:
                                                                         transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                          54.3%; Score 38; DB 1; Length 275; 50.0%; Pred. No. 40; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                  261 CLIWQRKWKKNR 272
                                                                                                                                                                                                                                                                                                                                 1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                       Local Similarity
                           A; Residues: 1-275 <WEI>
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                           g
```

Query Match
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-291 <STO>
A, Cross-references: GB:AE005176; PID:g12723619; PIDN:AAK04806.1; GSPDB:GN00146
A, Experimental source: strain II.1403
C, Genetics:
A, Gene: rmaB

A;Accession: D86713

4 WOREMRK 10

Search completed: February 21, 2003, 07:47:58 Job time : 10.65 secs

```
February 21, 2003, 07:25:55 ; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                    US-09-743-107B-86
70
1 CFQWQREMRKVR 12
                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                            Run on:
```

112892 Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | otion | homo sapien | camelus dro | capra hircu | mus musculu | chlamydomon | equus cabal | bos taurus | drosophila | saccharomyc | homo sapien | rattus norv | propionibac | caenorhabdi | caenorhabdi | ovis aries | homo sapien | sorghum bic | liberibacte | lactococcus | mus musculu | homo sapien | drosophila | archaeoglob | Balmonella | homo sapien | pseudomonas | caenorhabdi | homo sapien | escherichia | aquifex aeo | lactococcus | caenorhabdi | schizosacch |
|-----------|---------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|------------|-------------|-------------|----------------|-------------|-------------|-------------|-------------|----------------|-------------|
| | Description | P02788 | Omn160 | Q29477 | P08071 | Q39565 | 077811 | P12342 | Q9xz18 | P26448 | P48163 | P13697 | P11652 | 021988 | 019020 | P26898 | 015031 | P93528 | P41187 | Q9cg20 | P06801 | 015398 | Q24325 | 028816 | P37589 | P49771 | P36642 | 020351 | 013639 | P24204 | 067383 | 030418 | 60E60 0 | Ogute7 |
| SUMMARIES | | MAIN | MDR | APHI | MOUSE | 3_CHLRE | RSE | BOVIN |)ME | YEAST | HUMAN | ħ | PROFR | NEEL | NEEL NEEL | IEEP | JMAN | ORBI | BAF | TLA | OUSE | IMAN | COME | RCFU | D_SALTY | JMAN | PSEPU | CAEEL | (AN | ECOLI | AQUAE | ZEC . | CAEEL | SCHPO |
| SUM | OI (I | 딮 | TRFL CA | TRFL CAPHI | TRFL_MC | DYHBCE | TRFL HORSE | IL2A_BC | NLA DROME | BUB2 YE | | MAOX RAT | MUTA_PR | YNR2 CA | DYHC_CAEEL | IL2A_SHEEP | SYLM HU | PHYC SORBI | RPOB LI | DCE LAC | MAOX MOUSE | Y008 HU | T2D2_DR | YES6 ARCFU | PMRD_S7 | FL3L HUMAN | | TPSB C | 5H4 HUMAN | | ARLY AC | DCE LACLC | YOSI CA | MSS1_SC |
| | DB | - | Н | ٦ | н | Н | Н | Н | Н | ٦ | -1 | Н | H | Н | Н | Н | H | Н | Н | Н | Н | Н | Н | Н | н | Н | Н | , | ~ | - | Н | Н | Н | Т |
| | Length | 711 | 708 | 708 | 707 | 4568 | 692 | 275 | 292 | 306 | 572 | 572 | 637 | 783 | 4568 | 275 | 903 | 1135 | 146 | 466 | 572 | 765 | 1213 | 57 | 82 | 235 | 288 | 359 | 388 | 440 | 457 | 466 | 480 | 496 |
| de | Query | 92. | 77.1 | 77.1 | 71.4 | 65.7 | 57.1 | 54.3 | 54.3 | 54.3 | 54.3 | 54.3 | 54.3 | 54.3 | 54.3 | - | 52.9 | 52.9 | 51.4 | 51.4 | 51.4 | 51.4 | ٠. | 50.0 | | 50.0 | 50.0 | | 50.0 | ٠. | ٠. | ٠. | | 50.0 |
| | Score | 65 | 54 | 54 | 20 | 46 | 40 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 37 | 37 | 37 | 36 | 36 | 36 | 36 | 36 | 35 | 32 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 |
| | Result
No. | 1 | 2 | ო | 4 | S | 9 | 7 | 80 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 |

| Q9fg65 arabidopsis
Q9um07 homo sapien | P14632 sus scrofa
077698 bubalus bub | 035274 rattus norv
P36617 schizosacch | Q10201 schizosacch | 201371 neurospora | P57070 vibrio chol
P18132 cryptococcu |
|--|---|--|--------------------|-------------------|---|
| C911 ARATH | TRFL_PIG
TRFL_BUBBU | NEB2_RAT
RA16_SCHPO | YBX7_SCHPO | WC1 NEUCR | LOLB VIBCH PYRE CRYNE |
| н н | | | | 4 | 4 |
| 502 | 704 | 817 | 962 | 1167 | 211
225
225 |
| 50.0 | 50.0 | 50.0 | 50.0 | 50.0 | 4 4 4 4 8 . 6 . 6 . 6 . 6 . 6 . 6 . 6 . 6 . 6 . |
| 35 | 93 | 3
3
3
3 | 3
3
5
7 | , w , | , w.w. |
| 34 | 36 | യ ക
ന ന | 0 4 | 1 2 6 | 4.4 |

ALIGNMENTS

```
Sun X.L.,
                                             awamori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Mhan M., Parrell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker B.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                                                and
of
                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٦,
ت.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                           "The present state of the human lactotransferrin sequence. Study alignment of the cyanogen bromide fragments and characterization N- and C-terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutagenesis of the histidine ligand in human lactoferrin: iron
                                                                                                                                                                                    Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding properties and crystal structure of the histidine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "An 88 amino acid long C-terminal sequence of human
                                                                                human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 670:243-254 (1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                              comparisons with other transferring.";
Eur. J. Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acta Crystallogr. D 51:629-646(1995).
                                                                                                   Nucleic Acids Res. 18:4013-4013(1990)
                                                                                                                                          SECUENCE OF 20-711.
MEDLINE=85076667; PubMed=6510420;
                   TISSUE=Mammary gland;
mbbline=90326549; PubMed=2374734;
Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=82262043; PubMed=7049727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lactotransferrin.";
FEBS Lett. 142:107-110(1982).
  OF 3-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253-->methionine mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 609-711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resolution
                                                                                                                                                                                                                                                                                                                                                                            Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker E.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jolles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15]
REAL TRANSPORTED FOR THE SEASON OF THE SEASO
```

```
Rintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,

A Cumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,

Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,

B. Matri L., Irata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,

B. Hejtmancik J.F., Teng C.T.;

B. Hejtmancik J.F., Teng C.T.;

Hejtmancik J.F., Teng C.T.;

Corneal dystrophy): exclusion of linkage to lactoferrin gene.";

Mol. Vision 4:31-32(1998).

C. PINCTION: TRANSPERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUBLIY BICARBONATE.

-- FUNCTION: LACTOFERROXINS A, B AND C HAVE CPIOID ANTAGONIST

ACTIVITY: LACTOFERROXINS A, B AND C HAVE CPIOID ANTAGONIST

ACTIVITY: LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE

C. PORTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE

C. PORTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE

C. PORTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swigs Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION OF LACTOFERROXINS.
MEDDINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H. Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
                                  'Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                 Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335 (1998).
Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agric. Biol. Chem. 54:1803-1810(1990).
                                                                                                   Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC015822; AAH15822.1; -. BC015823; AAH15823.1; -. M73700; AAAS9479.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF332168; AAG48753.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X53961; CAA37914.1; -. EMBL; U07643; AAB60324.1; -. EMBL; M93150; AAA36159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M83202; AAA59511.1; -.
M83205; AAA58656.1; -.
M18642; AAA86665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAA37116.1; -.
AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS THR-30 AND ARG-48.
PubMed=9873069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from human lactoferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X52941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U95626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1LFI;
1LGB;
1LGC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLCF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1LFG;
1LFH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1BKA;
```

m

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                      (POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.1%; Score 54; DB 1; Length 708; 75.0%; Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                F -> S (IN REF. 2).
G -> A (IN REF. 2).
G -> D (IN REF. 2).
LLS -> PLF (IN REF. 2).
L -> F (IN REF. 2).
A -> P (IN REF. 2).
W, OBOCLT5A0B69D430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                         IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRFL_CAPHI STANDARD; PRT; 708 AA. Q29477; Q29479; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
BY SIMILARITY.
BY SIMILARITY
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     77211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 CAÓWORRMKKVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                  708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capra hircus (Goat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9925;
 9
           DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                              METAL
BINDING
BINDING
                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                          PARBOHYD
                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                           METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRFL_CAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Mammary gland,
Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.,
Submitted (JUN-1999) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORTENS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                         Gaps
                                                                                                                                                                                                                                                                  Camelus dromedarius (Dromedary) (Arabian camel),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                                                                                                                        STRAIN-Somali; TISSUB-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, 077811, 1BIX.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00402; TRANSFERIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                           ·,
           92.9%; Score 65; DB 1; Length 711; ilarity 91.7%; Pred, No. 0.00066; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                TRFL CAMDR STANDARD; PRT; 708 AA. O9TUMO; O9MZS5; 16-0CT-2001 (Rel. 40, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.
BY
BY
BY
BY
BY
BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ131674; CAB53387.1; -.
EMBL; AF165879; AAF82241.1; -.
                                                                   1 CFOWOREMRKVR 12
                                                                                              39 CFOWORNMRKVR 50
     Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364
364
364
134
134
350
350
350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signaî.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
                                                                                                                                        RESULT 2
TRFL CAMDR
```

HERETTELETER WAS BRANKE BRANK COURSE COURT BRANK BRANK

; 0

Gaps

```
0;
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR, 0125; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINIE; PR00422; TRANSFERRIN.
SMART; SM0094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.1%; Score 54; DB 1; Length 708; 72.7%; Pred. No. 0.055; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F2EDA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (PARTICE OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. . .)
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...
I -> V (IN REF. 2).
Q -> K (IN REF. 2).
Q -> K (IN REF. 2).
F -> P (IN REF. 2).
S -> P (IN REF. 2).
D -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
LACTOTRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77358 MW;
                                                                                                                                                                                                                                                                                                             EMBL; U53857; AAA97958.1; -. EMBL; X78902; CAA55517.1; -. HSSP; O77698; 1CE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signaî.
SIGNAL
CHAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
METAL
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
METAL
METAL
METAL
  SOLUTION OF THE STATE OF THE ST
```

1 CFQWQREMRKV 11 |:||||||38 CYQWQRRMRKL 48

à

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-14 FROM N.A. MEDILIBE-20240909; PubMed=1939212; MEDILIBE-20240909; PubMed=1939212; Liu Y., Teng C.T.; "Characterization of estrogen-responsive mouse lactoferrin promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol, Chem. 266:21880-21885 (1991)
-1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                    mouse
                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan, PF00405; transferin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSTIE; PS00205; TRANSFERRIN 1; 1.
PROSTIE; PS00206; TRANSFERRIN 2; 2.
PROSTIE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                   Pentecost B.T., Teng C.T.; "Lactotransferrin is the major estrogen inducible protein of
                                                                                                                                                                                                                                                                                                                                                     TISSUE=Uterus;
Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SUBLIARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
LACTOTRANSFERRIN.
TRFL MOUSE STANDARD; PRT; 707 AA. P08071; P70690; Q61799; Q922P2; 01-AUG-1988 (Rel. 08, Created) 15-UNG-2002 (Rel. 41, Last sequence update) 15-UNA-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                       uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                     TISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J03298; AAA40525.1; --
EMBL; D88510; BAA13633.1; --
EMBL; BC006904; AAH06504.1; --
EMBL; M74778; AAA39427.1; --
PIR; A22438; A28438
HSSP; P02788; LCB6.
MGD; MGI:96837; Ltf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
707
357
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
20
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
```

```
П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE THAT THAT THE STATE OF STATES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain genes.";
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELIA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYNEIN HAS ATPASE ACTIVITY.
SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                       ANION (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MR -> 1QG (IN REF. 1).
R -> Q (IN REF. 2).
M -> L (IN REF. 2).
S -> T (IN REF. 2).
A -> D (IN REF. 2).
E -> G (IN REF. 2).
L -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%; Score 50; DB 1; Length 707; 72.7%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F26AE0340A4C19A8 CRC64;
                                                                                                                                                                                                                                                               1 (BY SIMILARITY).
1 (BY SIMILARITY).
1 (BY SIMILARITY).
2 (BY SIMILARITY).
2 (BY SIMILARITY).
3 (BY SIMILARITY).
5 (BY SIMILARITY).
5 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                             ANION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
OMPHEN beta chain, flagellar outer arm.
ODA4 OR ODA-4 OR SUP1.
                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 4568 AA.
                                                                            SIMILARITY.
SIMILARITY.
                                                                                                                                                                          SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                               SIMILARITY
                                                                                                            SIMILARITY.
                                                                                                                                                        SIMILARITY
                                                                                                                           SIMILARITY
                                                                                                                                          SIMILARITY
                                                                                                                                                                                                                                                                  IRON 1
                                                                                                                                                                                                                                                                                               IRON 1
IRON 2
IRON 2
IRON 2
IRON 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonadaceae; Chlamydomonas
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                 210
271
271
413
4413
613
613
1139
1139
481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449
629
707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 CLRWONEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                       443
475
499
509
520
591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYHB CHLRE
REPEAT
DISULFID
DISULFID
                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                            BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                         DISULFID
                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                               SULFID
                                                                 SULFID
                                                                            DISULFID
                                                                                               SULFID
                                                                                                            DISULFID
                                                                                                                                                        DISULFID
                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      039565;
                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                             METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLRE
                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
DYHB_CH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resolution.";
J. Mol. Biol. 289:303-317(1999).

J. Mol. Biol. 289:303-317(1999).

J. FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ANTONS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.

J. SUBBUNIT: MONOWER.

J. SUBCELULIAR LOCATION: Secreted.

J. DOWAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

J. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P. "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus
                                                                                                                                                                                                                                                                                                                                                    COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                         InterPro; IPR004273; Dynein heavy.
Pfam; PF03028; Dynein heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 4568;
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "cDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.7%; Score 46; DB 1
50.0%; Pred. No. 9.4;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                  COILED COIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA; 519961 MW;
                                                                                                                                                                                                                        EMBL; U02963; AAA19956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     1650
1825
2045
2045
3162
3425
3425
3728
1926
22209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||| ::| ::
1852 CFQWQSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4568
                                                                                                                                                                                                                                                                                                                                                                                                                            1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3106
3339
3648
1919
2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2530
                                                                                                                                                                                                                                                                                                                                                                                                       614
                                                                                                                                                                                                                                                                                                                    Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRFL HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP BIND
NP BIND
NP BIND
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRFL_HORSE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                        R PDB; 1BTZ; 02-DE2-98.

R PDB; 1BTZ; 02-DE2-98.

R PDB; 1BTZ; 02-FEB-99.

R PDB; 1BTZ; 02-FEB-99.

R PDB; 1BTZ; 02-FEB-99.

R PF00405; transferrin; 2.

R PROMOD42; TRANSFERIN.

R MART; SM00094; TR FER; 2.

R PROSITE; PS00206; TRANSFERIN 1; 2.

R PROSITE; PS00206; TRANSFERIN 2; 2.

R PROSITE; PS00207; TRANSFERIN 2; 2.

R PROSITE; PS00207; TRANSFERIN 2; 2.

R A Signal; 3D-structure.

T NON TER 1 1 1

SIGNAL <1 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Length 695;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07BB84D50E1B165D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (P
                                                                                                                                                                                                                                      LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7

IL2A BOVIN

ID 1L2A BOVIN

STANDARD;

ID 112342;

DT 01-OCT-1989 (Rel. 12, Created)
                                                                                       EMBL; AJ010930; CAA09407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 653
681
681
531
532
636
66
66
759
759
759
759
759
759
759
759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 CAKFORNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482
695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                         MEDLINE=96116968; PubMed=8563178;
MEDLINE=96116968; PubMed=8563178;
MEDLINE=96116968; PubMed=8563178;
MEDLINE=96116968; PubMed=8563178;
MCO J., de Leon F.A., Stone R.T., Beattie C.W.;
"Cloning and chromosomal assignment of the bovine interleukin-2 receptor alpha (IL-2R alpha) gene.";
Mamm. Genome 6.751-753(1995).
-!- SUBUNIT: NON COVALENT DIERR OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN.
                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=88212503; PubMed=2835311;
Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
Reeves R., Magnuson J.A.;
"Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
Immunology 63:603-610(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                  Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Ammanla, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
W, 4901BBF9A4862390 CRC64;
01-OCT-1989 (Rel. 12, Last sequence update)
LeCCT-2001 (Rel. 40, Last annotation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERLEUKIN-2 RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.3%; Score 38; DB 1; Length 275; larity 50.0%; Pred. No. 13; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              - SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M20818; AAA51414.1; -.
BMBL; U42226; AA648487.1; -.
PIR; S07442; S07442.
HSSP; P01589; IIIM.
InterPro; IFR004456; Sushi_SCR_CCP.
Ffam; PF00084; sushi; 2.
SMART; SM00032; CCP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31238 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
243
262
275
78
185
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 CLTWORKWKKNR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109
275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
2442
263
122
122
122
152
152
152
152
152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            임
```

.; 0

Gaps

0;

3; Indels

Score 38; DB Pred. No. 14; 2; Mismatches

54.3%;

6; Conservative

Best Local Similarity

Matches

Query Match

2 FOWOREMRKVR 12

ò

EMBL; AF147700; AAD33987.1; -.
EMBL; AE003712; AAF55285.1; -.
Flybace; FB070026629; nla.
SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

8 H H S

```
RCHINES-CIGNOROR PLANES-10731132,
RAMININE-20186006; Pubmed=10731132;
RAMININE-20186006; Pubmed=107, RAMININE-M.; Refelfer B.D., RAMININE-M.; Barnd M., Barnden B.C., Releffer B.D., RAMININE-M.; Barnd M., Barnden B.C., Raminine-M.; Barnden B.C., Barnden B.C., Barnden B.C., Barnden B.C., Raminine-M.; Barnden B.C., Raminine-M.; Barnden B.C., Raminine-M.; Barnden B.C., Staden-Klamon G.S., Pan S., Pollard J., Puri V., Resee M.G., Ramer B., McInton R.M., Worlden B.C., Worley B.C., Wullen B.C., Staden-Klamon G.S., Pan S., Pollard J., Barnden B.C., Staden-Klamon B.C., Staden-Klamon B.C., Staden-Klamon B.C., Staden-Klamon B.C., Staden-Klamon B.C., Staden B.C., Staden-Klamon B.C., Staden B.C., Staden-Klamon B.C., Barnden B.C., Staden-Klamon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Edopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                     WcCormick A.V., Goldberg M.L.; "Gene required for elongation of Meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE. -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                         DIA DROME STANDARD; PRT; 292 AA. 09XZL8; Q9V391; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                Nebula protein.
                                                                                                                                                                                                                                                                                                                                                                          McCormick A.V.
                                                                                                                                                                                        NLA OR CG6072
                                                                                                                                                                                                                                                                                                                                                                                                                             females.
RESULT 8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and prevents premature exit from mitosis. This cell-cycle arrest depends upon inhibition of the G-protein Teml by the BFA1/BUB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: Part of a checkpoint which monitors spindle integrity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91330299; PubMed=1651171;
Hoyt M.A., Totis L., Roberts B.T.;
S. cerevisiae genes required for cell cycle arrest in response to loss of microcubule function.";
Cell 66:507-517(1991).
                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
BUB2 OR YMR055C OR YM9796.08C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21385309; PubMed=11493673;
Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D.
Johnston L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE TRAIN-S288c / AB972;
Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A39654; A39654.
SGD; S0004659; BUB2.
INTERPORT PRROUGUSS; RABGAP_TBC.
Pfam; PF00566; TBC; 1.
SWART; SW00164; TBC; 1.
CGL1 cyCle; Mitcsis.
SEQUENCE 306 AA; 35027 WW; Alddersers CRC64;
                                                                                                                                                                                     306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Interacts with BFA1.
-!- SUBCELLULAR LOCATION: Spindle poles.
-!- SIMILARITY: TO S.POMBE CDC16.
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulates cytokinesis.";
J. Cell Sci. 114:2345-2354(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M64706; AAA16885.1; -. EMBL; Z49703; CAA89765.1; -.
                                                                                                                                                                                     STANDARD;
150 FOWLRSFRER 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                  BUB2 YEAST
P26448;
                                                                                                                                               BUB2_YEAST
                                                                                                                                                                                                                    DATE OF STATE OF STAT
```

ω

0

Gaps

ö

Mismatches

5

```
4; Conservative
                                                                                                                                                                                                                                                    MAOX RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
Matches
                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               0
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                            P48163; Q16855; Q9BWX8; Q9UIX4; Q9H1W3;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last amotation update)
NADP-dependent malic enzyme (EC 1.11.40) (NADP-ME) (Malic enzyme 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 8-572 FROM N.A.
MEDLINE=96397682; PubMed=8804575;
Chou W.Y., Huang S.M., Chang G.G.;
"Nonidentity of the cDNA sequence of human breast cancer cell malic enzyme to that from the normal human cell.";
J. Protein Chem. 15:273-279 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loeber G., Dworkin M.B., Infante A., Ahorn H.;
"Characterization of cytosolic malic enzyme in human tumor cells.";
FEBS Lett. 344:181-186(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2)
                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 572;
                       Length 306;
                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 NADP (BY SIMILARITY).
138 P -> S (IN REF. 2).
64149 MW; EA4C8CB36F6C619C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
                       DB 1;
15;
                       Score 38; DB 1
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                       572 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%; Score 38; DB 33.3%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00072; MALOXRDTASE.
PROSITE; PS00331; MALIC_ENZYMES; 1.
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=White adipose tissue;
MEDLINE=94244767; PubMed=8187880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR001891, Malic_oxred.
Pfam; PF00390; malic; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AL391416; CAC36330.1; -. EMBL, AL136970; CAC19505.1; -. EMBL; AL049699; CAB52344.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X77244; CAA54460.1; -. EMBL; U43944; AAC50613.1; -.
                 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 27-572 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMOTETRAMER.
                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:6983; ME1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 AA;
                                                                                                                                                                                            108 CFAWOTOORR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                       Query Match
Best Local Similarity
                                                                                                                                       1 CFQWQREMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 154250;
                                                                                                                                                                                                                                                                                                                                    MAOX HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP BIND
                                                                                                                                                                                                                                                                         PRESULT 10
PROX HUMAN
PROX HUMAN
PACK HOMEN

                                                                            Matches
                                                                                                                                       ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                             01-0AN-1990 (Rel. 13, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-7UN-2002 (Rel. 41, Last annotation update)
MADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Malic enzyme 1).
MEI OR MOD1 OR MOD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morioka H., Magnuson M.A., Mitsuhashi T., Song M.K.H., Rall J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-35 FROM N.A. MEDIUTE-89096948; PubMed-3211151; MEDIUTE-89096948; PubMed-3211151; MOTIOKA H., Tennyson G.E., Nikodem V.M.; "Structural and functional analysis of the rat malic enzyme gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nikodem V.M.,
"Structural characterization of the rat malic enzyme gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:4912-4916(1989).
-!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2)
                                                                                                                                                                                                                                                                                                                                                    Nikodem V.M., Magnuson M.A., Dozin B., Morioka H.; "Coding nucleotide sequence of rat malic enzyme mRNA and tissue specific regulation by thyroid hormone."; Endocr. Res. 15:547-564 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley;
MEDINE=8611756; PubMed=3753699;
Magnuson M.A., Moricka H., Tecce M.F., Nikodem V.M.;
"Coding nucleotide sequence of rat liver malic enzyme mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
                                                                                                                 572 AA.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90235791; PubMed=2699453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Cell. Biol. 8:3542-3545(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 261:1183-1186(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M26594; AAA41563.1; ALT SEQ. EMBL; M26581; AAA41563.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89296914; PubMed=2740332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA41563.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA41563.1;
AAA41563.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA41563.1;
AAA41563.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA41563.1;
                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                   STANDARD;
                   |: | |::|::
556 CYSWPEEVQKIQ 567
1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M26589;
M26590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M26586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M26584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M26583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M26585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M26587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M26588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
```

```
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marsh E.N., Leadlay P.F.;
"Methylmalonyl-CoA mutase from Propionibacterium shermanii. Evidence for the presence of two masked cysteine residues.";
Biochem. J. 260:339-343(1989).
                                                                                                                                                                                                                                                                                                                                       Propionibacterium freudenreichii shermanii.
Bacteria, Actinobacteria, Actinobacteria (class); Actinobacteridae,
Actinomycetales; Propionibacterineae; Propionibacteriaceae;
Propionibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mancia F., Keep N.H., Nakagawa A., Leadlay P.F., McSweeney S., Rasmussen B., Bosecke P., Diat O., Evans P.R.; "How coenzyme B12 radicals are generated: the crystal structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NCIB 9885;
PubMed=9655823;
Mancia F., Evans P.R.;
Conformational changes on substrate binding to methylmalonyl CoA mutase and new insights into the free radical mechanism.";
Structure 6:711-720(1998).
-!- FUNCTION: CATALYZES THE ISOMERIZATION OF SUCCINYL-COA TO METHYLMALONYL-COA DURING SYNTHESIS OF PROPIONATE FROM TRICARBOXYLIC ACID-CYCLE INTERMEDIATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marsh E.N., McKie N., Davis N.K., Leadlay P.F.;
"Cloning and structural characterization of the genes coding for adenosylcobalamin-dependent methylmalonyl-CoA mutase from Propionibacterium shermanii.";
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 3-8; 95-99; 301-305; 472-477
                                                                                                                                                                                                                                                                                         01-0CT-1989 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methylmalonyl-CoA mutase small subunit (RC 5.4.99.2) (MCB-beta)
                                                                                                                                                                ;
0
                                                                                                                                       54.3%; Score 38; DB 1; Length 572; 33.3%; Pred. No. 28; ive 5; Mismatches 3; Indels
                                                                                                     ADP (BY SIMILARITY).
7D6EB48F3BA7D95B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylmalonyl-coenzyme A mutase at 2-A resolution.";
                                                                                                                                                                                                                                                                        637 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                    PERMIS, PR00390; malic; 1.
PRINTS; PR00372; MALOXEDIASE.
PROSTITE; PR00331; MALIC_ENZYMES; 1.
OXIGOTEGUCLASE; NADP.
NP_BIND 301 318 NADP (
SEQUENCE 572 AA; 64002 MW; 7D6E
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96398619; PubMed=8805541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89350816; PubMed=2569861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 514-517.
STRAIN-NCIB 9885;
MEDLINE-89350815; PubMed=2569860;
           EMBL; M26592; AAA41563.1; JOINED.
EMBL; M26593; AAA41563.1; JOINED.
PIR; A37228; DERIWX.
                                            interPro; IPR001891; Malic_oxred.
 EMBL; M26591; AAA41563.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. J. 260:345-352(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structure 4:339-350(1996).
                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                   |: | |::|::
556 CYSWPEEVQKIQ 567
                                                                                                                                                                                     1 CFQWQREMRKVR 12
                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-NCIB 9885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-NCIB 9885;
                                                                                                                                                                                                                                                                    MUTA PROFR
P11652;
                                                                                                                                                                                                                                              RESULT 12
MUTA PROFR
g
                                                                                                                                                                                      à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
CATALYTIC ACTIVITY: (R)-2-methyl-3-oxopropancyl-CoA = succinyl-
                                                                                        -i- PATHWAY: Propionic acid fermentation.
-i- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-i- SIMILARITY: BELONGS TO THE METHYLMALONYL-COA MUTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.3%; Score 38; DB 1; Length 637; 66.7%; Pred. No. 31; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Durbin R.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637 AA; 69333 MW; A9D8809A2C4C9150 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein R13G10.2 in chromosome III.
R13G10.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001629; MM CoA mutase.
InterPro; IPR004608; MmCoA mut beta.
Pfam; PF01642; MM CoA mutase; I.
PIGRPAMs; TIGR00642; mmCoA mut beta; 1.
PROSITE; PS00544; METWALONYL COA MUTASE; I.
ISOMERABE; Vitamin B12; CobaIt; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                 -!- COFACTOR: ADENOSYLCOBALAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X14965; CAA33089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      !- COFACTOR: FAD (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1REG; 27-JAN-97.

2REG; 24-JAN-98.

3REG; 24-JUN-98.

4REG; 13-JAN-99.

5REG; 12-AUG-98.

6REG; 09-SEP-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S04640; S04640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 QWEREVEKV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gardner A.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNR2 CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      021988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNR2 CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
```

```
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Verhagen A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL2A SHEEP
                                                                                                                                                                                                                          DOMAIN
NP_BIND
NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
DOMAIN
DOMAIN
DOMAIN
                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P26898;
                                                                                                                          DOMAIN
                                                                                                                                                    DOMAIN
                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL2RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL2A_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96114101; PubMed=8674131;
Lye R.J., Wilson R.K., Waterston R.H.;
"Genomic structure of a cytoplasmic dynein heavy chain gene from the
nematode Caenorhabditis elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS
-!- FUNCTION: DYNEIN HAS ETROGRADE MOTILITY OF VESICLES AND
ORGANELLES ALONG MICROTUBULES.
-!- SUBUNIT: CONSTSTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
INTERMEDIATE AND LIGHT CHAINS.
-!- SUBCELLULAR LOCATION: CYCOPLASMIC.
-!- SIBLIARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WormPep; T21E12.4; CE23997.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR004273; Dynein heavy.
Pfam; PF03028; Dynein heavy.
SMART; SM00382; AAA; I.
Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.
                                                                                                                                                                                                                                                  54.3%; Score 38; DB 1; Length 783; 50.0%; Pred. No. 38; 1:ve 2; Mismatches 4; Indels
                                                 EMBL; Z35602; CAA84671.2; -.
WormPep; R13G10.2; CES5088.
InterPro; IR9002937; Amino oxidase.
Pfan; PF01593; Amino_oxidase; 1.
Hypothetical protein; Oxidoreductase; Flavoprotein; FAD. NP BLND
PROME TABLE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Du Z., Maggi L.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Dynein heavy chain, cytosolic (DYHC). DHC-1 OR T21E12.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Motil. Cytoskeleton 32:26-36(1995).
       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L33260; AAC37251.1; -.
EMBL; U80440; AAK21472.1; -.
                                                                                                                                                                                                                                                                              Local Similarity 50.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                      540 CIDWGRDDRKVK 551
                                                                                                                                                                                                                                                                                                                                                          1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYHC CAEEL
Q19020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYHC_CAEEL
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEREER
                                                                                                                                                                                                                                                                                                                                                            ઠે
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 113:283-284(1992).
-1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
-1- SUBGNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
-1- SUBGNIT: NON COVALENT DIMER OF A HIGH AFFINITY DIMER, AN INTERNEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92241682; PubMed=1572550;
Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.;
"Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa protein, CD25.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-PEB-1996 (Rel. 33, Last amoctation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                              COLLEG COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 028E52684F381676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                (POTENTIAL).
                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; I
Pred. No. 2.3e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                   (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                         COIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
COILED COIL
                         COILED
                                                                                                                                                                                                                                                                                                                                   ATP
ATP
ATP
                                                                                                                                                                                                                                                                                                             ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                 521568 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z11560; CRA77652.1; -.
EMBL; X60149; CRA42723.1; -.
EMBL; A19167; CRA01447.1; -.
PIR; S18910; S18910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Cetar
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
587 65

814 84

1241 127

1324 134

11559 159

11964 139

3130 343

3707 373

3707 373

1865 187

2163 221

2537 254

2580 2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 CNRWVKEIRKV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWOREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATE THE THE TRANSPORT OF THE TRANSPORT
```

```
DR PIR; S18899; S18899.

DR HSP, T01113; UC1113.

DR HSPP; P01589; JULM.

ET SIGNAL

FT SIGNAL

FT DOWAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.

FT DOWAIN 22 275 FYPERLEUKIN-2 RECEPTOR ALPHA CHAIN.

FT DOWAIN 24 262 POTENTIAL.

FT DOMAIN 23 775 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 122 185 SUSHI 2.

FT DOMAIN 122 185 SUSHI 2.

FT DOWAIN 23 78 SUSHI 2.

FT DISULFID 123 168 BY SIMILARITY.

FT DISULFID 123 168 BY SIMILARITY.

FT CARBOHYD 80 N-LINKED (GLUNAC. .) (POTENTIAL).

FT CONFLICT 166 166 S -> T (IN REF. 2).

SEQUENCE 275 AA; 30904 MW; 1101A2DESACSA088 CRC64;
```

OY 1 CFGWQREMRKVR 12 | | | | | | | | | Db 261 CLTWQRRWKGNR 272

ô

Gaps

0;

Ouery Match 52.9%; Score 37; DB 1; Length 275; Best Local Similarity 50.0%; Pred. No. 20; Matches 6; Conservative 1; Mismatches 5; Indels

Search completed: February 21, 2003, 07:28:01 Job time : 5.6 secs

us-09-743-107b-86.rspt

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE DE DE OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q19133 caenorhabdi
Q91v34 neisseria m
Q9xt65 cryza sativ
Q9sml1 cicer ariet
Q9sml2 cicer ariet
Q9ffy4 salmonella
Q08f80 saccharomyc
Q9fhi9 arabidopsis
Q8u6f2 agrobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9xhp1 sesamum ind Q93780 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    097tq8 clostridium 09hpa3 halobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBtcd2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ovis aries
                                                            (without alignments)
118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo
                                                  February 21, 2003, 07:25:55; Search time 20.8 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ucy5 |
Q9tr80 (
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                   671580 segs, 206047115 residues
                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    097TQ8
09HPA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JV34
Q9XFD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9SML1
Q9SML2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09FHI9
                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TCD2
Q9UCY5
Q9TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9XHP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSUGF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            093780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09F7Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208580
                                                                                                                                                                                                                                                                                                                                                             sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                     sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                       sp_organelle:*sp_phage:*
                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                  US-09-743-107B-86
70
                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                        1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_rodent:*
                                                                                                                                                                                                                                                                                                                                            sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                   SPTREMBL 21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                    Database :
                                                                                                         Sequence:
                                                                                                                                                   Searched:
                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
```

| ENTS | ĄLIGNMENTS | | | | | |
|--------------------|-----------------|-----|------|---------|--------|-------------|
| | | | | | | |
| Q986a0 rhizobium l | Q986A0 | 16 | 205 | | 37 | 45 |
| Ø | Q8 <i>S</i> C55 | g | 108 | | 37 | 44 |
| 9 | 077856 | | 16 | | 37 | 43 |
| | 077855 | 15 | 91 | | 37 | 42 |
| | Q9FXD3 | 10 | 64 | | 37 | 41 |
| m | 052003 | | 979 | | 38 | 40 |
| a | 910380 | | 864 | | 38 | 39 |
| Q8srg3 encephalito | Q8SRG3 | | 864 | | 38 | 38 |
| 062582 encephalito | 062582 | _ | 864 | | 38 | 37 |
| Ogevos macaca rasc | C92007 | 0 0 | 780 | . 4. r. | ם
מ | ה עם
הית |
| | 094937 | | 632 | | 38 | 34
4. |
| O22188 arabidopsis | 022188 | | 543 | | 38 | 33 |
| 09ltd4 arabidopsis | Q9LTD4 | 10 | 531 | | 38 | 32 |
| 022185 arabidopsis | 022185 | | 515 | | 38 | 31 |
| Q95k28 macaca fasc | Q95K28 | - | 512 | | 38 | 30 |
| P96223 mycobacteri | P96223 | 16 | 489 | | 38 | 29 |
| coryr | Q9EUL5 | | 477 | | 38 | 28 |
| homo | Q9NUS2 | | 466 | 54.3 | 38 | 27 |
| Q9nzw3 homo sapien | O9NZW3 | | 460 | | 38 | 26 |
| рошо | OMZN6O | 4, | 459 | | 38 | 25 |
| 024366 Spinacia ol | 024366 | | 339 | • | 38 | 24 |
| 09qb73 yaba monkey | Q9QB73 | 7 | 329 | | 38 | 23 |
| Qêtax2 homo sapien | QETAX2 | - | 306 | 54.3 | 38 | 22 |
| Q9chml lactococcus | Q9CHM1 | 16 | 291 | | 38 | 21 |
| Q8xse2 ralstonia s | O8XSE2 | 16 | 279 | | | 20 |
| | OBWVX2 | 4 | 233 | 54.3 | 38 | 13 |
| OBu6k3 agrobacteri | 08U6K3 | 16 | 121 | 54.3 | | 18 |
| Ogne65 leishmania | 09NE65 | ις. | 1778 | 55.7 | 39 | 17 |

```
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                Length 711;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB-PROSTATE;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; --
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              85.7%; Score 60; DB 4;
90.9%; Pred. No. 0.022;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 A.A.
                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
QBTCD2
QBTCD2;
QBTCD2;
01-JUN-2002 (TEMBLEEL: 21,
01-JUN-2002 (TEMBLEEL: 21,
01-JUN-2002 (TEMBLEEL: 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOWOREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 CFOWORNMRKV 49
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 10; Conserv
                                                                                                          Lactotransferrin.
                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UCYS
ID Q9UCYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
```

0

σ

Tue Dec

```
"Molecular cloning of 11S globulin and 2S albumin, the two major seed
                                                                                                                                                                                                                                                                  57.1%; Score 40; DB 10; Length 148; 66.7%; Pred. No. 15; 3; Indels ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 40; DB 5; Length 275; 63.6%; Pred. No. 29; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OTN-2002 (TrEMBLrel. 21, Last annotation update)
Xre family DNA-binding domain and TPR repeats containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dobson R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81089; CAB03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                        148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 AA.
                       storage proteins in sesame.";
J. Agric. Food Chem. 47:4932-4938(1999).
EMBL; AF091841; AAD42943.1; -.
InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
InterPro; IPR001768; Try/amyl_inhbtr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                              Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00496; NAFIN.
SMART; SM00499; AAI; 1.
SEQUENCE 148 AA; 17524 MW: RAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 FOWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     54 CMOWMRSMR 62
                                                                                                                                                                                                                                                                                                                                                           1 CFQWQREMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F53H4.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pSOL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  093780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 097T08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             093780
ID 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q97TQ8
    à
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sesamum indicum (Oriental sesame) (Gingelly).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Lamiales; Pedaliaceae; Sesamum.
                                                                                                           Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          Score 56; DB 4; Length 38;
Pred. No. 0.0059;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP; O77698; 1CB2.
                                                                                                                                                                                                                    InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.3%; Score 52; DB 6; 63.6%; Pred. No. 0.026; iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AA
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                     seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995)
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                      MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                          80.0%;
                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                     2 FOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                               21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 CYÓWÓKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4182;
                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2S albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09XHP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09XHP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9TR80
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID DATA SERVICE OF THE SERVICE OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
```

```
Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=2022556; PubMed=10761919; ParkINE=20222556; PubMed=10761919; ParkINID. G. Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Ruherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                             Bukaryota: Metazoa, Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%; Score 40; DB 5; Length 932; 63.6%; Pred. No. 99; ative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Direct Submission.",
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, 105308; AAG24025.1; -
InterPro; IPR000731; HMGCR/patch_5TW.
PROSITE; PSS0156; SSD; 1.
Hypothetical protein.
SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Favello A., Gattung S., "The sequence of C. elegans cosmid F07C3."; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 57 AA; 6491 MW; A6D8781C29E212C5 CRC64;
      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 105.1 kba protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 AA.
                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitidis Z2491 ";
Nature 404:502-506(2000).
EMBL; AL162754; CAB84283.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein NMA1014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 FOWORSARLVK 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 FOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMA1014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JV34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
           du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20504483; PubMed=11016950; MEDLINE-20504483; PubMed=11016950; MEDLINE-20504483; PubMed=11016950; Medined S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                    STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE=21359325; PubMed=11466286;
Moselling J., Braton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobitylicum.";
J. Bacteriol. 183:4823-4838(2001)

EMBL, AE001438; ARK76786.1;
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 40; DB 16; Length 443; 50.0%; Pred. No. 47; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 40; DB 17; Length 584; 41.7%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                    INTERPRO, IPROD1440, ...
SMART; SM00530; HTH XRE; 1.
SMART; SM00028; TPR; 3.
nNa-binding; Plasmid; Complete proteome.
FOTHS MW; 726C5BD139BF91EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halobacterium sp. (atrain NRC-1).
Archaea, Buryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                584 AA; 65151 MW; 21BF5D5F0486CCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       932 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001646; Speptide repeat.
InterPro; IPR001622; K+channel_pore.
Pfam; PF00805; Pentapeptide; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0°
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || |:::| : |
445 CFTWRKDMERKR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 CYCWMKEYOK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQREMRK 10
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=64091;
```

09HPA3;

Q9HPA3

RESULT 7

δ

09HPA3

SEQUENCE

019153;

019153

RESULT 8 Q19153 ID Q1 AC Q1

à

ö

0; Gaps

ö

. 0

Q9XFD5

SOURCE COUNTY NEW NORTH NO. CONTROL OF THE SERVICE OF THE SERVICE

```
Cicer arietinum (Chickpea) (Garbanzo).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids 1; Fabales, Fabaceae, Papilionoideae, Cicereae, Cicer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Overkamp S., Hein F., Barz W.;

"Cloning and characterization of eight cytochrome P450 cDNAs from chickpea (Gicer arietinum L.) cell suspension cultures.";

Plant Sci. 155:101-108 (2000).

-! SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

BMBL; AJ249800; CAB56742.1;

Interpro; PR001128; Cytochrome_P450.

Pfam; PP00067; p450.

PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pJ.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                   Score 39; DB 10; Length 207;
Fred. No. 33;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.7%; Score 39; DB 10; Length 240; Best Local Similarity 71.4%; Pred. No. 38; Matches 5; Conservative 2; Mismatches 0; Indels
Pfam; PF00067; p450; 1.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.

Heme; Monocxygename; Oxidoreductase.

NON TER 1

SEQÜENCE 207 AA; 23476 MW; DEID9AAAEC2D1BFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA; 27150 MW; 19CB488E6E7C0407 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CV. ILC 3279; TISSUE=CELL SUSPENSION CULTURE;
PubMed=10773344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome P450 monooxygenase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 16, Created) (TrEMBLrel. 16, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                          Query Match 55.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 CFEWKRE 204
                                                                                                                                                                                                                                                                                                                                                                                              165 CFEWKRE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQRE 7
                                                                                                                                                                                                                                                                                                                                   1 CFOWORE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9SML2
Q9SML2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09F7Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9F7Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9F7Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SML2
                                                                                                                                                                                                                                                                                                                                                                                              .
අු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RXX OCCOORDINATION NAMED TO THE PROPERTY OCCOORDINATION OCCOUNTS AND THE PROPERTY OF THE PROPE
      RADE SO
                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnolophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Overkans, Journal F., Barz W.;
Overkans S., Hein F., Barz W.;
Cloning and characterization of eight cytochrome P450 cDNAs from chickpea (Cicer arietinum L.) cell suspension cultures.";
Plant Sci. 155:101-108(2000).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AJ249801; CAB56743.1; --
InterPro; IPR001128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu J., Yang J.; "Suppression subtractive hybridization (SSH) identified candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes that are differentially expressed at rice young panicle.", Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-1-SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AF140468; AAD2599-1.1.
InterPro; IPR01128; Cytochrome_P450.
PRIMTS; PR00085; P450; 1.
PRIMTS; PR00086; CYTOCHROME P450; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.7%; Score 39; DB 10; Length 105; 60.0%; Pred. No. 16; 2; Mismatches 2; Indels
      DB 16; Length 57;
                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CV. ILC 3279; TISSUE=CELL SUSPENSION CULTURE;
PubMed=10773344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P450 (Fragment).
                                                                                                                                                                                                                                                                                                                                      105 AA.
Query Match 55.7%; Score 39; DB 1
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome P450 monooxygenase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cicer arietinum (Chickpea) (Garbanzo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                         1 CFQWQREMRKVR 12
                                                                                                                                                                                 21 CFPSRREMGKVR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CFQWQREMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CFQWERLGKK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISSUE-PANICLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eurosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYP81E4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9SML1
                                                                                                                                                                                                                                                                                                                                                                  Q9XFD5
                                                                                                                                                                                                                                                                                                                                   O9XFD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                           RESULT 10
```

ô

Gaps

ö

Q9SML1

Ŋ

```
Search completed: February 21, 2003, 07:44:40 Job time : 21.8 secs
                                                                                                                                                              à
                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 5, Pl clone-MFC19.
Arabidopsis thaliana (Mouse-ear Cress).
Bukaryota; Viridiplanatae; Streptophyra; Embryophyta; Tracheophyta; Spermatophyta; endicotyledons; core eudicots; Rosidae; eurosids II. Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99397451; PubMed=10470850; Rankor T., Katch T., Sato S., Nakamura Y., Asamizu E., Kotani H., Miyajima N., Tabata S.; Ratchani H., Structural analysis of Arabidopsis thaliana chromosome 5. IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Rychlik I., Sebkova A.;
"Plasmid pJ of Salmonella enteritidis encoding hypothetical rep
                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                           55.7%; Score 39; DB 2; Length 329; 54.5%; Pred. No. 52; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.7%; Score 39; DB 3; Length 376; 60.0%; Pred. No. 60; ive 3; Mismatches 1; Indels
                              protein.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF268389; AAG17348.1; -.
InterPro; IPR000989; Rep.
Pfam; PF01446; Rep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z75101; CAA99406.1; -. SGD; S0005719; YOR193W. SGD; SEQUENCE 376 AA; 44131 MW; 976FDBCA43AB4F80 CRC64;
                                                                                                                           329 AA; 37819 MW; C3D88A9C0175155D CRC64;
                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ORF YORL93W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866 AA.
                                                                                                                                                                                                                                                                                                                                       376 AA
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                          Local Similarity 54.5
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                        308 FEWKTEVRKYR 318
                                                                                                                                                                                                                        2 FOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| |||:|:
181 FRWLREMKKL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FQWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=3702;
                                                                                                                            SEQUENCE
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      YOR193W
                                                                                                                                                                                                                                                                                                                                                      0085805
                                                                                                                                                                                                                                                                                                                                       008280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9FHI9
                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                          008280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9FHI9
RA
RIL
DR
DR
VW
SQ
                                                                                                                                                                                                                         ઠે
```

```
Sequence features of the regions of 1,011,550 bp covered by seventeen P1 and TAC clones.";
DNA Res 6.183-195(1999).
EMBL; AB018113; BAB09175.1; -.
SEQUENCE 866 AA; 100187 MW; 164FAB99H976D27D CRC64;
                                                                                                                                                                            Gaps
                                                                                                                                                                          0;
                                                                                                                            Query Match 55.7%; Score 39; DB 10; Length 866; Best Local Similarity 50.0%; Pred. No. 1.4e+02; Matches 6; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                            389 CFNWLLKFRKLR 400
                                                                                                                                                                                                                     1 CFQWQREMRKVR 12
                                                                                                                               Query Match
```

0

```
Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                             February 21, 2003, 07:37:21; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Geneseq 101002:*

| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78038
AAY78046
AAY78047
AAY78084
AAY78087
AAY78091
AAY78092
AAY78037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78072
                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                             US-09-743-107B-87
                                                                                                                                                                                                                                                                                                                 1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.5
97.0
97.0
97.0
97.0
97.0
                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      655
655
655
655
655
655
655
                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

| , | 1122 | 0 0 0 0
0 0 0 0
0 0 0 0 | 97.0
97.0
97.0 | 44.
6644. | 2222 | AAY78048
AAY78049
AAY78036
AAY78050 | ಐ ರಾ ಅ ೦ , | |
|--------------------------------|------------------------------|-------------------------------|----------------------|--------------------------------|----------------|--|------------------|---|
| | | | | 4 T L | | | ተ 4 ፕ | Human lactoferrin
Peptide for anti-u |
| | | | 97.0 | 15 | | | 1 1 10 10 | |
| | | | | 110 | | | ח הו | |
| | | | 97.0 | 19 | | | * 10. | |
| | | | | 17 | | | 4 | Human lactoferrin |
| | | | | 17 | | | 0 0 0 | |
| | | | | B 65 | | | | Ruman lactoferrin |
| | | | | 8 6 | | | | Human lactoferrin |
| | | | | 9 6 | | | | Amino acid sequen |
| | | | | 20 | | | | Anti microbial pep |
| . • | | | | 20 | | | - 1 (| Lactoferrin-relate |
| | | | | 202 | | | 0 - | Lactoferrin derive |
| | | | | 20 | | | · | Lactoferrin derive |
| | | | | 20 | | | 2.5 | Lactoferrin derive |
| | • | | | 7 0 | | | യ വ | Bowine lactoferrin |
| | | | | 20 | | | \ (1) | Anti-parasitic la |
| • | | | | 20 | | | 4 | iic 1 |
| . • | | | | 0 0 | | | | Peptide for anti-u |
| • | | | | 2 6 | | | 4 tr | Lactoferrin-deriv |
| , , | | | 97.0 | 200 | 17 | | 1 | Lactoferrin deriv |
| | | | | | | ALIGNMENTS | MENTS | |
| RESULT 1
AAY78072
ID AAY | LT 1
9072
AAY78072 | | standard; | . Peptide; | de; | 12 A. | | |
| A X | AAY78072; | .; | | • | • | | | |
| ž ti | 25-APR-2000 | 2000 | (first | st entry) | (, | | | |
| E Y | Human la | lactoferrin | errin | derived | | peptide SEQ | Q ID NO:72. | |
| X & & | Human; | lacto: | ferri | n; modi | fic | ation; in: | n'; | ion; tumour; |
| XX | urinary
bacteric | traci | t infe | ection;
servati | , co | urioar, intant infection; collitis; Candida
bactericidal; preservative. | inf | -microbial; and:-tumour;
ection; fungicidal; |
| XX 80 80 | Homo sar
Syntheti | sapiens
etic. | | | | | | |
| XX | WO200001730-A1 | 1730-4 | 41. | | | | | |
| X & : | 13-JAN-2000 | 2000. | | | | | | |
| X & I | 06-JUL-1999 | ,6661 | 166 | 9WO-SE0123 | 230 | | | |
| X | 06-JUL-1998;
17-JUL-1998; | 1998; | 986 | 98SE-0002441.
98SE-0002562. | 562 | | | |
| | 29-DEC-1 | 1998; | 386 | 3E-0004 | 614 | | | |

Dolphin GT;

Hanson LA, Mattsby-Baltzer I, Baltzer L,

WPI; 2000-147388/13

(ASCI-) A+ SCI INVEST AB.

K K X K X L X K

~

```
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired
                                                                                               AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                              anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, lactoferrin, modification; infection; inflammation; tumour;
food; infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urnary tract infection; colltis; Candida infection; fungicidal;
bactericidal; preservativa
             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                  98.5%; Score 66; DB 21; Length 12; 91.7%; Pred. No. 3.1e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltzer L,
                                                                Claim 22; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78038 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWARNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                   12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78038;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
```

AAY78001 to AAY78100 represent peptides having sequences based on human

```
0;
        binding to specific lattoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and way also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
lactoferrin. The peptides are taken up in the intestine through
                                                                                                                                                                                                                                                                                                                                                                 ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                            Length 12;
                                                                                                                                                                                                                                                                                                                          97.0%; Score 65; DB 21; Length 12
91.7%; Pred. No. 4.7e-05;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78046 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                            Local Similarity 91.7 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFÓWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78046;
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          d
8888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                         à
```

; 0

Gaps 0; m

; 0

Gaps

. 0

Length 12;

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/of prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammartions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and continual and the used clinically on a broad basis as lactoferrin at lower and and anti-infermations.
                 Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour;
 may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                       Score 65; DB 21;
Pred. No. 4.7e-05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                               AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 73; 102pp; English.
fungicidal and bactericidal and
                                                                                                                                                                                         97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                   1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-147388/13.
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                    12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                    Sequence
                                                                                                                                                                                                                         Matches
 88888888888
                                                                                                                                                                                                                                                                                                 엄
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through the opecific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, onlitis, and Candida infections and mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                              Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                      ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                  Score 65; DB 21; Length 12; Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.0%; Score 65; DB 21; Length 12; 91.7%; Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.7e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:84.
                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baltzer L,
                                                                                                                                                                                                                                         AAY78084 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 36; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I,
                                                97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0002562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                   bactericidal; preservative.
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                  Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                      1 CFQWXRNMRKVR 12
                                                                                                                                                     1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
                 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                                                                              25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                 Sequence
                                                                                                                                                                                                                                                                           AAY78084;
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                      Best Loca
Matches
                                                                                                                                                                                                                         AAY78084
XX SS
                                                                                                                      à
                                                                                                                                                   g
```

¥.

AAY78088 standard; Peptide; 12

Human lactoferrin derived peptide SEQ ID NO:88.

25-APR-2000

AAY78088;

4 Page

```
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                   Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection, fungicidal, bactericidal, preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.0%; Score 65; DB 21; Length 12; 100.0%; Pred. No. 4.7e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolphin GT;
                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 37; 102pp; English.
                                                                                                                    AAY78087 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0004614.
                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
                              1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-147388/13
CFQWXRNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
                                                                                                                                                                                       25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                      AAY78087;
                                                                                                d
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as curinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also an engicidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired ant: inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower costs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                    Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.0%; Score 65; DB 21; Length 12
100.0%; Pred. No. 4.7e-05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:91.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78091 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 37; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                   99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWXRNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 AA;
                                                                                                                                                                                                                                                     WO200001730-A1.
                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78091
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BXXXXX
```

.

Gaps 0;

12; Conservative

Matches

Best Local Similarity

1 CFQWXRNMRKVR 12

à

12

1 CFQWXRNMRKVR

RESULT 7

Tue Dec

Ŋ

```
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the directating. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78001 to AAY78100 represent peptides having sequences based on human
            Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.0%; Score 65; DB 21; Length 12; 91.7%; Pred. No. 4.7e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                                                              Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78092 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Page 38; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                        99WO-SE01230.
                                                                                                                                                                                                                                                          98SE-0002441.
                                                                                                                                                                                                                                                                           98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                   WO200001730-A1.
                                                                                                    Homo sapiens
                                                                                                                                                                                                                      06-JUL-1999;
                                                                                                                                                                                                                                                                             17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2000
                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                     13-JAN-2000
                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intential clactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower ceals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:37.
                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78037 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 38; 102pp; English
                                                                                                                                                                                                                               Hanson LA, Mattsby-Baltzer I,
                                                                                                                              98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999; 99WO-SE01230.
                                                                                                                                                             98SE-0004614.
                                                                                             99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bactericidal, preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 11; Conservative
                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWKRINMRKVR 12
                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MO200001730-A1.
                               WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                               06-JUL-1999;
                                                                                                                              06-JUL-1998;
                                                                                                                                                             29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JAN-2000
                                                              13-JAN-2000
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78037
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

0

ô

Gaps ö

Homo sapiens

φ

```
ö
                                                                                                                                                                                                                                                                                        through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as uninary tract infections, colitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fungicidal and bacteridal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would contain them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                             AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·
0
                                                                                                                                                                    New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 21; Length 13;
Pred. No. 5e-05;
0; Mismatches 1; Indels
                                                                                                        Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78048 standard; Peptide; 13 AA.
                                                                                                                                                                                                                Claim 12; Page 70; 102pp; English
                                                                                                       Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.0%;
91.7%;
                           98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-SE01230.
             98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.0
Best Local Similarity 91.7
Matches 11, Conservative
                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CFÓWQRNMRKVR 13
                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200001730-A1.
             06-JUL-1998;
                                          29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
AAY78048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
```

```
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                        AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó,
                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65, DB 21; Length 13;
Pred. No. 5e-05;
0, Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dolphin GT;
Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:49.
Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baltzer L,
                                                                                                           Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78049 standard; Peptide; 13 AA.
Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                  97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147388/13.
                              WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                      13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000
Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78049;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                        cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78049
à
```

0

ö

```
cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78050
                     8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                      havy8001 to havy8100 represent peptides having sequences based on human biactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment arrives infections, colitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicial and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 21; Length 13;
Pred. No. 5e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78036 standard; Peptide; 14 AA.
     Claim 18; Page 74; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapie
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78036;
\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{M}}{\times}\overset{\text{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infections and anti-tumoural properties they cannot be used clinically on a broad basis because of high production
urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                           97.0%; Score 65; DB 21; Length 14; 91.7%; Pred. No. 5.4e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78050 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-SE01230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                 Best_Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                 1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                         3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-147388/13.
                                                                                                                                                                                                                                     14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78050;
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                             Query Match
```

```
costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
```

14 AA; Sequence cost. 8888

Query Match Best Local Similarity 91.7 Matches 11; Conservative

Score 65; DB 21; Length 14; Pred. No. 5.4e-05; 0; Mismatches 1; Indels 97.0%; 1 CFQWXRNMRKVR 12 3 CFÓWORNMRKVR 14 ð

AAY78051 standard; Peptide; 14 AA. AAY78051; RESULT 15

Human lactoferrin derived peptide SEQ ID NO:51. 25-APR-2000 (first entry)

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative

Homo sapiens. Synthetic.

WO200001730-A1.

13-JAN-2000

99WO-SE01230. 06-JUL-1999;

98SE-0002441. 06-JUL-1998; 17-JUL-1998;

98SE-0002562. 98SE-0004614. 29-DEC-1998;

(ASCI-) A+ SCI INVEST AB.

Mattsby-Baltzer I, Hanson LA,

Dolphin GT;

Baltzer L,

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food WPI; 2000-147388/13.

Claim 18; Page 75; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also thugicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad beasis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and contact

14 AA; Sequence

Query Match

97.0%; Score 65; DB 21; Length 14;

0; Gaps ., 91.7%; Pred. No. 5.4e-05; tive 0; Mismatches 1; Indels 11; Conservative Best Local Similarity Matches 11; Conserv

1 CFQWXRNMRKVR 12 ð g

3 CFOWORNMRKVR 14

Search completed: February 21, 2003, 07:56:42 Job time : 28.093 secs

0;

Gaps

; 0

```
, Appli
, Appli
                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                       February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Ag
Sequence 1, Ag
Sequence 24, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, 1
Sequence 25, 1
Sequence 4, Ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8
Sequence 8
Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                            262574
                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-508-734-4
US-09-508-734-6
US-07-755-161A-10
US-07-891-174-10
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-891-174-3
US-08-204-487-1
US-08-256-771-24
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-508-734-8
US-07-755-161A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-381-984-24
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-693-274A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-464-182A-5
US-08-406-271-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -08-464-182A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-628-380-8
US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-891-174-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-204-487-7
                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      OM protein - protein search, using sw model
                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                    Issued Patents AA:*
                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                    1 CFOWXRNMRKVR 12
                                                                                                 US-09-743-107B-87
                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                      Sednence:
                                                                                                                                                                       Searched:
                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ño.
```

| Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 4, Sequence 4, Sequence 4, Sequence 6, Sequence 2, Sequen | |
|---|--|
| 2 US-08-406-271-2
3 US-08-724-586-2
4 US-09-932-190-2
2 US-08-655-640-4
1 US-08-655-640-4
1 US-08-655-640-4
1 US-08-461-333-4
1 US-08-461-333-4
3 US-08-461-333-4
4 US-08-476-798-4
1 US-08-476-798-4
4 US-08-453-703-2
1 US-08-453-703-2
2 US-08-455-106-2
3 US-08-455-106-2
3 US-08-455-106-2
4 US-09-265-577-2 | cation US/08204487 110N: WARMOTO, NAOKI WASHIMA, HIDEKI SBUCHI, WATARU WARKA, SHIGERAI SBAKO, SHUN'ICHI WASAKI, YOSHIHIRO HIDA, YOSHIHIRO TION: INHIBITORS FENDESS: BATERY ADMINISTRATOR, TESTA, HURWITZ & THIBBAULT STATE STREET NA ALENEIN PC-DOS/MS-DOS STATE STREET NA ALENEIN PC-DOS/MS-DOS STATE STREET NA ALENEIN PR-DOS/MS-DOS STATE STREET NA NUMBER: US/08/204,487 O2-MR-1994 ON: 514 INFORMATION: FELL FORM INFORM INF |
| 97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00
97.00 | |
| \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ | 87-3 3, App 1. 5565 1. 100R/R 1. 10 |
| 00000000000000000000000000000000000000 | SSULT 1 SSULT 1 SSULT 1 SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SETAT SETAT STAT STAT STAT STAT STAT S |

NAME/KEY: Peptide LOCATION: 1..18 OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE

TOPOLOGY: linear MOLECULE TYPE: peptide

FEATURE:

```
1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO ; FRAGMENT TYPE: US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                     07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                          ·
0
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: ENDPRODUCTS; AND METHODS OF THEIR USE
TITLE OF INVENTION: ENDPRODUCTS; AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.0%; Score 65; DB 2; Length 18; 91.7%; Pred. No. 3.6e-05; tive 0; Mismatches 1; Indels
                                                   Score 65; DB 1; Length 18; Pred. No. 3.6e-05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26,742
FR: 947-1-008A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-0
TELECOMMUNICATION INFORMATION:
TELEFAX: 201 343-1684
TELEFAX: 201 343-1684
TELEFAX: 201 343-1684
TELEFAX: 13521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TEMMOTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREH: 411 Hackensack Avenue
CITY: Hackensack
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                            ; Sequence 8, Application US/08485948
; Patent No. 5855882
 (20-37)"
                                                       97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIAME.
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                           Query Match
Best Local Similarity 91.75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWXRNMRKVR 12
OTHER INFORMATION:
                                                                                                                              1 CFOWXRNMRKVR 12
                                                                                                                                                                   1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Ne COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-485-948-8
                                                                                                                                                                                                                                              US-08-485-948-8
         ;
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                            RESULT 2
                                                                                                                                    à
                                                                                                                                                                   g
```

1 CFOWORINMRKVR 12

```
Sequence A Application US/0862380

PRESENTING A APPLICATION US/0862380

PRESENTING A SEQUENCE A APPLICATION OF ANTIBACTERIAL PROTEINS

TITLE OF INVESTMENT ON ANTION

NUMBERS DAYLORS A DAYLORS

APPLICANT: Has A DAYLORS A STREAM

APPLICANT: Has A DAYLORS A COMPANY IN SECURISES A COMPANY IN SECURIAE A COMPANY IN SECURISES A COMPANY IN SECURISES
```

```
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.0%; Score 65; DB 1; Length 20;
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19910905
CLASSIFICATION S 30
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTONNEY, AGENT INFORMATION:
NAME: WATTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRILING DATE:
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 2; I
Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEFRONE: 201,343-1684
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/07755161A Patent No. 5304633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELBEAK: 201 3-2 TELBEAK: 13351
TELEX: 13351
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acids STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: amine ar amnino acids strandeduction acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNMRKVR 12
                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                      07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-07-755-161A-3
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dd
```

us-09-743-107b-87.rai

Page

```
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
                                   OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 1; Length 20;
Pred. No. 4e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WACARNU
APPLICANT: TANAKA, SHICEKI
APPLICANT: TANAKA, SHICEKI
APPLICANT: TANAKA, SHUN'ICHI
APPLICANT: KAMASAKI, YOSHIMIRO
APPLICANT: KAMASAKI, YOSHIMIRO
APPLICANT: UCHIDA, TOSHIMI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATOMEVAGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08204487
Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
                                                                                                                                              NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CFÓWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                        JOURNAL:
                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                            VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                       ö
                                       Gaps
Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                       APPLICANT: Mamoru TOWITA et al.
IIILE OF INVENTION: Antimicrobial Peptides and an
IIILE OF INVENTION: Antimicrobial Agent
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: Ms-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           ; Sequence 3, Application US/07891174; Patent No. 5317084 care to GENERAL INFORMATION: APPLICANT: Mamoru TOMITA et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warren M. Cheek Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                 Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: modified site
                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-371-885
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE:
                                                                                                               2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                             1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                          US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY:
                                       Matches
                                                                               ŏ
```

us-09-743-107b-87.rai

```
US-08-256-771-24
                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                  Query Match 97.0%; Score 65; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                          ; LOCATION: 1..20; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN" US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/256,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,
FILING DATE: UNJY 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELEPRONMUNICATION INFORMATION:
TELEPRONMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 amino acids
                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                       MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                     NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS: Bil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                          RESULT 9

US-08-256-771-25

US-08-256-771-25

; Sequence 25, Application US/08256771

; Sequence 25, Application US/08256771

; GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING

TITLE OF INVENTION: PRODUCTS THEREWITH

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "Cys residues are protected to OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25
Score 65; DB 1; Length 20;
Pred. No. 4e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.0%; Score 65; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
IDENTIFICATION METHOD:
                                                                                          1 CFQWXRNMRKVR 12
                                                                                                                                2 CFOWORINMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRY: U.S.A.
20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
```

us-09-743-107b-87.rai

```
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REPERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR PRILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR PLING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "the specified peptide as well as peptides including the specified peptide as a fragment there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
OCHER INFORMATION: /note= "cysteine residues at positions 2
(OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.0%; Score 65; DB 1; Length 20; 91.7%; Pred. No. 4e-05; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                      COMPUTER ERADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IRM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
  805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                           US/08/381,984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-508-734-4; Sequence 4, Application US/09508734; Patent No. 6423509
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/38 FILING DATE: April 11, 1995 CLASSIFICATION: 252 PRICR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warten M. Cheek, Jr.
RECISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD:
OTHER INFORMATION: /n
OTHER INFORMATION: pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                            RY: U.S.A.
20005
                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note= "cysteine residues at positions 2 OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 1; Length 20;
Pred. No. 4e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NOWER: US/08/381,984 FILLNG DATE: APPLI 11, 1995 CLASSIFICATION: 252
                                                                                                                                                       ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE 32
ADDRESSEE: Wenderoth, Lind & Ponack
Sequence 24, Application US/08381984
                     Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                      STATE: D.C
                                                                                                                                                                                                                                                                 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-381-984-24
                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

0;

```
IDENTIFICATION METHOD:
OTHER INPORMATION: / hote= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 1;
Pred. No. 5e-05;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                33,367
                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-371-8850
                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.08;
91.78;
                    ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: modified site LOCATION: 4
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                     TELEFAX: 202-371-885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: the PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                           TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICANTION NUMBER: US/09/508,734
CURRENT FILING DATE: 1099-07-14
PRIOR APPLICATION NUMBER: RR1999-29351
PRIOR APPLICATION NUMBER: KR1999-29351
PRIOR APPLICATION NUMBER: KR1999-29351
RNOMER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 6
LIENGTH: 24
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                       ;
                                                                                             Query Match 97.0%; Score 65; DB 4; Length 22; Best Local Similarity 91.7%; Pred. No. 4.4e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 97.0%; Score 65; DB 4; Length 24; I Similarity 91.7%; Pred. No. 4.8e-05; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-175-161A-10

Sequence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: Diskette, 5.25 inch, 500Kb
COMPUTER: Displaying SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09508734 Patent No. 6423509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19910900 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                         1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 805 Fiftee CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                              2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           US-09-508-734-6
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                              g
```

ö

Gaps

```
THE OFF MARINET NATIONAL TOWNS AND A SEQUENCE OF SEQUE
```

```
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.0%; Score 65; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 5e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 21, 2003, 08:04:25 Job time : 8.93023 secs
                                                                                                                                                                                                                                                                                    FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                          DATE:
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                    US-07-891-174-10
                                                                                                                                                   JOURNAL:
                                                                                                                                                                                                                        PAGES:
                                                                                                                                                                                               ISSUE:
                                                                                                                                TITLE:
```

```
(without alignments)
54.162 Million cell updates/sec
                                                                                                                                                                                February 21, 2003, 08:08:15; Search time 6.88372 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: / cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: / cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
3: / cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
4: / cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: / cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
6: / cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: / cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
8: / cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
9: / cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: / cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: / cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: / cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: / cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: / cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
14: / cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156504 segs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                        US-09-743-107B-87
                                                                                                                                                                                                                                                                                                                                                                      1 CPQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                            Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

| | | Description | Sequence 2, Appli | 20, | Sequence 2, Appli | Sequence 6, Appli | Sequence 3, Appli | Sequence 23, Appl | 7, 4 | Sequence 4, Appli | 22, | 2, | Sequence 8, Appli | Sequence 29, Appl | ~ | Sequence 47985, A | Sequence 5715, Ap | Sequence 1031, Ap | 19, A | 119, | Sequence 119, App |
|-----------|--------|--------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|------------------|-----------------|-------------------|-------------------|------------------|---------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| SOMMERTES | | ID | US-09-798-869-2 | US-09-798-869-20 | US-10-023-096-2 | 9-698-861-60-SN | US-09-798-869-3 | US-09-798-869-23 | US-09-798-869-7 | US-09-798-869-4 | US-09-798-869-22 | US-09-888-320-2 | US-09-798-869-8 | US-09-798-869-29 | US-09-798-869-30 | US-09-864-761-47985 | US-09-738-626-5715 | US-09-764-864-1031 | US-09-978-295A-119 | US-09-978-697-119 | US-09-978-192A-119 |
| | | DB | 9 | σ | σι | σ | σ | 0 | 9 | σ | σ | σ | σ | σ | σ | 10 | σ | 10 | σ | σ | σ |
| | | Match Length | 15 | 25 | 694 | 15 | 15 | 25 | 15 | 15 | 25 | 489 | 15 | 15 | 15 | 21 | 98 | 95 | 338 | 338 | 338 |
| * | Query | Match | 97.0 | 97.0 | 97.0 | 85.1 | 71.6 | 71.6 | 59.7 | 58.2 | 58.2 | 55.2 | 53.7 | 53.7 | 53.7 | 52.2 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 |
| | | Score | 65 | 65 | 65 | 57 | 48 | 48 | 40 | 39 | 39 | 37 | 36 | 36 | 36 | 35 | 34 | 34 | 34 | 34 | 34 |
| | Result | No. | - | 7 | m | 4 | Ŋ | 9 | 7 | œ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |

| Sequence 119, App
Sequence 119, App
Sequence 14, Appl
Sequence 6, Appli
Sequence 24, Appli | Sequence 23, Appl
Sequence 32, Appl
Sequence 2, Appli
Sequence 2, Appli | | വവ | Sequence 12129, A
Sequence 13026, A
Sequence 26, Appl
Sequence 107, App | Sequence 2, Appli
Sequence 36085, A
Sequence 13, Appl
Sequence 33, Appl |
|--|--|---|--|--|---|
| 9 US-09-999-832A-119
9 US-09-978-189-119
9 US-09-796-753-14
10 US-09-981-649A-6 | 10 US-09-981-649A-32
10 US-09-981-649A-32
10 US-09-795-691-2
10 US-09-981-649A-28 | | 9 US-10-219-248-5
9 US-10-219-247-5
10 US-09-855-722-5
10 US-09-944-849-4
10 US-09-864-761-46393 | 10 US-09-815-242-12129
10 US-09-815-242-13026
9 US-09-796-753-26
10 US-09-867-852-107 | 9 US-09-759-508B-2
10 US-09-864-761-36085
9 US-09-956-206A-13
9 US-09-735-056-33 |
| 338
338
553
553 | , ៧ ៧ ៧ ៧
, ៧ ៧ ៧ ៧
, 4 4 6 0 | 846
1212
1212
1212 | 1238
1238
1238
1238 | 62
62
333
1258 | 26926
28
31
344 |
| 50.7 | 50.7 | 50.7 | 50.7
50.7
50.7
50.7 | 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 49.3
47.8
47.8
67.8 |
| W W W W W | 1 41 41 41 4
1 60 60 60
1 61 41 41 41 41 | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | | 32233 |
| 01222 | 2 2 2 2 2 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 9 9 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | 6 8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 | 8 6 4 4
8 6 0 H | ል ቁ ቁ ቁ
ሪ ዬ ቁ ጊ |

ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 9; Length 15;
Pred. No. 1.8e-05;
0; Mismatches 1; Indels
Sequence 2, Application US/09798869
Sequence 2, Application US/0979869
Selection No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANTON: BIOACTIVE PEPTIDES
FILE REFERENCE: ASJOSP - PCT-USA-A
CURRENT FILING DATE: 2001-02-27
FRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
SOFTWARE: FASELED ION WINDER: GENORE SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKOAL; APPLICANT: BALDUR SVEINBJ (RNSSON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ωp
```

0;

```
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: CAPRINE
                                                                                                                                                                                                          9-698-861-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10023096

Sequence 2, Application US/10023096

Patent No. US20020160941A1

GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kruzel, Marian L.
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                            Score 65; DB 9; Lengtn 20, Pred; No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Jacobson, Price, Holman & Stern 400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT PEPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FESTEREQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10505/P58185C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 30-SEPT-1996
APPLICATION UNDRER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAWE: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                           97.08;
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 393-5950
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington D.C.
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWXRNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CFÓWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens) OTHER INFORMATION: sequence)
US-09-798-869-6
                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
Score 65; DB 9; Length 694;
Pred. No. 0.00066;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.1%; Score 57; DB 9; Length 15; 83.3%; Pred. No. 0.00044; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.6%; Score 48; DB 9; Length 15; 63.6%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                  CONTRACTOR APPLICATION US/08798869

PUBLICATION NO. US20030022821A1

GENERAL INFORMATION:

APPLICANT: USTEIN REKDAL

APPLICANT: (YSTEIN REKDAL

APPLICANT: LARS VORLAND

APPLICANT: LARS VORLAND

APPLICANT: LARS VORLAND

TITLE OF INVERTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798.869

CURRENT PILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: CT/GB99/02851

PRIOR APPLICATION NUMBER: GB9818938.4

PRIOR PRIOR DATE: 1999-08-31

PRIOR PRILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: GB9818938.4

PRIOR PRILING DATE: 1999-08-38

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FABELSEQ FOR WINDOWS VERSION 4.0

SERVICE IN NO 65 SEQ ID NOS: 300

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: (YSTEIN REGOLA
APPLICANT: (YSTEIN REGOLA
APPLICANT: EARS VORTAND
APPLICANT: LARS VORTAND
TILLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-36
NUMBER OF SEQ ID NOS: 30
SOFTWARE: RESURED FOR WINDOWS VERSION 4.0
SCOTTWARE: PASKEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION: APPLICANT: JOHN SIGURD SVENDSEN
     97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Seguence
Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                           1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWXRNMRKVR 12
                                                                                                                                                         22 CFÓWQRINMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CFOWOWNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.2%; Score 39; DB 9; Length 15; 54.5%; Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.2%; Score 39; DB 9; Length 25; 54.5%; Pred. No. 0.97; 1ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                    APPLICANT: O'GNI SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO: SEQ ID WINDS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSEEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                    Sequence 4, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 54.5
hes 6; Conservative
         1 CFQWXRNMRKV 11
                                                    3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CLRWONEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-798-869-22
                                                                                                                                                  US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 22
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: synthetic peptide (modified form of homo sapiens OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.6%; Score 48; DB 9; Length 25; 63.6%; Pred. No. 0.026; tive 2; Mismatches 2; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.7%; Score 40; DB 9; Length 15; 54.5%; Pred. No. 0.4; Live 2; Mismatches 3; Indels
2; Mismatches
                                                                                                                                                                                                                                                                            APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDOR SVEEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9918938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 23
LENGTREE: AsstSEQ for Windows Version 4.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LARS VORLAND
TITLE OF INVENTION: BICACTIVE PEPTIDES
TITLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                              ; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/09798869
; Publication No. US20300202821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserva
                                          1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CYQWQRRMRKL 13
                                                                                              3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: CAPRINE US-09-798-869-23
                                                                                                                                                                                        US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7-698-867-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
  Matches
```

à

, 0

ö

```
US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                      Sequence 2. Application US/0988320
Publication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: Debarber, Andrea E.
APPLICANT: Miluli, Khisimuzi
APPLICANT: He Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFERENCE: 015280-413100US
CURRENT APPLICATION NUMBER: US/09/888,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
. ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.2%; Score 37; DB 9; Length 489; 54.5%; Pred. No. 36; 3; Indels trive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.7%; Score 36; DB 9; Length 15; 54.5%; Pred. No. 2; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: A34.049-PCT-USA-A
FILE REFERENCE: A34.049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: G99-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 30
SEQ ID NOS: 30
SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09798869; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYEINBJ (RNSSON
APPLICANT: BALDUR SYEINBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54...
And 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 COKWPRRMRKM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CLRWQWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 489
RESULT 10
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.7%; Score 36; DB 9; Length 15; 45.5%; Pred. No. 2; 2; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.7%; Score 36; DB 9; Length 15; llarity 45.5%; Pred. No. 2; Conservative 3; Mismatches 3; Indels
RESULT 12
US-09-798-869-29
Sequence 29, Application US/09798869
Sequence 29, Application US/09798869
PUDLICATION. US20030022821A1
GENERAL INFORMATION:
APPLICANT: UOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVENDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BIODCTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FESESEQ FOR WINDOWS VETSION 4.0
SEQ ID NO 30
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-798-869-30
. Sequence 30, Application US/09798869
. Publication No. US20030022821A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CFRWOWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CFRWQWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: BOVINE
US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: BOVINE
```

```
2 FOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::| :||:|
73 FEYRROLRKIR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-738-626-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5715
LENGTH: 86
                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
APPLICANY: Rank, David R.
APPLICANY: Chen, Wensheng
ITILE REPRENEEMES: According STATE STERRESION ANALYSIS BY MICROARRAY
ITILE REPRENEEMES: According STATE STERRESION ANALYSIS BY MICROARRAY
ITILE REPRENEEMES: According STATE STERRESION ANALYSIS BY MICROARRAY
CORREMY THING DATE: 2001-05-24
FRICK APLICATION NUMBER: 2001-05-24
FRICK APLICATION NUMBER: 2004-03-24
FRICK APLICATION NUMBER: 2006-03-24
FRICK APLICATION NUMBER: 2007-03-24
FRICK APLICATION NUMBER: 2007-03-36
FRICK 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

OTHER INFORMATION: MAP TO AL096701.14

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

US-09-864-761-47985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 10; Length 21; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
```

.; 0

Gaps

0;

1; Indels

0; Mismatches

RESULT 15
US-09-738-626-5715
Sequence 5715, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:

g

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 9; Length 86;
Pred. No. 23;
4; Mismatches 2; Indels
                                                                                                                                                                                           FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/737484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159163
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: February 21, 2003, 08:11:55 Job time: 7.88372 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Corynebacterium glutamicum
MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 50.7%; Similarity 45.5%; 5%; Conservative
                                      HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                  OZAKI, AKIO
```

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec Run on:

US-09-743-107B-87 67 Title: Perfect score:

1 CFQWXRNMRKVR 12

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | lactotransferrin | lactoferrin - goat | - 1 | μ | | | En/Spm-like transp | | dynein beta heavy | apolipoprotein B-1 | probable monooxyge | hypothetical sh3-c | | Fl511.22 [imported | | probable proteinas | | MAP1 protein - myx | histidyl-tRNA synt | hypothetical prote | | protein F21H11.2 [| carcinoembryonic a | 26S proteasome SU | | pyridoxamine 5'-ph | probable pyridoxam | hypothetical prote | hypothetical prote |
|-----------|-----------------------|------------------|--------------------|--------|--------|--------|--------|--------------------|------------|-------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|-------------------|--------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ID | TEHUL | JC2323 | S52107 | AB0858 | T22597 | A28438 | A84471 | T24218 | T08030 | B60950 | C70655 | T39801 | C84325 | C96582 | AD2346 | A24470 | 137477 | B36418 | F81660 | T25415 | A45687 | D88450 | D33876 | E90094 | H97451 | AB2670 | 44 | 70 | AB2154 |
| | DB |
 rd
 | 7 | N | N | N | Н | 7 | 0 | 7 | N | 7 | 7 | 7 | ~ | 7 | N | N | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | N | N | ~ | 7 |
| | Length | 711 | 708 | 33 | 511 | 275 | 707 | 531 | 536 | 4568 | 274 | 489 | 501 | 584 | 124 | 298 | 361 | 365 | 369 | 428 | 742 | 749 | 2700 | 114 | 205 | 206 | 206 | 208 | 376 | 649 |
| ale | Query
Match Length | 97.0 | 71.6 | 67.2 | 61.2 | 58.2 | 58.2 | 26.7 | 26.7 | 26.7 | 55.2 | 55.2 | 55.2 | 55.2 | • | 53.7 | | 53.7 | | | 53.7 | 53.7 | | • | 52.2 | | | 52.2 | | 52.2 |
| | Score | 65 | 48 | 45 | 41 | 39 | 39 | 38 | 38 | 38 | 37 | 37 | 37 | 37 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 35 | 35 | 32 | 35 | 32 | 35 | 35 |
| | Result
No. | П | Ŋ | 3 | 4 | ហ | 9 | 7 | c c | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 |

| hypothetical prote | RNA 1a protein - b | phytochrome C - so | pyruvate carboxyla | pyruvate carboxyla | probable helicase | trichohyalin like | resistance protein | protein UNC-89 - C | vif protein - simi | hypothetical prote | arginyltransferase | signal peptidase I | 33.3K hypothetical | conserved hypothet | hypothetical prote |
|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T28820 | P1BVBB | T14803 | C97686 | AE2911 | T41378 | B85431 | T30563 | T29757 | 807989 | D89836 | AI3401 | E87515 | G86403 | C82234 | T33211 |
| 0 | Н | (1 | 7 | N | ~ | N | ~ | 7 | ~ | ~ | 7 | N | N | N | 7 |
| 932 | 996 | 1135 | 1174 | 1174 | 1213 | 1432 | 1804 | 6642 | 214 | 224 | 249 | 255 | 289 | 323 | 335 |
| 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 |
| 35 | 35 | 35 | 32 | 35 | 35 | 35 | 35 | 35 | 34 | 34 | 34 | 34 | 34 | 34 | 34 |
| 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

| | RESULT 1
TFHUL |
|---|---|
| | lactotransferrin precursor [validated] - human
N;Alternate names: lactoferrin |
| | C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #fext change 08-Dec-2000 |
| | C;Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74 |
| | submitted to the EMBL Data Library, March 1994 |
| | A;Reference number: G06820 |
| _ | A;Accession: G01394 |
| _ | A;Status: preliminary; translated from GB/EMBL/DDBJ |
| | A; Molecule type: mRNA |
| | A;Residues: 1-711 <cho></cho> |
| | A; Cross-references: EMBL: U07643; NID: q467236; PIDN: AAB60324.1; PID: q467237 |
| | R; Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. |
| | Nucleic Acids Res. 18, 5288, 1990 |
| | A; Title: Complete nucleotide sequence of human mammary gland lactoferrin. |
| | A; Reference number: S11228; MUID: 90384839; PMID: 2402455 |
| _ | A;Accession: S11228 |
| | A;Molecule type: mRNA |
| | A;Residues: 1-148,'T',150-422,'C',424-711 <rey></rey> |
| | A; Cross-references: EMBL: X53961; NID: q34415; PIDN: CAA37914.1; PID: q34416 |
| _ | R; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T. |
| | Mol. Endocrinol. 6, 1969-1981, 1992 |
| | A; Title: Differential molecular mechanism of the estrogen action that regulates lactofer |
| | A;Reference number: A45401; MUID:93125571; PMID:1480183 |
| | A;Accession: A45401 |
| | A; Molecule type: DNA |

A)Residues: 1-15 <TEN>

A,Gross-references: GB:SS2659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A,Experimental source: placenta A,Experimental source: placenta A,Note: sequence extracted from NCBI backbone (NCBIP:122202) R;Powell, M.J.; Ogden, J.E. Nucleic Acids Res. 18, 4013, 1990 A;Title: Nucleic Gequence of human lactoferrin cDNA. A;Reference number: S10324; MUID:90326549; PMID:2374734 A;Accession: S10324

A; Molecule type: mRNA A; Residues: 3-711 < POW>

A,Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-3155, 1991
A;Tile: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066
A;Accession: S15853

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 20-31 <ST1>

A,Accession: \$20841 A,Molecule type: protein A,Residues: 20-28,'X',30-31 <ST2>

ó

```
71.6%;
Query Match
Best Local Similarity 63.5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-33 <QIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 CYOWOKKOMRKL 29
                                                                                                                                                                                                         1 CFOWKRNMRKV 11
                                                                                                                                                                                                                                                                                          38 CYOWORRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-511 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                         852107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Reb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Date: 20-Reb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2329
B;Accession: JC2323; MulD:9438047; PMID:8093048
A;Reference number: JC2323; MulD:94380047; PMID:8093048
A;Accession: JC2323
A;Accession: JC2323
A;Accession: JC3233
A;Accession: JC3233
A;Accession: JC3233
A;Accession: JC333
A;Accession: JC3333
A;Accession: JC33333
A;Accession: JC3333
A;Accession: JC3333
A;Accession: JC33333
A;Accession: JC33333
A;Accession: JC33333
A;Accession: JC33333
A;Accession: JC33333
A;A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 3-701, 'SWKEVN' <PAN>
A;Experimental Source: normal breast tissue
R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Bur. J. Blochem. 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A;Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein

A; Molecule type: protein

A; Residues: 20-140,142-1169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4

A; Note: this is the final paper in a series

R; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

B; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

A; Houen, G.; Lactoferrin. 241, 393-308, 1996

A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin

A; Reference number: S74119; MUID:97054624; PMID:8898921
                                                                                     띹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65,39-56,135-218,177-193,130-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbobydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                                                                                                                                                                                                                                                                                                         A, Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyd
                                                                                 οĘ
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 398-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression
A;Reference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                A Molecule type: mRNA
A,Residues: 436-487,'A', 489-711 cRAD>
A,Cross-references: EMBL:M18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%; Score 65; DB 1; Length 711
91.7%; Pred. No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: duplication; glycoprotein; iron binding; milk F;1-15/Domain: signal sequence #status predicted <5:To
F:20-711/Product: lactotransferrin #status experimental <MAT> F:21-356/Domain: transferrin repeat homology <TRH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A61169; MUID: 91235214; PMID: 1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:119368; OMIM:150210
A;Map position: 3q21-3q23
C;Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CFOWORNIMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A61169
                                                                                                                                                              A; Accession: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S74119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactoferrin - goat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB:LTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
hypothetical protein STY1070 [imported] - Salmonella enterica subsp. enterica serovar T C, Species: Salmonella enterica subsp. enterica serovar Typhi A,Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CjAccession: AB0658

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Ajathora: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. Ajtitle: Complete genome sequence of a multiple drug resistant Salmonella enterica sero A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Biolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: S52107; MUID:95127729; PMID:7827104
A;Accession: S52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AL513382; PIDN: CAD06049.1; PID: 916504016; GSPDB: GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F53H4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                      lactoferrin - sheep (fragment)
C,Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C,Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.2%; Score 41; DB 2; Length 511; 58.3%; Pred. No. 9.1;
Length 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.2%; Score 45; DB 2; Length 33; 54.5%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
   Score 48;
Pred. No.
```

.. 0

ö

Best Loca Matches

à

ò

```
C;Accession: T08030
R;Mitchell, D.R.; Brown, K.S.
A;Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: Z16302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ajntrons: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nucleotide binding; P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
A,Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUD:20083487; PMID:10617197
A,Rocession: A84471
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-536 <WIL>
A;Residues: EMBL:Z35602; PIDN:CAA84671.1; GSPDB:GN00021; CESP:R13G10.2
                                                                                                                                                                                                                  A;Cross-references: GB:AE002093; NID:g4586022; PIDN:AAD25641.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g05550
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R13G10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dynein beta heavy chain - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-4568 <MIT>
A,Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R)Gardner, A.
Submitted to the EMBL Data Library, August 1994
A)Reference number: Z19857
A)Accession: T24218
A)Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB Pred. No. 34; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.7%; Score 38; DB 50.0%; Pred. No. 34; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T08030
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: clone R13G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain 21gr
                                                                                                                                                                                                                                                                                                                                                                   56.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: CESP:R13G10.2
A,Map position: 3
A,Introns: 64/3; 194/1; 404/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 CIDWGRDDRKVK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                          A)Residues: 1-531 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 ÓWFRNMKK 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 QWXRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: ODA4
A, Map position: IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactoferrin precursor - mouse

Nathernate names: lactoferrin

Shalternate names: lactortransferrin

Arritle: Lactortransferrin is the major estrogen inducible protein of mouse uterine secre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A84471

K;Lin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, M.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4 A;Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Liu, Y.; Teng, C.T.
J. Biol. Cham. 266, 21880-21885, 1991
A;Title: Charcterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A84471
En/Spm-like transposon protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                          A;Nap position: X
A;Introns: 67/1; 155/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.2%; Score 39; DB 2; Length 275; 63.6%; Pred. No. 12; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.2%; Score 39; DB 1; Length 707; Best Local Similarity 54.5%; Pred. No. 29; Matches 6; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C'Superfamily: transferrin; transferrin repeat homology C'Keywords: duplication; glycoprotein F;1-19/Domain: signal sequence #status predicted <SIG>F;20-707/Product: lactotransferrin #status predicted <MAT>F;358-695/Domain: transferrin repeat homology <TRH2>
                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                       R,Dobson, R. submitted to the EMBL Data Library, October 1996 A;Reference number: Z19587 A;Recession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 63.6%;
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 3-707 <PEN>
A;Cross-references: EMBL:J03298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A41205
A;Molecule type: DNA
A;Residues: 1-15 <LIU>
A;Cross-references: GB:M74778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 FOWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 CLRWONEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWXRNMRKV 11
                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-275 <WIL>
                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

Best Loca Matches

ö

.; 0

Gaps

Matches

g

```
Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsc Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Mature 408; Hughes, B.; Huizar, L. Alanser, C.J.; Hughes, D.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nature 408; Muster, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali A.; Rooney, T.; Rowley, D.; Sakano, H. A.; Luros, J.S.; Maiti, R.; Marziali A.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Sun, H.; Tallon, A;Reference and analysis of Chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MuID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84325
K;Ngy, W. V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, i. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; I. A;Althe: Genome sequence of Halobacterium species NRC-1.
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T39801. R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, July 1999
A;Reference number: Z21880
A;Accession: T39801
A;Accession: T39801
A;Residues: L-501 *MD>
A;Residues: L-501 *MD>
A;Residues: L-501 *MD>
A;Cross-references: EMBL-AL109731; PIDN:CAB52037.1; GSPDB:GN00067; SPDB:SPBC19C2.10
A;Experimental source: strain 972h-; cosmid c19C2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: GB: AE004437; NID: g10581192; PIDN: AAG19967.1; GSPDB: GN00138
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fi5il.22 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2; Length 584;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.2%; Score 37; DB 2; Length 501; 60.0%; Pred. No. 48; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 41.7%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 CFTWRKDMERKR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Gene: SPDB:SPBC19C2.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-584 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWXRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 CTRWVRNMDK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: C84325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: VNG1732C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 196/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
C;Accession: B60950
R;Law, A.; Scott, 100-1120, 1990
J. Liple: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A;Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Note: authors translated the codon ATA for residue 8 as Val
C,Superfamily: apolipoprotein B
C,Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable monooxygenase - Mycobacterium tuberculosis (strain H37RV)
[5] Species: Mycobacterium tuberculosis
[5] Species: T. Juliania Mycobacterium tuberculosis
[6] Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Davies, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature, 393, 537-544, 1998
[A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Reference number: A70500; MUID:98295987; FMID:9634230
[A.Accession: C70655
[A.Accession: C70655]
[A.Accession: P.MA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-489 <COL>
A;Cross-references: GB:283864; GB:AL123456; NID:G3261687; PIDN:CAB06212.1; PID:e301250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T39801
hypothetical sh3-containing protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                        Score 38; DB 2; Length 4568; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.2%; Score 37; DB 2; Length 274; Best Local Similarity 66.7%; Pred. No. 27; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.2%; Score 37; DB 2; Length 489; llarity 54.5%; Pred. No. 47; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                            4; Indela
                                                  F;2202-2209/Region: nuclectide-binding motif A (P-loop) F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein B-100 - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Experimental source: strain H37Rv C; Genetics:
                                                                                                                                                                   h 56.7%;
Similarity 41.7%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       1852 CPÓWQSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                       1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 COKWPRRMRKM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-274 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 WDRNLRKFR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 WXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: B60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: Rv3854c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

RESULT 11 C70655

원 ð

RESULT 12

g à

ö

Gaps

A;Status: preliminary

```
0
A;Molecule type: DNA
A;Residues: 1-124 <STO>
A;Crossicues: 1-124 <STO>
A;Cross-references: GB:AE005173; NID:g4587555; PIDN:AAD25786.1; GSPDB:GN00141
C;Genetics:
A;Gene: F1511.22
A;Map position: 1
                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                         Query Match 53.7%; Score 36; DB 2; Length 124; Best Local Similarity 50.0%; Pred. No. 19; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                           2 FOWXRNMRKV 11
                                                                                                                                                                                                                                                                           ð
```

11 FRWSRSRKI 20

q

Dypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)

Dypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)

A,Note: Nostoc sp.

A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C,Bate: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C,Accession: AD2346

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sh. (2012)

A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A,Stelence number: AB1807; MUD:21595285; PMID:11759840

A,Status: preliminary

A,Status: preliminary

A,Reseidues: 1-298 «KUR>

A,Coss-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179

A;Gene: alr4323

Score 36; DB 2; Length 298; Pred. No. 45; 3; Indels 0; Mismatches Query Match 53.7%; Best Local Similarity 66.7%; Matches 6; Conservative (

o;

0; Gaps

Search completed: February 21, 2003, 08:02:43 Job time : 11.6047 secs

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2003, 07:28:06; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec Run on:

US-09-743-107B-87 67

1 CFQWXRNMRKVR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | %
Query
Match | ,
,
, | 9 | SUMMARIES | |
|--------|--------|---------------------|-------------|-----|------------|--------------------|
| Score | - : | datch | rength | H - | 1D | Description |
| 9 | 2 | | 711 | Н | TRFL HUMAN | 80 |
| 4 | 80 | | 708 | Н | TRFL_CAMDR | _ |
| 4 | 80 | i, | 708 | Н | TRFL CAPHI | Q29477 capra hircu |
| 4 | 0 | 59.7 | 292 | Н | NLA DROME | ~ |
| 4 | 0 | φ. | 695 | Н | TRFL HORSE | |
| M | σ | 58.2 | 707 | Н | TRFL MOUSE | |
| m | æ | 56.7 | 146 | Н | RPOB_LIBAF | P41187 liberibacte |
| m | 80 | 56.7 | 783 | Н | YNR2_CAEEL | |
| m | 89 | 56.7 | 4568 | Н | DYHB CHLRE | Q39565 chlamydomon |
| m | 9 | 53.7 | 365 | Н | 1A34 HUMAN | |
| m | 9 | 53.7 | 369 | ۲ | SPI1 MYXVL | |
| m | 9 | 53.7 | 428 | Н | SYH CHLMU | Q9pjj9 chlamydia m |
| æ | 9 | 53.7 | 749 | Н | VP4 ROTGA | Q04916 rotavirus (|
| c | ι
Ω | 52.2 | 62 | Н | RL28 THETN | Q8r9ul thermoanaer |
| e | Ŋ | 52.2 | 996 | ⊣ | V1A BBMV | |
| m | ιÙ | 52.2 | 1135 | ٦ | PHYC SORBI | |
| m | 4 | 50.7 | 214 | Н | VIF SIVS4 | |
| m | | 50.7 | 422 | Н | PAFA_CHICK | |
| m | 4 | 50.7 | 428 | Н | SYH_CHLTR | |
| m | 4, | 50.7 | 430 | Н | SYH CHLPN | Q9z7p1 chlamydia p |
| m | 4 | 50.7 | 455 | Н | YKYL CABEL | Q19910 caenorhabdi |
| m | | 50.7 | 480 | н | YQS1_CAEEL | Q09309 caenorhabdi |
| m | 4 | 50.7 | 200 | ч | | |
| | 4 | 50.7 | 522 | Н | COR1_SCHPO | O13688 schizosacch |
| 5 | | 50.7 | 663 | Н | PDI1 HUMAN | Q9ulc6 homo sapien |
| | | 50.7 | 765 | Н | YOOR HUMAN | 8 homo |
| M | 4 | 50.7 | 989 | Н | T100 HUMAN | 075448 homo sapien |
| | | 50.7 | 1202 | Н | JAG2 RAT | P97607 rattus norv |
| m | | 50.7 | 1238 | Н | JAG2_HUMAN | Q9y219 homo sapien |
| m | 4 | 50.7 | 1247 | Н | JAG2 MOUSE | |
| m. | | 50.7 | 2151 | Н | RRPL_SEOU8 | 4. |
| m | 4 | 50.7 | 4568 | Н | | \sim |
| 33. | Ŋ | 20.0 | 727 | H | KDGA RAT | P51556 rattus norv |

| 088673 mus musculu
099up4 staphylococ
P16903 ovine lenti
058118 methanococc
P32174 escherichia
P46421 arabidopsis
09kd18 bacillus ha
Q55185 synechocyst
P16710 vaccinia vi
P26929 lactobacill
P26929 lactobacill
095125 homo sapien | |
|--|--|
| KDGA MOUSE RL28 STAAM RL28 STAAM YOUVS YOU METJA FDOI ECOLI CCDA BACHH CCDA BACHH Y495 SYNY3 VA16 VACCV URBI LACFE Z202 HUMAN | |
| аанаааааааа | |
| 730
1444
1744
1722
1722
1722
1723
173
173
173
173 | |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | |
| ип п п п п п п п п п п п п п п п п п п | |
| W W W W W W W W W W W W W W W W W W W | |

ALIGNMENTS

| RESULT 1 TREL HUMAN AC 096KZ AC 096KZ DDT 121-UU DDT 12 |
|--|
|--|

a

```
SEQUENCE OF 237-711 FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Mhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N. Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan T., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis
and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
                                                                                                                                                                                                            MEDLINE=82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                             Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031, PubMed=3477300;
Rado T.A., Weil X., Benz E.J. Jr.,
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutagenesis of the histidine ligand in human lactoferrin: iron
                                                                                                    MEDLINE-85076667; PubMed-6510420; Mazurier J., Schoentgen F., Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F., Hegrand D., Spik G., Montravil J., Jolles P.; "Human lactotransferrin: amino acid sequence and structural comparisons with other transferrins.";
                                                                                                                                                                                                 PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding properties and crystal structure of the histidine-253-->methionine mutant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                          Jolles P.;
"An 88 amino acid long C-terminal sequence of human
                                      Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353
MEDLINE=97156796; PubMed=9003186;
                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 670:243-254(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acta Crystallogr. D 51:629-646(1995).
                                                                 Nucleic Acids Res. 18:4013-4013(1990)
                                                                                                                                                                       J. Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                              MEDLINE=82262043; PubMed=7049727;
                          MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 142:107-110(1982).
SEQUENCE OF 3-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood 70:989-993(1987).
             TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 609-711
                                                                                         SEQUENCE OF 20-711.
                                                                                                                                                                                                                                                                                                                                                                                    lactotransferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resolution
                                                                                                                                                                                                                                        Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker E.N.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING DF AN ANION, USUALLY BICARBONATE.
PUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY. LACTOFERROXIN A SHOWS PREPERBRINGE FOR MU-RECEPPORS, WHILE IACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREPERBINGE FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE-911.66929; PubMed=136923;
Tani F., Io K., Chiba H. Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kilithworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
Hejtmancik J.F., Teng C.T.;
Hejtmancik J.F., Teng C.T.;
"Familial eubepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.";
Mol. Vision 4:31-32(1998)
                                                                                                                                                                                                  Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N., Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Secreted.
-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DCMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agric. Biol. Chem. 54:1803-1810(1990).
                                                                                      Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                             MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF332168; AAG48753.1; -. BC015822; AAH15822.1; -. BC015823; AAH15823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M73700; AAAS9479.1; -.
X52941; CAA37116.1; -.
U95626; AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M83202, AAA59511.1, -.
M83205, AAA58656.1, -.
M18642, AAA86665.1, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X53961; CAA37914.1; -: EMBL; U07643; AAB60324.1; -. EMBL; M93150; AAA36159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS THR-30 AND ARG-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from human lactoferrin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1LCF; 31-AUG-94.
1LCT; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-JUL-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-0CT-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96-NON-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9873069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $11228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1LFH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1LGB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1VFD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Mammary gland;
Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (UUN-1999) to the EMBL/Genbank/DDBJ databbases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORD WITH THE BINDING OF AN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                  · 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PERINTS; PRO0425; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
            97.0%; Score 65; DB 1; Length 711; 91.7%; Pred. No. 0.00015; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                           Camelus dromedarius (Dromedary) (Arabian camel).
                                                                                                                                                                                                                      TRFL_CAMDR STANDARD; PRT; 708 AA. 09TUM0; 09MZS5; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AJ131674; CAB53387.1; -- MBLL, AR16899; AAF82241.1; -- HSSP, O77811, 1B1X. InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.
BY
BY
BY
BY
BY
BY
                            Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
708
363
463
708
708
192
192
200
264
399
                                                                                    1 CFOWXRNMRKVR 12
                                                                                                                           39 CFOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
SIGNAL
CHAIN
REPEAT
REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                               RESULT 2
TRFL CAMDR
                                              Matches
                                                                                                                       g
                                                                                                                                                                                                                                          HERETERETERED BREEF BREE
```

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IN-LINKED (GLUNC. ...) (POTENTIAL).
IN-LINKED (GLUNC. ...) (POTENTIAL).
IN-LINKED (GLUNC. ...) (POTENTIAL).
ILLS -> PLF (IN REF. 2).
ILLS -> PL (IN RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.6%; Score 48; DB 1; Length 708; 66.7%; Pred. No. 0.21; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRFL_CAPHI STANDARD; PRI; 708 AA. 029477; 029479; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 CAQWORRMKKVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642 (
708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=9925;
        DISULFID
                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                    DISULFID
                                                                                                                                               DISULFID
                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                        METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                    METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRFL_CAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
```

```
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                 NIA DROME STANDARD; PRT; 292 AA. 09XZL8; 09V391; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                Nebula protein.
NLA OR CG6072.
                                                                                                                                                                                                                                                                                                                                                                              females.
                                                          NLA DROME
                                                                                             DETICATION OF THE STANTANT OF 
                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ( POTENTIAL) ( POTENTIAL) ( POTENTIAL) ( POTENTIAL) (
                                                                                                                                                                                                                                                                                                                                                                                             fransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.6%; Score 48; DB 1; Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F2EDA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - V ( IN REF. 2).

- N (IN REF. 2).

2 - N (IN REF. 2).

5 - P (IN REF. 2).

5 - N (IN REF. 2).

5 - O (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.21;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
N-LINKED
N-LINKED
I -> V (II
L -> R (II
Q -> K (II
F -> P (II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                           PEGM, PF00405, transferrin, 2.
PRINTS, PR00422, TRANSFERRIN.
SMART; SM00094, TR. FER, 2.
PROSITE; PS00205, TRANSFERRIN 1, 2.
PROSITE; PS00206; TRANSFERRIN 2, 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
                                                                                                                                                                                                                                                             InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77358 MW;
                                                                                                                                                                                                     EMBL, U53857; AAA97958.1; -. EMBL, X78902; CAA55517.1; -. HSSP; O77698; ICE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
```

```
REGUENCE EXECUTED STREET STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE -!- SIMILARITY: BELONGS TO THE DSCRI FAMILY.
```

Gaps

; 0

7; Conservative

à

```
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its modified and profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFORINS ARE IRON BINDING TRANSFORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.; "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                59.7%; Score 40; DB 1; Length 292; 54.5%; Pred. No. 2.6; 2; Indels iive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.,
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                     EMBL; AR147700; AAD33987.1; -.
EMBL, AB003712; AAF55285.1; -.
FYPase; FBGM0026629; nla.
SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1- SUBCELLULAR LOCATION: Secreted,
1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                           695 AA.
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99296631; PubMed=10366507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ010930; CAA09407.1; -.
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 181X; 02-DEC-98.
PDB; 187U; 02-FEB-99.
PDB; 187Z; 02-FEB-99.
                                                                                                                                                                                                                                                            ||| |: |::|
150 FQWLRSFRRLR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: MONOMER
                                                                                                                                                                                                                                    2 FOWXRNMRKVR 12
                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissum=Milk;
                                                                                                                                                                                                                                                                                                                                                                                  TRFL HORSE
077811;
                                                                                                                                                                                                                                                                                                                                                                  TRFL_HORSE
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                          RESULT 5
HE TO THE PROPERTY OF THE PROP
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pentecost B.T., Teng C.T., "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         SLWILLE.

(GLCNAC. .) (PULDNILL)

(GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.7%; Score 40; DB 1; Length 695; 58.3%; Pred. No. 6.1; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07BB84D50E1B165D CRC64;
                                                                                                                                                                                                                                                                                       IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
LACTOTRANSFERRIN.
1.
2.
                                                                                                                                                                                                                                                                                                                                                                                                   ANON (BY SIMILARI
ANION (BY SIMILARI
N-LINKED (GLCNAC,
N-LINKED (GLCNAC,
N-LINKED (GLCNAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P08071; P70690; Q61799; Q922P2;
01-AUG-1988 (Rel. 08, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Uterus;
MEDLINE=87280033; Pubmed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :: |||:|||
CAKFORNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 rissum=uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRFL MOUSE
                                 REPEAT
DISULFID
                                                                                                                  DISULFID
DISULFID
DISULFID
                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
BINDING
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                             DISULFID
                                                                                                       DISULFID
                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                              DISULFID
                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                      REPEAT
                                                                                                                                                                                                                                                                                                                                METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
TRFL_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
```

0;

```
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                               SEQUENCE
                                                                 Query Match
CONFLICT
                                                                                                                                                                 RPOB_LIBAF
                                                                                                                                                       RESULT 7
                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                         ð
STEETS
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch):
                                     Liu Y., Teng C.T.;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266:21880-21885(1991).

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MR -> 1QG (IN REF. 1).
R -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                         HSEP, P02788; 1CBC.

MGD; MGI:95837; Lbf.

InterPort, Irgollis6; Transferrin.
Pfam; PF00405; transferrin; 2.

PRINTS; PR00422; TRANSFERRIN.

SMART; SM00094; TR FER; 2.

PROSITE; PS00206; TRANSFERRIN 1; 1.

PROSITE; PS00206; TRANSFERRIN 2; 2.

PROSITE; PS00207; TRANSFERRIN 3; 2.

Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (POTENTIAL).
ANION (POTENTIAL).
                                                                                                       -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
LACTOTRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                   SEQUENCE OF 1-14 FROM N.A.
MEDLINE=92042099; PubMed=1939212;
                                                                                                                                                                                                                          EMBL; J03298; AAA40525.1; -.
EMBL; D88110; BAA13633.1; -.
EMBL; BC006904; AAH06904.1; -.
EMBL; M74778; AAA39427.1; -.
PIR; A28438; A28438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1191
1299
1263
1389
1402
1523
1523
1605
170
170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210
271
271
413
441
613
613
613
481
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366
376
4423
4423
4443
509
509
643
643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {RNA}(N).
SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
11-NOV-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (RC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.7%; Score 38; DB 1; Length 146; 60.0%; Pred. No. 3; ive 0; Mismatches 4; Indels
                                                                                                                                                                     DB 1; Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U09675; AAA19557.1; -.
InterPro; IPR001572; RNA_pol_B.
Pfam; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_FOL_BETA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
NON_TER 146 146
SEQÜENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                                    4; Indels
82 M -> L (IN REF. 2).
359 S -> T (IN REF. 2).
482 A -> D (IN REF. 1).
449 E -> G (IN REF. 1).
77865 MW; P26AE0340A4C19A8 CRC64;
                                                                                                                                                                  h Se.2%; Score 39; DB 1
Similarity 54.5%; Pred. No. 9.6;
6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
         82
359
382
344
449
629
670 AA;
                                                                                                                                                                                                                                                                   1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                 37 CLRWONEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWKRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 CVOWSRGARK 19
                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                   RPOB LIBAF
P41187;
```

-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS. -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.

DYNEIN HAS ATPASE ACTIVITY.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                          Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Cell Sci. 107:635-644 (1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, fiagellar outer arm.
0DA4 OR 0DA-4 OR SUP1.
Chlamydomonas reinhardrii.
Eukaryota, Viridiplantee; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: FAD (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 1; Length 783;
Pred. No. 16;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                         Gardner A.E.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; INTERPOS 337; Amino oxidase.

Ffam; PF01593; Amino oxidase; 1.

Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.

NP_BIND 311 366 FAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                        Durbin R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8D087E96464DC908 CRC64;
                                                              15-DEC-1998 (Rel. 37, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Hypothetical protein R13G10.2 in chromosome III.
                                   783 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 4568 AA.
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 366 F.
783 AA, 88799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z35602; CAA84671.2; -: WormPep; R13G10.2; CE25088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                            Rī3G10.2.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 CIDWGRDDRKVK 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                           STRAIN=Bristol N2;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3055;
                                 CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYHB CHLRE
                                                                                                                                                                                                                                                                                                        REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                             021988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q395<u>6</u>5
RESULT 8
YNR2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
DYHB_CH
                                               à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=93235211; PubMed=8475492;
Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit B.D., Parham P.;
"Structural diversity in the HLA-Al0 family of alleles: correlations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=99056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HAA-A, B antigens of black populations formed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIA-A OR HLAA.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                        EMBL; U02963; AAA19956.1; -.
InterPro; IPR004273; Dynein_heavy.
Pfam; PF03028; Dynein_heavy; 1.
Motor_protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.7%; Score 38; DB 1; Length 4568; 41.7%; Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                         COIL (POTENTIAL)
COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                         COLLED COIL (POTENTIAL)
COLLED COIL (POTENTIAL)
COLLED COIL (POTENTIAL)
                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 95;
3; Mismatches
                                                                                                                                                                                                                                               COIL
                                                                                                                                                                                                                                                              COIL
                                                                                                                                                                                                                                               COILED
                                                                                                                                                                                                                                                                                    COILED
                                                                                                                                                                                                                                                                          COILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         519961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1A34 HUMAN STANDARD; F P30453; P30454; Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interallelic conversion
                                                                                                                                                                                                                                                                                    1650
1825
2045
2848
                                                                                                                                                                                                                                                                                                                                           3162
3425
3728
                                                                                                                                                                                                                                                                                                                                                                                 1926
2209
2537
                                                                                                                                                                                                                                                           1175
                                                                                                                                                                                                                                                                                                                                                                                                                           2886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||| :| ::
1852 CFQWQSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                       4568 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                         3106
3339
3648
                                                                                                                                                                                                                                                                                                                                                                                 1919
                                                                                                                                                                                                                                Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1A34 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
ACT SITE CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serpin;
SOLITE THE REAL PROPERTY OF THE PROPERTY OF TH
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (BY SIMILARITY). BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                               -!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
            Tissue Antigens 41:72-80(1993).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMURE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 365; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              063BF63E6E6E01F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW-34 (A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .I -> V (IN A*3402).

/FIId=VAR 004379.

K -> N (IN A*3402).

/FIId=VAR 004380.

/FIId=VAR_04381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Au=VAR 004381.

P -> S (IN A*3402).

/FIId=VAR 00430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L -> I (IN A*3402).
/FTIG=VAR 004384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d=VAR 004382.
R (IN A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> L (IN A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> R (IN A*3402)
FTId=VAR 004383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41055 MW;
                                                                                                                                                                                                                                                                                                        EMBL, X61704; CAA43873.1; -. EMBL; X61705; CAA43874.1; -. PIR; S16767; S16767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
Pfam; PF00129; MFC I; 1.
Probom; PD000050; MFC I; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHC I; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                           PIR; $16771; _____HSSP; 019673; 1HSB. MTM; 142800; _____OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WXRNMRKVR 12
with serology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                    A*3401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

369 AA.

PRT;

STANDARD;

RESULT 11 SPI1\_MYXVL ID \_SPI1\_MYXVL

84 WDRNTRKVK 92

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91049428; PubMed=2173255;
Upton C., Macen J.L., Wishart D.S., McFadden G.;
Wyxona virus and malignant rabbit fibroma virus encode a serpin-like protein important for virus virulence.";
Virology 179:618-631(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Upton C., McFadden G.; "DNA sequence homology between the terminal inverted repeats of Shope fibroma virus and an endogenous cellular plasmid species."; Mol. Cell. Biol. 6:265-276(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease inhibitor; Virulence.
3 319 320 REACTIVE BOND (BY SIMILARITY).
1 16 MKYLVLVLCLTSCACR -> MFNVVRV (IN REF. 2
                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=87030884; PubMed=3021526;
Upton C., Carrell R.W., McFadden G.;
"A novel member of the serpin superfamily is encoded on a circular plasmid-like DNA species isolated from rabbit cells.";
FEBS Lett. 207:115-120(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.7%; Score 36; DB 1; Length 369; 85.7%; Pred. No. 18; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8DB31CE131C218A0 CRC64;
01-0CT-1989 (Rel. 12, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UTM-2002 (Rel. 41, Last annotation update)
Serine proteinase inhibitor 1 (Serpin 1) (Serp-1).
SERPI OR MOOS.1L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND THE GENE IS DERIVED FROM MYXOMA VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
MEDLINE=87064296; PubMed=3023828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF170726; AAF15055.1; -. EMBL; AF170726; AAF14896.1; -.
                                                                                                                                                 Myxoma virus (strain Lausanne)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 AA; 41556 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M35233; AAA46629.1; -.
EMBL; M12333; AAA81567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; PO5121; 1B3K.
InterPro; IPR000215; Serpin.
Pfam; PR00079; Gerpin; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A24470; A24470.
PIR; B36418; B36418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                              Leporipoxvirus.
NCBI_TaxID=31530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

9 06:51:49 2003

Tue Dec

```
Coat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RL28 THETN
Q8R9Ū1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RL28 THETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID DIT DO DE DIT DE DE DIT DE DE DIT DE DE DIT DE DE DIT D
             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W. DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae AR39.";

Nucleic Acids Res. 28:1397-1406(2000).

-!-CATALYTIC ACITUTY: ATP + L-histidine + tRNA(His) = AMP + diphosphate + L-histidyl-tRNA(His).

-!-SUBUNIT: HOWODINER (BY SIMILARITY).

-!-SUBCELLULAR LOCATION: Cytoplasmic.

-!-SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002106; AAtRNA ligaseII.
InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004156; HisS.
InterPro; IPR002314; FRNA-synt 2b.
Pfam; PF00587; tRNA-synt 2b; 1.
Pfam; PF03129; HGTP anticodon; 1.
TIGRFAMS; TIGR00442; hisS; 1.
AMINOACYI-FRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.7%; Score 36; DB 1; Length 428; 44.4%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428 AA; 48939 MW; 9CF859ED0E689DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBL_TaxID=83560;
                                                                                                                                                                                                                        428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VP4_ROTGA STANDARD;
004916;
01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE002349; AAF39630.1; -.
HSSP; O32422; 1QE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MoPn / Nigg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 CFSWAKHLR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWXRNMR 9
                                                           235 WIRNMRK 241
4 WXRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                   (HISS OR TC0830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; TC0830;
                                                                                                                                                                                                                     SYH CHLMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            HIBRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
VP4_ROTGA
                                                                                                                                                                                 SYH_CHLMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC DI
                                                                                                                                                                                                                     HIDDEN NEW TOOLS COURSE TO THE PROPERTY OF THE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          Mackow B.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.; "Identification and baculovirus expression of the VP4 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
-!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL)
                                                                                                Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                                 J. Viról. 67:2730-2738 (1993).
-1- SUBCELLULAR LOCATION: Outer capsid.
-1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 749;
Pred. No. 36;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D1223527DEAE0F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
25 ribosomal protein L28.
RPMB OR TTE1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MB4 / JCM 11007;
MEDLINE=21992816; PubMed=11997336;
                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=93233240; PubMed=8386274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                             human group B rotavirus ADRV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN 2002 (Rel. 41, Created)
15-JUN 2002 (Rel. 41, Last seq
15-JUN 2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, M91434; AAA47338.1; -.
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 CFTWDMNCANVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
109
133
407
527
568
620
681
698
749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=119072;
                                                                                                                                           NCBI_TaxID=12705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

.,

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  0;
              This SWISS-PROT entry is copyright. It is produced through a collaboration
                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/anmounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dzianott A.M., Bujarski J.J., mrhe nucleotide sequence and genome organization of the RNA-1 segment in two bromoviruses: broad bean mottle virus and cowpea chlorotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 185:553-562(1991).
-!- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CONTAINS AN HELICASE DOWAIN AND A METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.2%; Score 35; DB 1; Length 966; 46.7%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO LA PROTEIN FROM CCMV, CMV, PSV AND TAV.
                                                                                                                                                                                                                                        Score 35; DB 1; Length 62;
Pred. No. 4.6;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  966 AA; 109621 MW; DF592681D7231C8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002588; V methyltransf.
InterPro; IPR000606; Viral_helicasel.
Pfam; PF01443; Viral_helicasel; 1.
Pfam; PF01600; Vmethyltransf; 1.
Helicase; APP-binding; Transferase; Methyltransferase.
NP_BIND 690 697 ATP (POTENTIAL).
                                                                                                                                                                                      Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UUL-1993 (Rel. 26, Created)
1-UUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last amotation update)
1A protein [Includes: Helicase, Methyltransferase].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92074218; PubMed=1962437;
                                                                                                                                                                    EMBL; AE013107; AAM24713.1; -.
                                                                                                                                                                                                                                              52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M65138; AAA42740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Broad bean mottle virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A41699; PIBVBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                          3 QWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              27 RWKPNIRKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mottle virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bawden;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            V1A BBMV
Q00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

1 CFQ----WXRNMRKV 11

```
Db 347 CFKENKDWTENMRSV 361
```

Search completed: February 21, 2003, 07:51:35 Job time : 6.2093 secs

```
1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 CFOWORNMRKV 49
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheri
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                               Q8TCD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UCY5
                                                                                                                                                                                                                                                                               RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UCY5
                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8r2a4 mus musculu
Q9u4m9 leishmania
Q9fhi9 arabidopsis
Q8sc5s stx2 conver
O81653 hemerocalli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogtcd2 homo sapien
Ogtc80 ovis aries
Ogtc80 ovis aries
Og2462 salmonella
Og25p1 sesamum ind
O31090 rhizobium li
O33780 caenorhabdil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9sic0 arabidopsis
Q77855 human immun
Q77856 human immun
Q9czq7 mus musculu
                                                          (without alignments)
114.078 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                          671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                - protein search, using sw model
                                                                                                                                                                                                            Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   031090
Q93780
Q8R2A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9U4M9
Q9FHI9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      081653
Q9SIC0
Q77855
Q77856
Q9CZQ7
                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UCY5
Q9TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29XHP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8SC55
                                                                                                                                                                                                                                          sp archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                         sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                               sp_vertebrate:*
                                                                                                                                                                                                                                                                                                     sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                Bp_rvirus:*
Bp_bacteriap:*
                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                 US-09-743-107B-87
                                                                                                 1 CFOWXRNMRKVR 12
                                                                                                                                                                                                   Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                 sp archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
10
10
10
11
11
11
11
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length DB
                                                                                                                                                                                                                                     SPTREMBL 21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
273
275
341
415
866
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110...
                                                                                        Perfect score:
                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                OM protein
                                                                                                   Seguence:
                                                                                                                                          Searched:
                                                                                                                                                                                                                                   Database
                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429788798794
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
```

```
Q88487 zea mays (m Q9hpa3 halobacteri Q9v346 drosophila G9xfd5 oryza sativ G9ygc1 human immun G9ygc0 human immun G9yqb human immun G9yjl human immun G8q454 human immun G8q454 human immun G8yl human immun G9yjl anabaena sp Q8raz homo sapien G9yusz homo sapien G9syl drosophila G9sz30 drosophila
                                                                                                        Q91mq5 lumpy skin
Q9dhk5 yaba-like d
P96223 mycobacteri
Q9uud0 schizosacch
Q8s487 zea mays (m
                                                             mus musculu
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
29d4x5 mus musculu
96m21 homo sapien
                               28xse2 ralstonia s
                                              yaba monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                           0x6p60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.6%; Score 60; DB 4; Length 711; 90.9%; Pred. No. 0.003; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEPCINGE PROSTATE;
Strausberg R.; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08TCD2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Lactotransferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         711 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                        Q9D9X0
Q9JIT1
Q91MQ5
Q9DHK5
P96223
                                                                                                                                                                                                    Q9V346
Q9XFD5
                                                                                                                                                                                                                                  09YQC1
09YQC0
09YQB9
09YQB8
                                                                                                                                                                                                                                                                                                                                                                                                             Q9VI18
Q9SP27
Q9XZ30
                                          090B73
09DAJ3
                                                                                                                                                                                                                                                                                                               Q9YIJ2
Q8Q454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                      085487
                                                                                                                                                                                       Q9HPA3
                                                                                                                                                                                                                                                                                                                                                              Q8YP77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                OSTAX2
                                                                                                                                                                                                                                                                                                                                                                                               Q9NUS2
                                                                                                                                                                                                                                                                                                                                                                                                                           2 5
 Best_Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
Homo sapiens (Human).
\\
```

ď

; 0

```
STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 2S albumin, the two major seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Haque A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Hintehead S., Barrell B.G.;
Mhitehead S., Barrell B.G.;
Mature 413:848-822(2001).

EMBL; ALG27276; CADGG0491; -
Hypotherical protein; Complete proteome.
SEQUENCE 511 AA; 58126 MM; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Lamiales, Pedaliaceae, Sesamum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-GAT-1998 (TrEMBLrel. 18, Last annotation update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 31.0 kDa protein.
Hypothetical bactein leguminoaarum (biovar viciae).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 16; Length 511;
Pred. No. 9.9;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%; Score 40; DB 10; 66.7%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sesamum indicum (Oriental sesame) (Gingelly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 storage proteins in sesame.";
J. Agric. Food Chem. 47:4932-4938(1999).
EMBL; AF091841; AAD42943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
InterPro; IPR0001769; Try/amyl_inbbtr.
Pfam; PF00234; tryp_alpha_amyl_i.
PRINTS; PR00496; NAPIN.
SMARY; SM00499; AAI; 1.
SEQUENCE 148 AA; 17524 MW; BA46B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        61.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 CFAWDMIKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 CMOWMRSMR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWXRNMR 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2S albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              031090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09XHP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              031090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9XHP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              031090
1D 02
02
04
07
07
07
07
08
08
08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9XHP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SO DE RETAREDE DE PARENTE DE PARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ωp
            SWARERERERES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEALN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                             Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries (Sheep).
Sukaryota, Metazoca, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae, Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 6; Length 33;
Pred. No. 0.098;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    83.6%; Score 56; DB 4; Length 38; 90.9%; Pred. No. 0.00085; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                              Pfam, PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490BSEBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95127729; PubMed=7827104;
Qian z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP; O77698; 1CE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-MAR-2002 (TYEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 AA
                                                                                                                                                                                                                                                    Jpn. J. Îegal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
InterPro; IPR001156; Transferrin.
                                                                                                                             MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.2%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 90.9
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                          seminal plasma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi
                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08Z462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9TR80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9TR80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8Z462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OC SERVICE SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   рp
```

ö

Gaps

0;

ö

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                        SEQUENCE FROM N.A. STATE-128XI/SVJ;
STRAIN=128XI/SVJ;
MEDLINE=21676859; PubMed=11802169;
Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.;
"Multiple new and isolated families within the mouse superfamily of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ravel C., Dubessay P., Blaineau C., Lignon M.-F., Bastien P., Dedet J.-P., Pages M.;
"Leishmania major chromosome 5 complete sequence.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF163772; AAF14642.1;
InterPro: IPR003409; MORN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                58.2%; Score 39; DB 11; Length 341; 55.6%; Pred. No. 16; 2; Indels Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.2%; Score 39; DB 5; Length 415; 66.7%; Pred. No. 20; 2; Indels iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 341 AA; 39632 MW; B3D8259F7AD11130 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46701 MW; 3E3AD710BF23691E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last amnotation update)
Genomic DNA, chromosome 5, Pl clone:MFC19.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        866 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                              Vlr vomeronasal receptors.";
Nat. Neurosci. 5:134-140(2002).
EMBL; AY065506; AAL47911.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 55.6
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02493; MORN; 4
SEQUENCE 415 AA; 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 CFTWTRNIK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 CGEWFRINK 280
                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWXRNMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Eugler
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWXRNMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                   Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09U4M9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09FHI9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9U4M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FHI9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9U4M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FHI9
              ଟ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAC OCC OCC OCC SERVICE SERVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                     Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G., Ksenzenko V.N.;
Ksenzenko V.N.;
"Structural and functional organization of the exopolysaccharide
biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39.";
Mol. Biol. (Mosk) 32:797-804 (1998).
EMBL; AF028810; AAB88891.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                      Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%; Score 40; DB 2; Length 273; 60.0%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.2%; Score 39; DB 5; Length 275; 63.6%; Pred. No. 13; 3; Indels iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dobson R.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81089; CAB03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                            MEDLINE=99113394; PubMed=9914965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 21, C
(TrEMBLrel. 21, L
(TrEMBLrel. 21, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02,
01-AUG-1998 (TrEMBLrel. 07,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vomeronasal receptor VIRE6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.67
المراجعة 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| :||| |
262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 RWLRNLRKLR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 QWXRNMRKVR 12
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F53H4.4 protein.
NCBI_TaxID=387;
                                                                                                                                                                                                                     STRAIN-VF39;
                                                                               STRAIN=VF39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBR2A4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          093780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBR2A4
```

RESULT 7

à

0

RESULT 8 Q8R2A4

GE H H H H H H

0

Gaps

0

Length 372; 1; Indels

56.7%; Score 38; DB 10; 71.4%; Pred. No. 27; tive 1; Mismatches 1

```
NON TER 1 1 SEQUENCE 372 AA, 41909 MW; 55FB3EAF9699595E CRC64;
Plant Mol. Biol. 40:237-248(1999).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AF082028; A5424853.1; -
INTERPRO; IPR001128; Cytochrome_P450.
Pfam; PR00667; P450; 1.
PRINTS; PR00385; P450.
PRINTS; PR00386; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                             Heme; Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                    Query Match
Best Local Similarity
5, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 QWFRNMKK 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 QWXRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                              328 CFEWDRN 334
                                                                                                                                                                                                                                                                                                                                1 CPQWXRN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AT2G05650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9SIC0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q77855
ID Q7
AC Q7
DT 01
DT 01
                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
         STARBARTS
                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CV. STELLA D.ORO; TISSUE=SENESCING PETALS;
MEDLINE=99339248; PubMed=10412903;
PEDLINE=99339249; PubMed=10412903;
PEDRAVAS T., Pikula A., Reld D.D., Rubinstein B., Walker B.L.;
"Identification of senescence-associated genes from daylily petals.";
                                           Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu B., Kotani H., Miyajima N., Tabata S., "Structural analysis of Arabidopsis thaliana chromosome 5. IX. Sequence features of the regions of 1,011,550 bp covered by seventeen
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T., Yamasaski S., Takeda Y., "Genomic sequence of Shiga toxin 2-converting phage isolated from Escherichia coli 0157:H7 Okayama strain and comparison with other Shiga toxin 2-converting phages.", Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, AP004402; BAB87947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Asparagales;
Hemerocallidaceae; Hemerocallis.
NCBI_TaxID=80862;
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                         58.2%; Score 39; DB 10; Length 866; 50.0%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.7%; Score 38; DB 9; Length 108; 60.0%; Pred. No. 7.5; ttive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                Pl_and TAC clones.";
DNA_Res. 6:183-195(1999).
EMBL, AB018113, BAB09175.1;
SEQUENCE 866 AA; 100187 MW; 164FAB99B4976D27D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 108 AA; 12279 MW; 2FF2E76690C78BA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-070-2002 (TrEMBLrel. 21, Created) 01-070-2002 (TrEMBLrel. 21, Last sequence update) 01-UN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 12.3 kDa protein.
Stx2 converting bacteriophage 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Senescence-associated protein 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA
                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                         MEDLINE=99397451; PubMed=10470850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemerocallis hybrid cultivar.
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           389 CENWLLKFRKLR 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-STX2 PHAGE-I;
                                                                                                                                                                                                                                                                                                                                1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFOWXRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 CFOWISDNRK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=180816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8SC55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   081653
081653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       088055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
001653
10 001653
AC 001655
AC 001650
DT 01-NO
D
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
QBSC55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Н
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
    ð
                                                                                                                                                                                                                                                                                                                                                                         д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;

MEDLINB=20083487; PubMed=10617197;

Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo, H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.7%; Score 38; DB 10; Length 531; 75.0%; Pred. No. 39; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007170; AAD25641.1; -.
InterPro; IPR004264; Transposase_23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Рбам, РР03017; Transposase 23; 1. SEQUENCE 531 AA; 60512 МW; 57ВЗАС60С976А4В9 СRС64;
                                                           (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              077855 PRELIMINARY, PRT; 91 AA.
077855,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
531 AA
                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
PRT;
                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last
En/Spm-like transposon protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. COLUMBIA;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                MEDINE-59191002; PubMed-7884875; Kuiken C.L., Dekker J.,
MULDET-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J.,
Mulder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J.,
A Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;
I "Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is unrelated to time of HIV-1 RNA positivity in the child.";
J. Virol. 69:2285-2286(1995).
R EMBL; Z47867; CARAR7881.1;
R. InterPro; IPRO0777; G9120.
R PEMP; CARAR7881.1;
R A ALDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95191002; PubMed=7884875; Milder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J., Scherpbier H.J., de Perre P., Boer K., Goudsmit J., Scherpbier H.J., de Perre P., Boer K., Goudsmit J., "Similarity H. or and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is J. Virol. 69:2285-226(1995).

EMBL: 247868; CA887882.1; -. InterPro; IPRO0777; GP120.

Fiam; PRO0516; GP120.

Fam; PRO0516; GP120.

AMDS: Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.2%; Score 37; DB 15; Length 91; 60.0%; Pred. No. 9.9; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.2%; Score 37; DB 15; Length 91; Best Local Similarity 60.0%; Pred. No. 9.9; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                         91 91
91 AA; 10530 MW; 8B10C62011F305D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 AA; 10519 MW; EB20C63A22DA1288 CRC64;
                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 QWNRTLQKVR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
91
                                                                                                                                                                                                                                                                                                                          NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q77856
Q77856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 077856
     Dp
```

Search completed: February 21, 2003, 08:00:42 Job time : 21.6744 secs

3 QWXRNMRKVR 12 || | ::||| 67 QWDRTLQKVR 76

ઠે

```
Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         actoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              actoferrin
                                                                                                                                                         (without alignments)
56.918 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_101002:*

| SiDS2/gcddata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SiDS2/gcddata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1981.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1982.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1983.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1984.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1985.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1985.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1986.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1988.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1989.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1989.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1989.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1989.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1989.DAT:*
| SiDS2/gcddata/geneseqp-emb1/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SIDS2/gcgdata/geneseq_geneseq_embl/AA1990.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1990.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1991.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1993.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1993.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1994.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1995.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1995.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1995.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1999.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA1000.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA2001.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA2001.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA2001.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA2001.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA2001.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA2001.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/AA2002.DAT:
                                                                                                                               February 21, 2003, 07:37:21 ; Search time 28.093 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
Human
Human
Human
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                            908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78038
AAY78046
AAY78047
AAY78084
AAY78087
AAY78091
AAY78091
AAY78037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78072
                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                       US-09-743-107B-88
                                                                                                                                                                                                                                                                 1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3222222222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.0
97.0
97.0
97.0
97.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.
```

| д н н н в в в в в в в в в в в в в в в в | | Human lactoferrin Human lactoferrin Human lactoferrin Advanced glycosyla Human lactoferrin Amino acid sequenc Human lactoferrin | 44444 | Anti-parasitic lac
Anti-parasitic lac
Anti-parasitic lac
Peptide for anti-u
Lactoferrin-derive
Lactoferrin derive
Lactoferrin derive |
|--|--|---|--|--|
| AAY78048
AAY78049
AAY78036
AAY78050
AAY78051 | AAY78035
AAY78062
AAY78031
AAY78064
AAY78065
AAY78065 | AAYY8066
AAYY8067
AAW13397
AAY78033
AAY78032
AAY78032 | AAR4841
AAR4853
AAR57461
AAR57462
AAR86698
AAR86699 | AAR80263
AAR80264
AAR8553
AAR303045
AAR90607
AAR87621 |
| 221 221 221 221 221 221 221 221 221 221 | 222222 | 12
112
12
12
13
14
15
17
17 | 112
112
112
114
116 | 16
117
117
117 |
| 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 112
112
114
116
116 | 7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 00000000 | 000000000000000000000000000000000000000 |
| L L L L L L L L | | | 97.0
97.0
97.0
97.0
97.0 | |
| | , 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | | | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 |
| 11
12
13
14
15 | 23 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 25 2 2 2 2 2 4 4 3 3 2 9 9 8 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 1 CL | 20 0 11 41 41 41 42 42 43 43 43 43 43 43 43 43 43 43 43 43 43 |

ALIGNMENTS

```
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative
                                                                                                                                                                                                                                                                                                                         Dolphin GT;
                                                                                 Human lactoferrin derived peptide SEQ ID NO:72.
                                                                                                                                                                                                                                                                                                                         Baltzer L,
                     AAY78072 standard; Peptide; 12 AA
                                                                                                                                                                                                                                                                                                                         Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                         98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                               98SE-0004614.
                                                                                                                                                                                                                                     99WO-SE01230
                                                            25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                    (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                              WPI; 2000-147388/13.
                                                                                                                                                                                           WO200001730-A1
                                                                                                                                                           Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                     06-JUL-1999;
                                                                                                                                                                                                                                                        06-JUL-1998;
                                                                                                                                                                                                                                                                     17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                13-JAN-2000
                                        AAY78072;
RESULT 1
           AAY78072
```

lactoferrin lactoferrin

Human lactoferrin

lactoferrin

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                     Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                           98.5%; Score 66; DB 21; Length 12; 91.7%; Pred. No. 3.1e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78038 standard; Peptide; 12 AA.
                                                                   Claim 22; Page 35; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWARNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                            12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78038
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78038
ò
```

. 0

```
.
              binding to specific lattoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collis, and Candida infection on a mucosal membrane), inflammations and/or tummours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tunours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
lactoferrin. The peptides are taken up in the intestine through
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                              97.0%; Score 65; DB 21; Length 12; 91.7%; Pred. No. 4.7e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78046 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-SE01230,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0004614,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                         12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASCI-) A+ SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200001730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78046;
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                           à
```

us-09-743-107b-88.rag

ô

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and nable them to be used for the same purposes as lactoferrin at lower
             Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                 Gaps
fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                     97.0%; Score 65; DB 21; Length 12; 91.7%; Pred. No. 4.7e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dolphin GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                 AAY78047 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page 73; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                    1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-147388/13.
                                                                                                                                                                                                           Local Similarity
                                                                                                                                                  12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                    Sequence
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ношо
                                                                                                                                                                                                                                                                                                                                                                           AAY78047
8888888888888
                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                  g
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through the opecific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections are used membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such and and also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                   Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                 Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 97.0%; Score 65; DB 21; Length 12; Best Local Similarity 91.7%; Pred. No. 4.7e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolphin GT;
                                               Score 65; DB 21;
Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                    Human lactoferrin derived peptide SEQ ID NO:84.
                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Page 36; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattsby-Baltzer I,
                                                                                                                                                                                                                                             AAY78084 standard; Peptide; 12
                                               97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                       bactericidal; preservative.
                                                                                                                                                                                                                                                                                                               25-APR-2000 (first entry)
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB
                                                                                                                     CFOWXRNMRKVR 12
                                                                                                                                                    1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-147388/13.
                                             Query Match
Best Local Similarity
              12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1998;
                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
              Sequence
                                                                                                                                                                                                                                                                              AAY78084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                  Matches
                                                                                                                     Н
                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                              AAY78084
X S
                                                                                                                                                   qq
                                                                                                                     ð
```

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

99WO-SE01230

06-JUL-1999;

13-JAN-2000

WO200001730-A1.

Homo sapiens.

Synthetic.

Human lactoferrin derived peptide SEQ ID NO:88.

(first entry)

25-APR-2000

AAY78088;

AAY78088 standard; Peptide; 12 AA.

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the disculation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                       food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                      Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.0%; Score 65; DB 21; Length 12;
100.0%; Pred. No. 4.7e-05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 37; 102pp; English
                                                                                                                                 AAY78087 standard; Peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-SE01230.
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASCI-) A+ SCI INVEST AB.
CFOWXRNMRKVR 12
                                  1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1998;
                                                                                                                                                                                                            25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                       AAY78087;
                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                               d
```

```
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.0%; Score 65; DB 21; Length 12;
100.0%; Pred. No. 4.7e-05;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78091 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22; Page 37; 102pp; English:
                                                                                                                                                                                                                                                                                                                                  98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AA;
                                                                                                                                                                                                                                                                                                                                   36-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78091
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                田林田林本は田
```

ö

Gaps

; 0

RESULT 7

us-09-743-107b-88.rag

വ

Page

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment and be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammantions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
                             Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 21; Length 12, Pred, No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 22; Page 38; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AA;
                                                                                                                                                                                                                                                                                                                                                          WO200001730-A1.
                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-2000
                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                              Homo
80 X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B
```

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through be becific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would cannot be used for the same purposes as lactoferrin at lower

12 AA;

Seguence

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 22; Page 38; 102pp; English.

Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13

(ASCI-) A+ SCI INVEST AB.

17-JUL-1998; 29-DEC-1998;

99WO-SE01230 98SE-0002441. 98SE-0002562. 98SE-0004614

06-JUL-1999; 06-JUL-1998;

13-JAN-2000

WO200001730-A1

Synthetic.

```
..
0
                                                                                                                                                                                                                                                 Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                            Gaps
                           .
97.0%; Score 65; DB 21; Length 12; ilarity 91.7%; Pred. No. 4.7e-05; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:37.
                                                                                                                                           AAY78037 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             99WO-SE01230,
                                                                                                                                                                                                                                                                                        bactericidal; preservative
                                                                                                                                                                                              25-APR-2000 (first entry)
                                                  1 CFOWXRNMRKVR 12
                                                                            1 CFOWKRNMRKVR 12
             Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                     AAY78037;
Query Match
                                                                                                                   RESULT 10
                                                                                                                                  AAY78037
                                                  à
```

0;

Gaps

.. 0

0; Mismatches

11; Conservative

Matches

Best Local Similarity

Query Match

1 CFOWXRNMRKVR 12

ð

1 CPOWKRNMRKVR 12

97.0%; 91.78; Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

Human lactoferrin derived peptide SEQ ID NO:92.

(first entry)

25-APR-2000

AAY78092;

AAY78092 standard; Peptide; 12 AA.

AAY78092

```
WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JAN-2000.
 Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78049;
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
 g
                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to apecific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, lactoferrin, modification, infection, inflammation, tumour,
food, infant formula, anti-inflammatory, anti-microbial, anti-tumour,
urinary tract infection, colitis, Candida infection, fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                           New peptides used for treatment and prevention of infections,
                                                                                                                                       inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                               97.0%; Score 65; DB 21; Length 13; 91.7%; Pred. No. Se-05; 1; Indels ive 0; Mismatches 1; Indels
                                                                                Dolphin GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:48.
                                                                               Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                             Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78048 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-SE01230.
                     98SE-0002562
98SE-0004614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASCI-) A+ SCI INVEST AB.
                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CFOWORINMRKVR 13
                                                                                                     WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200001730-A1.
                     17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000
                                                                                Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78048;
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                    cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ношон
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
δ
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also such though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٠;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 21; Length 13;
Pred. No. 5e-05;
0; Mismatches 1; Indels
Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson LA, Mattsby-Baltzer I, Baltzer L,
Baltzer L,
                                                                                                                                                                                                                                                                                  Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78049 standard; Peptide; 13 AA.
Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-147388/13.
                                                                           WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13 AA;
```

. 0

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                        Score 65; DB 21; Length 13;
Pred. No. 5e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolphin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78036 standard; Peptide; 14 AA.
Claim 18; Page 74; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                          97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                          91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 91.7
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                        13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78036;
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
AAY78036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
ð
```

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-liflammatory anti-infections and anti-tumoural properties they cannot be used clinically on a broad basis because of high production
urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                       Score 65; DB 21; Length 14; Pred. No. 5.4e-05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78050 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattsby-Baltzer I,
                                                                                                                                                                                                                                       97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0002441.
98SE-0002562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98SE-0004614
                                                                                                                                                                                                                Query Match
Best Local Similarity 91....
Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                             3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                                                                                                                                                                                                     14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78050;
                                                                                                                                                                                                       Sequence
                                                                                                                                                                   cost.
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78050
     886666666666888888
                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-informatory anti-infectious and anti-informatory anti-infectious and anti-informatory and anti-informatory anti-information of peptides based on lactoferrin would costs. Therefore, provision of peptides based on lactoferrin at lower and anti-them to be used for the same purposes as lactoferrin at lower
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                              Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                 Gaps
                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                             97.0%; Score 65; DB 21; Length 14; 91.7%; Pred. No. 5.4e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                               AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB.
                                                                                                                                11; Conservative
                                                                                                                                                               1 CFQWXRNMRKVR 12
                                                                                                                                                                                            3 CFOWORINMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-147388/13.
                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 AA;
                                                                14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                               25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                              AAY78051;
                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                Query Match
                                                                                                                                Matches
                                                                                                                                                                                                                                             cost.
888888
                                                                                                                                                               ò
                                                                                                                                                                                            g
```

97.0%; Score 65; DB 21; Length 14;

Query Match

```
ö
               Gaps
              ;
0
              Indels
 91.7%; Pred. No. 5.4e-05;
tive 0; Mismatches 1;
               11; Conservative
Best Local Similarity
Matches 11; Conserv
```

```
1 CFOWXRNMRKVR 12
```

3 CFOWORNMRKVR 14

Search completed: February 21, 2003, 07:56:43 Job time : 29.093 secs

```
BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                           US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
Appli
Appli
Appli
                                                      February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-755-161A-10

US-07-891-174-10

US-08-204-487-7

US-09-208-734-8

US-07-95-161A-8

US-07-891-174-8

US-08-256-771-30

US-08-381-984-29

US-08-464-182A-6

US-08-406-271-6

US-08-693-274A-7
                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-891-174-3
US-08-204-487-1
US-08-256-771-24
US-08-381-984-24
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-464-182A-5
US-08-406-271-5
                                                                                                                                                              262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   OM protein - protein search, using sw model
                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                             US-09-743-107B-88
                                                                                                              1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                   Database
                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                       Result
```

| Appl | Ann | A | 100 | 1000 | Appl | Appl | Ann | Ann | Ann | Appl | 4 | 700 | 72.4 | 1 | Taddy | Appli | Appli |
|------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| Sequence 2. | Semience 2 | Semience 2 | | C entremes | Semence 2. | | Semience 4 | Semience 4 | Semience 4 | Segmence 4 | Segment A | Semience 2 | Section 2 | C endermen | Semience 2, | Sequence 2, | Sequence 2, |
| US-08-464-182A-2 | US-08-406-271-2 | US-08-724-586-2 | US-09-421-632-2 | US-09-932-190-2 | US-08-655-640-2 | US-08-655-640-4 | US-08-154-019-4 | US-08-461-333-4 | US-08-464-167-4 | US-09-158-313-4 | US-08-476-798-4 | US-08-145-681-2 | US-08-250-308-2 | US-08-453-703-2 | US-08-456-106-2 | US-08-456-108-2 | US-09-265-577-2 |
| 7 | 7 | m | 4 | 4 | N | 7 | 7 | ч | m | m | 4 | Н | r-1 | - | N |) (r) | 4 |
| 54 | 24 | 694 | 694 | 694 | 705 | 708 | 711 | 711 | 711 | 711 | 711 | 711 | 711 | 711 | 711 | 711 | 711 |
| 97.0 | 97.0 | 97.0 | 97.0 | 97.0 | 97.0 | 97.0 | 97.0 | 97.0 | 97.0 | 97.0 | 97.0 | 92.5 | 92.5 | 92.5 | 92.5 | 92.5 | 92.5 |
| 9 | 9 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 9 | 62 | 62 | 62 | 62 | 62 | 62 |
| 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
| | | | | | | | | | | | | | | | | | |

ALIGNMENTS

```
RESULT 1

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-487-3

19-68-204-204-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-204-30-3

19-68-20
```

OTHER INFORMATION: (20-37)"

```
JOHN TOPOLOGY: 1110ca.
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                          STREET: 411 PACKEDS CITY: Hackensack STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
TELEX: 1
                                              US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                              RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ਨੇ
                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                Gaps
                                                                                                                                                                                          RESULT 2
US-08-485-948-8

US-08-485-948-8

; Sequence 8, Application US/08485948

; Patent No. 5855882

; GENERAL INFORMATION:

; APPLICANT: YONG MING LI
APPLICANT: HELBN VLASSARA

; APPLICANT: HILD OF INVENTION: REMAINS FOR BINDING TO ADVANCED GLYCOSYLATION

; TITLE OF INVENTION: EXDPRODUCTS, AND METHODS OF THEIR USE
                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%; Score 65; DB 2; Length 18; 91.7%; Pred. No. 3.6e-05; 11ve 0; Mismatches 1; Indels
                                            Length 18;
                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                        Score 65; DB 1; I
Pred. No. 3.6e-05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26,742
ER: 947-1-008A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
FILING DATE: APRLL 7, 1995
CLASSIFUCATION NUMBER: 08/418,642
FILING DATE: APRLL 7, 1995
GLASSIFUCATION: 436
ATTORNEY/AGENT INFORMATION:
RAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
FELEPHONE: 2004 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELERAL
TELERAL: 13321
INFORMATION FOR SEQ.
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                        97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                        Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FRAGMENT TYPE: internal US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                          1 CFQWXRNMRKVR 12
                                                                                                                                          1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFÓWQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
;
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                       Dp
                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            П
```

```
ö
Sequence 8, Application US/08628380
Patent No. 5891341
GENERAL INFORMATION:
APPLICANT: LI, YONG MING
APPLICANT: VASSARA, HELEN
APPLICANT: VASSARA, HELEN
APPLICANT: VASSARA, ANTHONY
TITLE OF INVENTION: ACE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STRET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08475055;
Patent No. 5562245
GENERAL INFORMATION:
APPLICANT: YOUR MING II
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: BUDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.0%; Score 65; DB 2; Length 18; Best Local Similarity 91.7%; Pred. No. 3.6e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION NUMBER: US 08/418,642
ATTONENTY/AGENT INFORMATION:

NAME: Jackson Esg., David A.

REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REJERRENCE/DOCKET NUMBER: 947-1-008 CIP
TELECOMMUNICATION INFORMATION:
TELEPAK: 201 487-580
TELEPAK: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
WIBLIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.0%; Score 65; DB 2; Length 18; 91.7%; Pred. No. 3.6e-05; Live 0; Mismatches 1; Indels
                                                                                                                                 COMPUTER CASA COMPUTER CASA COMPUTER CASA COMPUTER Floppy disk COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055 FLING DATE:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3. Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Wenderoch, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STRTE: D.C. COUNTRY: U.S.A. ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
               ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
                                                                                 STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNMRKVR 12
                                                           Hackensack
                                                                                                                        07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-07-755-161A-3
```

```
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: modified site
LOCATION:
LOCATION:
LOCATION
LOCATION:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
         SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                              NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCK/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 19
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
CHROMOSOME/SEGMENT
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
```

Length 20;

97.0%; Score 65;

```
LOCATION: 19

IDBNIFTCATION METHOD:
OTHER INFORMATION: ()note= "thiol group of OTHER INFORMATION: ()s residue at location 19 connected by disulfide bond with OTHER INFORMATION: ()s residue at location 19 connected by Alsulfide bond with PUBLICATION INFORMATION: () A scend of () a residue at location 2" AUTHORS:
AUTHORS:
                                                  OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19" FEATURE: NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YARAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MATARIMA, HIDEKI
APPLICANT: MATARIMA, SHIGBAKI
APPLICANT: TANAKA, SHIGBAKI
APPLICANT: TOSAKO, SHINY ICHI
APPLICANT: WAMASAKI, YOSHIMIRO
APPLICANT: UCHIDA, TOSHIMKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 1; Length 20; Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT STREET: 53 STATE STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FJN-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08204487; Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGIETRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
         LOCATION: 2
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109
                                                                                                                                                                                                                                                                                                                                          JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                          PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                              0
  91.7%; Pred. No. 4e-05;
tive 0; Mismatches 1; Indels
                                                                                                                                                                   RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; Patent No. 5317084
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
; VUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
; COTTY: Machington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: Modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                  1 CFQWXRNMRKVR 12
                                                                                                       2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                       g
                                                                  ð
```

ö

Gaps

us-09-743-107b-88.rai

```
GENERAL INFORMATION:
APPLICANT: MAMORIA et al.
APPLICANT: MAMORIA DE ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ANDRESS: A
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                          Score 65; DB 1; Length 20;
Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                          /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IDEN COMPATIBLE FOR COMPUTER: DISKETTE, 5.25 inch, 500 kb COMPUTER: DISK COMPUTER: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
FRICR APPLICATION: 514
PRIOR APPLICATION BATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/08256771
Patent No. 5656591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24:
TELEPAX: (617) 248-7100
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNBY/AGENT INFORMATION:
NAME: Warren M. Cheek, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 amino acids
                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-256-771-24
                                                                                                                                                                                                                                                                US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
```

```
Gaps
                                                                                                                                                                                                                                                                         Sequence 25, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to;
; OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25
                                        ch 97.0%; Score 65; DB 1; Length 20; 1 Similarity 91.7%; Pred. No. 4e-05; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
97.04; Score 65; DB 1; Length 20;
Best Local Similarity 91.74; Pred. No. 4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warten M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FEATURE:
                                                                                                                            1 CFQWXRNMRKVR 12
                                                                                                                                                            2 CFQWQRNMRKVR 13
                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RY: U.S.A.
20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                     US-08-256-771-25
US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                            Query Match
                                                                                  Matches
                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
```

```
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REPERBACE: PALSYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.0%; Score 65; DB 1; Length 20; 91.7%; Pred. No. 4e-05; 1; Indels tive 0; Mismatches 1; Indels
         805 Fifteenth Street, N.W., #700
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                    CUMPUTER: DISKette, 3.5 inch, 1. COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/381,984 FILLING DATE: April 11, 1995 CLASSIFICATION: 252 PRIOR APPLICATION: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1.2
US-09-508-734-4
; Sequence 4, Application US/09508734
Patent No. 6423509
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CFOWORNMRKVR 13
                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                             20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "the specified peptide as well as

; OTHER INFORMATION: peptides including the specified peptide as a fragment thereo

US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 1; Length 20;
Pred. No. 4e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IDN Compatible
OPERATING SYGTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
         Sequence 21, April 2004555

BALLINGRAMINON:
APPLICANT: Mamoru TOMITA et al.
ITITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/08381984
Fatent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
Sequence 24, Application US/08381984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 97.0%;
1 Similarity 91.7%;
11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CFÓWORNMRKVR 13
                                                                                                                                                                        STREET: 805 Fifte CITY: Washington STATE: D.C.
                                                                                                                                                                                                                     D.C.
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                              20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
```

g ð

```
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.0%; Score 65; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 5e-05; Matches 11; Conservative 0; Mismatches 1; Indels
             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10
                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH. 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified site LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified site LOCATION: 21
                                                                                                                                                                     TELEFAX: 202-371-8856
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE:
CELL TYPE:
CELL LINE:
CRL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                           Patent No. 6425169

Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

Sequence 7, Application US/09508734

Sequence 7, Application US/09508734

GENERAL INFORMATION: Mass production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: Useful microorganism thereof

TITLE OF INVENTION: Useful microorganism thereof

FILE REPRESENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: US/09/508,734

PRIOR APPLICATION NUMBER: KR1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                   0;
                                                                                                              97.0%; Score 65; DB 4; Length 22; 91.7%; Pred. No. 4.4e-05; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.0%; Score 65; DB 4; Length 24; 91.7%; Pred. No. 4.8e-05; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INPORMATION:
APPLICANT: Manoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSES: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRI.

ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
"MEDIUM TYPE: IBM COMPATIBLE
"MEDIUM TYPE: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                    TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                   1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                               2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CPOWORNMRKVR 14
                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-755-161A-10
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

0;

Gaps

```
ISSUE:
                                                                                                                                                                                                             PAGES:
                                                                                                                           TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΩĐ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21" FEATURE:
                                Sequence 10, Application US/07891174

GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCES: Washington Street, N.W., #700
STREET: 805 Fifteenth Street, N.W., #700
STATE: 0.6.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
COMPUTER: DisplayWrite
COMPUTER: DisplayWrite
COMPUTER: DisplayWrite
COMPUTATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 5330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFA: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified site LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE:
CELL TYPE:
CELL LINE:
CRLL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL:
RESULT 15
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY:
```

```
DEMTIFICATION METHOD:

OTHER INFORMATION: Cys residue at location 21
OTHER INFORMATION: Cys residue at location 4"
OTHER INFORMATION: thiol group of Cys residue at location 4"
DUBLICATION INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
TITLE:
JOURNAL:
OUGUNAL:
PAGES:
DATE:
PAGES:
DATE:
PAGES:
DATE:
PRILIAG DATE:
PUBLICATION DATE:
PUBLIC
```

us-09-743-107b-88.rapb

```
Sequence 22, Appl
Sequence 2, Appli
Sequence 8, Appli
Sequence 29, Appl
Sequence 30, Appl
Sequence 5715, Ap
Sequence 1031, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 119, App
Sequence 119, App
Sequence 119, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, App.
Sequence 6, App.
                                                                                                           (without alignments)
54.162 Million cell updates/sec
                                                                                      February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               | Cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-864-761-47985
US-09-738-626-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-764-864-1031
US-09-978-295A-119
US-09-978-697-119
US-09-978-192A-119
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-023-096-2
US-09-798-869-6
US-09-798-869-3
US-09-798-869-2
US-09-798-869-4
US-09-798-869-4
US-09-888-320-2
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-798-869-29
US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-2
                                                                                                                                                                                                                                                             156504 Begs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                     US-09-743-107B-88
67
                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                   1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
```

| Sequence 119, App
Sequence 119, App | 14, 7 | . 4 | 30, | Sequence 32, Appl | 2, | 5 | 4 | Sequence 3. Appli | Sequence 3. Appli | Sequence 3. Appli | Sequence 5. Appli | 'n | | Sequence 4. Appli | Segmence 46393. A | Sequence 12129, A | Sequence 13026, A | Sequence 26, Appl | Seguence 107. App | Sequence 2. Appli | Semience 36085 A | Semience 13, Appl | Sequence 33, Appl |) | |
|---|---|----------------------|----------------------|----------------------|--------------------|----------------------|------|-------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|------------------------|------------------------|------------------------|--------------------|----------------------|--------------------|------------------|---------------------|-------------------|---|--|
| 9 US-09-999-832A-119
9 US-09-978-189-119 | 9 US-09-796-753-14
10 US-09-981-649A-6 | 10 US-09-981-649A-24 | 10 US-09-981-649A-30 | 10 US-09-981-649A-32 | 10 US-09-795-691-2 | 10 US-09-981-649A-28 | | 9 US-10-219-248-3 | 9 US-10-219-247-3 | 10 US-09-855-722-3 | 9 US-10-219-248-5 | 9 US-10-219-247-5 | 10 US-09-855-722-5 | | 10 US-09-864-761-46393 | 10 US-09-815-242-12129 | 10 US-09-815-242-13026 | 9 US-09-796-753-26 | 10 US-09-867-852-107 | 9 US-09-759-508B-2 | 0 | 9 US-09-956-206A-13 | | | |
| 338
338 | 553
553 | 553 | 554 | 554 | 256 | 559 | 846 | 1212 | 1212 | 1212 | 1238 | 1238 | 1238 | 1238 | 40 | 62 | 62 | 333 | 1258 | 26926 | | -1 | | | |
| 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 49.3 | 49.3 | 49.3 | 49.3 | 49.3 | 49.3 | 47.8 | 47.8 | 47.8 | | |
| 4.4. | ю с
4 4 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 32 | 32 | 32 | | |
| 0 10 0 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 8
8
8 | ტ
ლ | 40 | 41 | 42 | 43 | 44 | 45 | | |

ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
97.0%; Score 65; DB 9; L
Best Local Similarity 91.7%; Pred, No. 1.8e-05;
Matches 11; Conservative 0; Mismatches 1:
                      Sequence 2, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OGHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: HALDUR SVEINAD (RNSON)
TITLE OF INVENTION: BICACTIVE PEFTIDES
ITLE REFERENCE: A34449-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR PILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR PILING DATE: 1998-08-31
PRIOR PILING DATE: 1998-08-31
PRIOR PILING DATE: 1998-08-31
PRIOR PILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-798-869-20
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

0

```
Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                   22 CFÓWORNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CFOWOWNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: CAPRINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kruzeki, Tomasz
APPLICANT: Gollick, Paul D.
APPLICANT: Gollick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
                                                                                                                                                                                                                                                                                                                                                                                 97.0%; Score 65; DB 9; Length 25; 91.7%; Pred. No. 2.9e-05; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILLING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PCASLED NOS: 30
SOFTWARE: PCASLED FOR WINGOWS VERSION 4.0
SERIOTH 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAX-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/10023096 ; Patent No. US20020160941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Player, William E.
REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear;
MOLECULE TYPE: protein
US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CFOWORINMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens; OTHER INFORMATION: Sequence)
US-09-798-869-6
                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
               Length 694;
Score 65; DB 9; Length 694
Pred. No. 0.00066;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 9; Length 15;
Pred. No. 0.00044;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.6%; Score 48; DB 9; Length 15; 63.6%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCORPATION US/09798869
FUBLICATION NO. US20030022821A1
GENERAL INFORMATION:
FAPPLICANT: USED STGRED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
ITTLE OF INVENTION: BIOLOR SVETINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
SEQ ID NOS: 30
SEQ ID NOS: 30
LENGHRE: FABELSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQUARED SOURCE SOUR SOURCE SOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 85.1%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                   1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
```

7;

Matches

```
58.2%; Score 39; DB 9; Length 15; 54.5%; Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.2%; Score 39; DB 9; Length 25; 54.5%; Pred. No. 0.97; 4; Indels cive 1; Mismatches 4; Indels
                                                                                                                                                                                                                APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: RESEREQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLODGTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/G899/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: REACERQ for Windows Version 4.0
                                                                                                                                                            ; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.5%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                   1 CFQWXRNMRKV 11
                                                      3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWXRNWRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CPOWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-798-869-22
                                                                                                                                    US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
             ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: SYNTHELIC PEPTIDE (modified form of homo sapiens; OTHER INFORMATION: Sequence)
US-09-798-869-7
        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.6%; Score 48; DB 9; Length 25; 63.6%; Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.7%; Score 40; DB 9; Length 15; Best Local Similarity 54.5%; Pred. No. 0.4; Matches 6; Conservative 2; Mismatches 3; Indels
    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                             RESULT 6

US-09-798-869-23

Sequence 23, Application US/09798869

PUDLICATION NO. US2003002281A1

GENERAL INFORMATION:
APPLICANT: JOHN SIGHED SVENDSEN
APPLICANT: GYBEIN REXDLE
APPLICANT: HALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT-GB99/02851
PRIOR APPLICATION NUMBER: PCT-GB99/02851
PRIOR APPLICATION NUMBER: PSP816B998-4
PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDOR SVEEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: AJ4049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CT/GB99/02651
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
SOFTWARE: FEASTEQ FOR Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.00
-20 7; Conservative
Conservative
                                    CFOWXRNMRKV 11
                                                                           3 CYÓWORRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CYOWORRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                    à
```

0

Gaps

0

·.

Gaps

.;

```
; Sequence 29, Application US/09798869; Publication No. US2030022821A1; GENERAL INFORMATION: APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-864-761-47985
US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó,
         Sequence 2, Application US/0988320
Publication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Barry II, Clifton E.
APPLICANT: DeBarber, Andrea E.
APPLICANT: Bekker, Linda-Gail
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
CURRENT APPLICATION NUMBER: US/09/888,320
CURRENT FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.2%; Score 37; DB 9; Length 489; 54.5%; Pred. No. 36; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.7%; Score 36; DB 9; Length 15; 54.5%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BALDUR SYBINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE RFFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SVENDSEN; APPLICANT: (XSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.5%,
'-hos 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 COKWPRRMRKM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CLRWQWEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8-698-867-80-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.7%; Score 36; DB 9; Length 15; 45.5%; Pred. No. 2; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.7%; Score 36; DB 9; Length 15; 45.5%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
APPLICANT: (YSTEIN REKOAL)
APPLICANT: (YSTEIN REKOAL)
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/G899/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PREUSEQ for Windows Version 4.0
SCO ID NO 29
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: (YSTEIN REPORT
APPLICANT: (YSTEIN REPORT
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/G899/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 47985, Application US/09864761; Patent No. US20020048763A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CFRWQWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CFRWQWRMKK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 5; Conserv
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 9; Length 86;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: J000-12-18
PRIOR PELICATION NUMBER: JP 99/377484
PRIOR FLING DATE: 1999-12-16
PRIOR PELICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280989
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF FILING DATE: 300
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 21, 2003, 08:11:55
Job time : 6.88372 secs
                                                                                                                                                                                                                                                                             APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5715
                                               MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                              YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                    NAKAGAWA, SATOSHI
                                                                                                     HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              · 2 FOWXRNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 FEYRROLRKIR 83
                                                                                                                                                                                                                    APPLICANT:
                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                    APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEA4, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
US-09-864-761-47985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 52.2%; Score 35; DB 10; Length 21; Similarity 83.3%; Pred. No. 4.1; 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47985
LENGTH: 21
                                                                                                                                               TITLE REPRENCE: Acomica_X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-24
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/203,366
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00664
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR AFFLANCE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: ACT/US01/00670
PRIOR APPLICATION NUMBER: ACT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-01-50
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-01-30
APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
```

ó

Gaps

.; 0

1; Indels

0; Mismatches

; Sequence 5715, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:

ð

RESULT 15 US-09-738-626-5715

ö

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec Run on:

US-09-743-107B-88

1 CFQWXRNMRKVR 12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Begs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\* Database :

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lactotransferrin p lactoferrin - goat lactoferrin - shee hypothetical prote lactoferrin precur En/Spm-like transp MAP1 protein - myx histidyl-tRNz ermt F1511.22 [imported hypothetical prote hypothetical prote outer capsid prote apolipoprotein B-1 probable monooxyge hypothetical sh3-c probable proteinas histoc carcinoembryonic a Mypothetical prote dynein beta heavy 26S proteasome SU protein F21H11.2 hypothetical MHC class I Description S52107 AB0858 T22597 A28438 A84471 T24218 T08030 B60950 A45687 D88450 E90094 Query Match Length DB Score . 90 Result

| hypothetical prote | RNA 1a protein a h | phytochrome C and | portivate carboxyla | nvrivate carboxyla | probable beliese | trichohvalin like | registance arctein | Drottein INC. 89 | Tif protein and | himothetical proto | ardinyltransfersos | Signal mentidace I | 33 3K himothetical | conserved himsthat | hypothetical prote | |
|--------------------|--------------------|-------------------|---------------------|--------------------|------------------|-------------------|--------------------|------------------|-----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| T28820 | P1BVBB | T14803 | C97686 | AE2911 | T41378 | B85431 | T30563 | T29757 | 807989 | D89836 | A13401 | E87515 | G86403 | C82234 | T33211 | |
| N | ⊣ | 7 | 7 | 7 | 7 | 7 | ~ | 8 | N | N | N | N | 0 | N | 7 | |
| 932 | 996 | 1135 | 1174 | 1174 | 1213 | 1432 | 1804 | 6642 | 214 | 224 | 249 | 255 | 289 | 323 | 335 | |
| 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 52.2 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | |
| 35 | 35 | 35 | 35 | 35 | 35 | 32 | 35 | 32 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | |
| 30 | 31 | 32 | 93 | 34 | 35 | 36 | 37 | 38 | 99 | 40 | 41 | 42 | 43 | 44 | 45 | |

ALIGNMENTS

| TEHUL |
|--|
| lactotransferrin precursor [validated] - human |
| N;Alternate names: lactoferrin |
| C;Species: Homo sapiens (man) |
| C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change no no non- |
| C; Accession: G01394; S11228; A45401; S10324; S15853. |
| R;Cho, Y. |
| submitted to the EMBL Data Library. March 1994 |
| A; Reference number: G06820 |
| A; Accession: G01394 |
| A;Status: preliminary; translated from GB/EMBL/DDBJ |
| |

A; Molecule type: mRNA A; Residues: 1-711 < CHO>

A,Cross-references: BMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237 R,Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucleic Acids Res. 18, 5288, 1990 A,Title: Complete nucleotide sequence of human mammary gland lactoferrin. A,Reference number: S11228; MUID:90384839; PMID:2402455

A; Accession: S11228

A Molecule type: mRNA
A;Residues: 1-148, T'.150-422, C', 424-711 <REY>
A;Crosz-references: EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416
A;Crosz-references: EMBL:X53961; Nalmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A;Tille: Differential molecular mechanism of the estrogen action that regulates lactofern A;Reference number: A45401; MUID:93125571; PMID:1480183

prote

A; Molecule Lype: DNA
A; Residues: 1-15 < TEN>
A; Residues: 1-15 < TEN>
A; Residues: 1-15 < TEN>
A; Experimental sources: GB: 552659; NID: 9263311; PIDN: AAB24877.1; PID: 9263312
A; Experimental source: placenta
A; Note: sequence extracted from NCBI backbone (NCBIP: 122202)
B; Powell: M.J.; Oqden, J.B.
Nucleic Acids Res. 18, 4013, 1990
A; Title: Nucleotide sequence of human lactoferrin cDNA.
A; Reference number: \$10324; MUID: 90326549; PMID: 2374734

A; Accession: S10324

A Molecule type: mRNA
A, Residues: 3-711 < POW>
A, Residues: 3-711 < POW>
A, Crosser references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
A, Crossell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A, Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A, Reference number: 815853; MUID:91264786; PMID:2049066

A)Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Accession: 20-31 <671.>
A;Accession: 20-31 <671.>
A;Accession: 20-2841
A;Molecule type: protein
A;Residues: 20-28, X', 30-31 <572.>

pyridoxamine 5'-ph probable pyridoxam hypothetical prote hypothetical prote

S67085 AB2154

H97451

Pyridoxamine 5'-ph

; 0

Gaps

0

```
Pypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typic (imported) - Salmonella enterica serovar Typic (iSpecies: Salmonella enterica serovar Typic)
A;Note: this species has also been called Salmonella typhic (iDate: Obligate: 09-Nov-2001 #text_change 09-Nov-2001 #text_change 09-Nov-2001 #text_change 09-Nov-2001 R;Parkhill, J; Dougan, G;; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parrar, N.S.; Moule, S.; O'Gaora, P.
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tille: Complete genome sequence of a multiple drug resistant Salmonella enterica seron
                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: 552107
C;Accession: 552107
B;Othm. Biophys. Acta 1243, 25-32, 1995
B;Ochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Accession: 552107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F53H4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: i5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                           Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.2%; Score 45; DB 2; Length 33; 54.5%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Modecule type: protein
A;Residues: 1-33 <QIA>
C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                       Score 48; DB 2,
Pred. No. 0.65;
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB;
Pred. No. 9.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                               2,
                                                       71.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.2%;
58.3%;
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       lactoferrin - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 CFAWDMINKAKVR 361
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                         38 CYQWQRRMRKL 48
                                                                                                                                                                           1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-511 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWXRNMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T22597
                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T22597
                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                  Æ
                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 436-487, /A', 489-711 < RAD>
A; Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A;Note: this is the final paper in a series
R;Houen, G.; Hoegdall, B.V.; Barkholt, V.; Norskov, L.
Bur. J. Biochem. 241, 303-308, 1996
A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A;Reference number: S74119; MUID:97054624; PMID:8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Blochem. 145, 659-666, 1984
A;Title: Human lactorransferrin: amino acid sequence and structural comparisons with oth A;Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2233
R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A;Reference number: JC2323; MUID:94380047; PMID:8093048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;21-356/Domain: transferrin repeat homology <TRH1>
F;30-69/Domain: transferrin repeat homology <TRH2>
F;30-65/39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Recession: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Accession: JC2233
A,Molecule type: mRNA
A/Residues: 1-708 - LEEP-
C.Superfamily: transferrin; transferrin repeat homology
C.Superfamily: transferrin; glycoprotein
F:359-696/Domain: transferrin repeat homology <TRH2>
F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 1; Lengtn ....
Pred. No. 0.0005;
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Cross-references: GDB:119368; OMIM:150210
A;Map position: 3421-3423
C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplication; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-711/Product: lactotransferrin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                               A; Reference number: A61169; MUID: 91235214; PMID: 1674448
                                                                                                                                                                                                                                                                                                                                                                                                              A, Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A;Residues: 'G', 23-24,'R', 26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: normal breast tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 3-701, 'SWKPVN' <PAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 CFOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A61169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S74119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactoferrin - goat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB:LTF
```

C;Genetics:

Query Match

Matches

ð qq

·,

Gaps

;

0

Gaps

ö

0

Gaps

0;

```
C)Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: T08030
R;Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 334/3; 3666/3; 3882/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nucleotide binding; P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
                       A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: Z35602; PIDN: CAA84671.1; GSPDB: GN00021; CESP:R13G10.2
                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-531 <STO>
A;Cross-references: GB:AE002093; NID:g4586022; PIDN:AAD25641.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein R13G10.2 - Caenorhabditis elegans
C;Species: Ceenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999
C;Accession: T24218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-4568 <MIT>
A,Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
                                                                                                                                                                                                                                                                                                                                   56.7%; Score 38; DB 2; Length 531; 75.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z19857
A;Accession: T24218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 2;
Pred. No. 34;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dynein beta heavy chain - Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R,Gardner, A.
submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: clone R13G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain 21gr
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: CESP:R13G10.2
A,Map position: 3
A,Introns: 64/3; 194/1; 404/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 CIDWGRDDRKVK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-536 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 OWFRIMKK 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                3 QWXRNMRK 10
                                                                                  A; Accession: A84471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T08030
                                                                                                                                                                                                                    C;Genetics:
A;Gene: At2g05650
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Map position: IX
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: ODA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A24818; A41205
B;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
A;Reference number: A32596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  En/Spm-like transposon protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84471
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                 A;Residues: 1-275 <WIL>
A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A.Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A.Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: DNA
A,Residues: 1-15 <LIU>
A,Residues: 1-15 <LIU>
A,Residues: 1-15 <LIU>
A,Cross-references: GB:M/4/78
C,Superfamily: transferrin; transferrin; transferrin; transferrin; transferrin; transferrin; E/20-107/Product: lactotransferrin #status predicted <MGI>
F;20-707/Product: lactotransferrin #status predicted <MGI>
F;28-695/Domain: transferrin repeat homology <TRHI2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                         A;Map position: X
A;Introns: 67/1; 155/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2; Length 275;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.2%; Score 39; DB 1; Length 707; 54.5%; Pred. No. 29; 1. Mismatches 4; Indels
                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
R,Dobson, R. submitted to the EMBL Data Library, October 1996 A;Reference number: 219587 A;Referestion: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactoferrin precursor - mouse
N,Alternate names: lactotransferrin
                                                                                                                                                                                                                            A; Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                  58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Accession: A28438
A.Molecule type: mRNA
A.Residues: 3-707 <PEN>
A.Cross-references: EMBL:J03298
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLRWQNEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                 A; Gene: CESP: F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A41205
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                       C; Genetics:
```

ö

Gaps

; 0